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Baker et al.(10) **Pub. No.: US 2003/0027262 A1**(43) **Pub. Date: Feb. 6, 2003**(54) **SECRETED AND TRANSMEMBRANE
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IRVINE, CA 92614 (US)(73) Assignee: **Genentech, Inc.**(21) Appl. No.: **10/173,700**(22) Filed: **Jun. 17, 2002****Related U.S. Application Data**(63) Continuation of application No. 10/052,586, filed on
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C07K 14/435; C07H 21/04;
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(52) **U.S. Cl.** **435/69.1**; 435/320.1; 435/183;
435/325; 530/350; 536/23.2(57) **ABSTRACT**The present invention is directed to novel polypeptides and
to nucleic acid molecules encoding those polypeptides. Also
provided herein are vectors and host cells comprising those
nucleic acid sequences, chimeric polypeptide molecules
comprising the polypeptides of the present invention fused
to heterologous polypeptide sequences, antibodies which
bind to the polypeptides of the present invention and to
methods for producing the polypeptides of the present
invention.MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLAFGGSKKGKNLGQA
YPCSSDKECEVGRYCHSPHQGSSACMVCRRKKRCHRDGMCCPSTRCNGICIPVTESILTPHIPALDGTTRHRDR
NHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRSSDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGL
EIFQRCDCAKGLSCKVWKDATYSSKARLHVCQKI**Signal peptide:**
amino acids 1-25

Related U.S. Application Data

which is a continuation of application No. 09/380,138, filed on Aug. 25, 1999, now abandoned, and which is a continuation of application No. 09/380,139, filed on Aug. 25, 1999, now abandoned, and which is a continuation of application No. 09/380,142, filed on Aug. 25, 1999, now abandoned, and which is a continuation of application No. 09/403,297, filed on Oct. 18, 1999, now abandoned, and which is a continuation of application No. 09/423,844, filed on Nov. 12, 1999, now abandoned, and which is a continuation of application No. 09/644,848, filed on Aug. 22, 2000, and which is a continuation of application No. 09/664,610, filed on Sep. 18, 2000, now abandoned, and which is a continuation of application No. 09/665,350, filed on Sep. 18, 2000, and which is a continuation of application No. 09/709,238, filed on Nov. 8, 2000, now abandoned, and which is a continuation of application No. 09/747,259, filed on Dec. 20, 2000, and which is a continuation of application No. 09/816,744, filed on Mar. 22, 2001, and which is a continuation of application No. 09/854,208, filed on May 10, 2001, and which is a continuation of application No. 09/854,280, filed on May 10, 2001, and which is a continuation of application No. 09/866,028, filed on May 25, 2001, and which is a continuation of application No. 09/874,503, filed on Jun. 5, 2001, and which is a continuation of application No. 09/908,827, filed on Jul. 18, 2001, and which is a continuation of application No. 09/918,585, filed on Jul. 30, 2001, and which is a continuation of application No. 09/924,419, filed on Aug. 6, 2001, now abandoned, and which is a continuation of application No. 09/929,404, filed on Aug. 13, 2001, now abandoned, and which is a continuation of application No. 09/931,836, filed on Aug. 16, 2001, and which is a continuation of application No. 09/941,992, filed on Aug. 28, 2001, and which is a continuation of application No. 09/946,374, filed on Sep. 4, 2001.

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Aug. 29, 2001	(WO).....	PCT/US01/27099

FIGURE 1

GAAGGCTGCCTCGCTGGTCCGAATTCCGGTGGCGCCACGTCCGCCCGTCTCCGCCTTCTGCATCGCGGCTTCGGCG
GCTTCCACCTAGACACCTAACAGTCCGCGGAGCCGGCCCGTCTGAGGGGGTCCGGACGGGGAGTCCGGCGGTCT
TGTGCATCTTGGCTACCTGTGGGTCCGAAGATGTCGGACATCGGAGACTGGTTTCAGGAGCATCCCGGCGATCACGC
GCTATTGGTTCGCGCCACCGTCCCGTGGCCCTTGGTCCGCAAACTCGGCCTCATCAGCCCGGCCCTACCTCTTCC
TCTGGCCCGAAGCCTTCTTTATCGCTTTCAGATTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGGGTC
CAGGAAGTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTCTACGCGACTTGAAACAGGAGCTT
TTGATGGGAGGCCAGCAGACTATTTATTTCATGCTCCTCTTTAACTGGATTTGCATCGTGATTACTGGCTTAGCAA
TGGATATGCAGTTGCTGATGATTCTCTGATCATGTCTAGTACTTTATGTCTGGGCCCAGCTGAACAGAGACATGA
TTGTATCATTTTGGTTTGGAAACACGATTTAAGGCCGTCTATTTACCCTGGGTATCCTTGGATTCAACTATATCA
TCGGAGGCTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTTCTAATGTTTCAGATACC
CAATGGACTTGGGAGGAAGAAATTTCTATCCACACTCAGTTTTTGTACCGCTGGCTGCCAGTAGGAGAGGAG
GAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGCTGCTGATCAGAATGGCGGAGGCGGGAGACACA
ACTGGGGCCAGGGCTTTCGACTTGGAGACCAGTGAAGGGGCGGCCCTCGGGCAGCCGCTCCTCTCAAGCCACATTT
CCTCCCAGTGTGGGTGCACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTC
TTTCAGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCCACAAGTTTCACGATTCTCATTCA
AGTCTTACTGCTGTGAAGAACAAATACCAACTGTGCAAATGCAAACTGACTACATTTTTTGGTGTCTTCTCT
TCTCCCCTTTCCGTCTGAATAATGGGTTTTAGCGGGTCCCTAATCTGCTGGCATTGAGCTGGGGCTGGGTACCAA
ACCCTTCCCCAAAAGGACCTTATCTCTTTCTTGACACATGCCCTCTCTCCCACTTTTCCCAACCCCCACATTTGCA
ACTAGAAAAAGTTGCCCATAAAATTGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGT
CACAACAATCATATTCACGTTATTTTCCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAGAAGACAGCCACG
GATGAAGCGTTTCTCAGCTTTTGGAAATTGCTTCGACTGACATCCGTTGTTAACCCTTTGCCACTCTTCAGATATT
TTTTATAAAAAAAGTACCACTGAGTTCATGAGGGCCACAGATTGGTTATTAATGAGATACGAGGGTTGGTGCTGG
GTGTTTGTTCCTGAGCTAAGTGATCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTAGGTTTAAACCATGGG
GGATGCACCCCTTTGCGTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGTTA
GGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCTGGGCATTGATTCCCATTTCATC
TCATTCTGATATGTGTTTATTGAGTAAAGGAGGAGAGACCCTCATACGCTATTTAAATGTCATTTTTTGCCTA
TCCCCCGTTTTTTGGTCATGTTTCAATTAATTGTGAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTA
AAGCTAATGTAAGCACATCTAAGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCAATTGGGTTTGAGG
GTGTGTTATTTTGGTTCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTTTCGTA
GGTGGGCTTTTCCATCAGAGCTTGGCTCATAACCAATAAAGTTTTTTGAAGGCCATGGCTTTTCACACAGTTA
TTTTATTTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGTATTGAGTGGCTGTACACTTTGAGGCAACTA
AAAAGGCTTCAAACGTTTTGATCAGTTTCTTTTCAGGAAACATTGTGCTCTAACAGTATGACTATTCTTTCCCC
ACTCTTAAACAGTGTGATGTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTCTCATTTTGAATAGAGTTT
GTGTGTACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTATGTTTTGT
TGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAAATTTTAGAGGCCATTACTCCAATTATGTTGCACGTACAC
TCATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATATTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGT
ACCCTCTTACCAGTCAGCTGCCTGCGAGCAGTCATTTTTTCTTAAAGGTTTACAAGTATTTAGAAGTTTTTCAGTT
CAGGGCAAAATGTTTCATGAAGTTATTCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGA
TTATGTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTGTGACTTGACAAGGCAAAACATGACAGTGGAT
TCTCTTTACAAAATGGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCCTTTTTGTAAACTAATCCTTTTTTAT
TGGTAAAAATTGTAAATTAAATGTGCAACTTG

FIGURE 2

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYFPVGPGTGFLYLVN
LYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIPLIMSVLYVWAQLNRDMIVSFWFGTRF
KACYLFWVILGFNYIIGGSVINELIGNLVGHLYFFLMFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPA
SMRRAADQNGGGGRHNWGQGFRLGDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 3

GAGCGAGGCCGGGACTGAAGGTGTGGGTGTGAGCCCTCTGGCAGAGGGTTAACCTGGGTCAAATGCACGGATT
CTCACCTCGTACAGTTACGCTCTCCCGGGCACGTCCGCGAGGACTTGAAGTCCTGAGCGCTCAAGTTTGTCCGT
AGGTTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCC
CCGAGTCTTTTGCTGCCGAAGCTGTGACTGCCGATTCCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGT
CCCAGAGCCCTATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAAT
TTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAATACC
AGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCATAACCGGTTTGATGCTGT
GCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTTCGTTATGGCTGGCGCTGGGGTTGGAGAAGTGCAGTGTT
TGTGACTATATTCAACACAGTGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAT
TGCAGGAGCTGTACCGGAAGTCTTTTTAGGATAAACTAGGCCTGCGTGGCCTGGTGGCTGGTGGCATAATTGG
AGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTGGTGAGACTGTTTCAGGAAAG
AAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAACTGGAAGAGTGGAAGGCAGACTACAAGTTACTGAGCA
CCTCCCTGAGAAAATTGAAAGTAGTTTACGGGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCT
AAACCTTCCTAGAAACCTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACCTTGAAACTCACTG
GAGAGCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGCTGACAAATT
TAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTCTTTTCTTTTAACTAAGAATGGGGCTGTT
GTACTCTCACTTTACTTATCCTTAAATTTAAATACATACTTATGTTTGTATTAATCTATCAATATATGCATACAT
GGATATATCCACCCACCTAGATTTTAAGCAGTAAATAAAACATTTGCAAAAGATTAAAGTTGAATTTACAGTTT

FIGURE 4

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELFQKDEQQRISKDLA
NICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDAVQSAHRAATRGFIRYGWRWGWRTAVFVTIFN
TVNTSLNVYRNKDALS HFVIAGAVTGSLFRINVGLRGLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDR
KALHELKLEEWKGR LQVTEHLPEKIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD
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Important Features:**Signal Peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

FIGURE 5

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGCGCCTGAAGTCGGC
GTGGGCGTTTGGGAAGCTGGGATACAGCATTAAATGAAAAATTTATGCTTAAGAAGTAAAAATGGCAGGCTTCC
TAGATAATTTTCGTTGGCCAGAATGTGAATGTATTGACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCG
CAGGTATATTGTTTTTTACAGGCTGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGA
ACCATGCCTTTCACACATGTGGTGTATTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTCAGG
TGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTTTTCATTGGTTTCATGT
TGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGCATATGTTACCCAAAATACTGATGTTTATC
CGGGACTAGCTGTGTTTTTTCAAATGCACTTATATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAG
AGCTATGGACCTGAGATCACTTCTTAAGTCACATTTTCCTTTTGTTATATTCTGTTTGTAGATAGGTTTTTTATC
TCTCAGTACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTCTGAGTT
TTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTATATAATACAAGACTATATG
AATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAACTTGATCTACTCCCTGAGCCAGGGTTACATCA
TCTTGTCATTTTAGAAGTAACCACTCTGTCTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTT
TGGGAGGCCGAGGCGGGCCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATC
TACTAAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCGTGAATCCCAGCTACCTGGGAGGCTGAGGCAGG
AGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTGCGCCACTGCACTCTAGCCTGGGGGAGAA
AGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATCTCTGATTTCTGAAGATGTACAAAAAATATAGCTT
CATATATCTGGAATGAGCACTGAGCCATAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGT
TTTTTTGGTAAAGAAAAATATTTGTTCTTATGTATTGAAGAAGTGTACTTTTATATAATGATTTTTTAAATGCC
CAAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

FIGURE 6

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCGVFSTLAFFMINAV
SNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQNTDVYPGLAVFFQNALIFFSTLIYKF
GRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 7

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCACG
TATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAGGATGTGCGTTCTTC
CACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAAACAGTGGAAATGGAAAAACAGTGCTGTAGTCATCCTGTAATA
TGCTCCTTGTCACAATGTATACATTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTA
GTGAAGTATTCTGCCAATGAAGAAAACAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTGGTG
AAGCTAGTTTTCTGTGTGCTTGTGTCAATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATATGCT
TCCTGGAAGGAATTCCTGATTTTCATGAAGTGGTCCATTCTGCTTTCTTTATTTCTGGATAACTTGATTGTC
TTCTATGTCCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTT
CTATTCAGGATAGTGCTGAAGAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATT
GTGGCCTTGACTGCCGGGACTAAACTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCCTTTTTTC
AGCCCTTCCAATTCCTGCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTGTACAGCAAAGGAATGGACT
TTCTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTCACATCCGTCTTGGCATGGGCCATGTTCTTATT
ATAGTCCAGTGTTTTATTTCTTCAATGGCTAATATCTATAATGAAAAGATACTGAAGGAGGGGAACCAGCTCACT
GAAAGCATCTTCATACAGAACAGCAAACCTATTTCTTTGGCATTCTGTTAATGGGCTGACTCTGGGCCCTTCAG
AGGAGTAACCGTGATCAGATTAAGAAGTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCCCTTATTTTT
GTAACCTGCATTCCAGGGCCTTTTCAGTGGCTTTTCATTCTGAAGTTCTGGATAACATGTTCCATGTCTTGATGGCC
CAGGTTACCACTGTCAATTATCACAACAGTGTCTGTCTGGTCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTG
GAAGCCCCATCAGTCTTCTCTCTATATTTATTTATAATGCCAGCAAGCCTCAAGTTCGGAATACGCACCTAGG
CAAGAAAGGATCCGAGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTT
ACCAAACCCCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCAGCTCTCTTGAAC
CTTATTTTTCACATTTTCAGTGTGTTGTAATATTTATCTTTTCACTTTGATAAACAGAAATGTTTCTAAATCCTAA
TATTTCTTGCATATATCTAGCTACTCCCTAAATGGTTCCATCCAGGCTTAGAGTACCCAAAGGCTAAGAAATTC
TAAAGAACTGATACAGGAGTAACAATATGAAGAAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATAT
GTGCAGATTATTTTCTTGGCCTTCAAGCTTCCAAAAAACTTGTAAATAATCATGTTAGCTATAGCTTGTATATAC
ACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGTCTTCTCTTTTAAACA
TTATAAAAGCTAGGTTGTCTCTTGAATTTTGAGGCCCTAGAGATAGTCATTTTGCAAGTAAAGAGCAACGGGACC
CTTTCTAAAAACGTTGGTTGAAGGACCTAAATACCTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAA
ATATTTTGCTGAAGAAGCAGTTTCTCAGACACAACATCTCAGAATTTTAATTTTGTAGAAATTCATGGGAAATGG
ATTTTGTGAATAATCTTTTGATGTTTTAAACATTGGTTCCCTAGTCACCATAGTTACCACTTGATTTTTAAGTCA
TTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGATGTCAATTACTCTGAATTA
TTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACTAATTCAAGCTGTGACTATTGTATATCTTTCC
AAGAGTTGAAATGCTGGCTTCAGAATCATACCAGATTGTCAGTGAAGCTGATGCCTAGGAACTTTTAAAGGGATC
CTTTCAAAAGGATCACTTAGCAAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAA
AGACCAGTAATATATAAGTCACTTTACAGTGTCTACTTCACACTTAAAGTGTCATGGTATTTTTCATGGTATTTTG
CATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAAAAATTAGCAAACAAAAGTGAC
TTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGGCTTTAACTGGCAGGCCTGTATGTTTACAGACTAC
CATACTGTAAATATGAGCTTTATGGTGTCAATTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTC
ATGCAGATGAATATAAGGTAATATACTATTATATAATTCAATTTGTGATATCCACAATAATATGACTGGCAAGAAT
TGGTGGAAATTTGTAATTAAATAATTTATTAACCT

FIGURE 8

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVKLVFCVLVSFCVIK
KDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAVIFS NFSIITTALLFRIVLKRRLNWIQ
WASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFFSPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFS
HIRLGMGHVLIIVQCFISSMANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFY
GHSAFSVALIFVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFTYNA
SKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLT KPKSDESDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293, 298-318,
328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 9

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATGAGCAGGTCTG
AAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTC
CTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACTCCACCAT
ATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTA
AATATTGCGGCAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAG
AACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGGGAACTGAGTTGTTTAGGACTTTCTATTGTGGCA
AACTTCCAGAAAACAACCTTTTGTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCATTATAT
ATGTTTGTTCAGACCATCCTTTCTACCAAATGCAGCCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTG
TTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTT
GGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACTACTGCA
GCAGAATGGTCTATGTCATTTCTTCTTTGGTTTTTTCTTGACTTACATTCTGATTTTTAGAAAATTTCTTTA
CGGGTGGGAAGCCAATTTACATGGATTAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGG
CTACTTTCCAGAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCT
GATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTATTAAAAACA
CCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAGACTATG

FIGURE 10

MWWFQQGLSFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATYVRY
KQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFGMGSLYMFVQTILSYQMOPKI
HGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT
YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTRLLSRDI

FIGURE 11

CCCACGCGTCCGCCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGGCCGGGGTGCGGAG
 CCGACATGCGCCCCGCTTCTCGGCCCTCCTTCTGGTCTTCGCCGGCTGCACCTTCGCCTTGTAATTGCTGTGACGC
 GACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGGAGGCTGGAGGCAGGTCGCTGTGGTTCCCCTCCGACCTGG
 CAGAGCTGCGGGAGCTCTCTGAGGTCCCTTCGAGAGTACCGGAAGGAGCACCAGGCCCTACGTGTTCTCTGCTCTTCT
 GCGGCGCTTACCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTTGAATGTTTTAGCTGGTGCCTTGT
 TTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGCTGCTACCTGCTCTCCA
 GTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGTGGCCCTGCTGCAGAGAAAGGTGGAGGAGA
 ACAGAAACAGCTTGTTTTTTTTCTTATTGTTTTTGAGACTTTTCCCCATGACACCAAACCTGGTTCTTGAACCTCT
 CGGCCCAATTCTGAACATTCCCATCGTGCAGTTCCTTCTTCAGTTCTTATCGGTTTGATCCCATATAATTTCA
 TCTGTGTGCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTGTCTTTA
 AGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCCTCATTAAAAAATTTAGTCAGAAACATCTGCAAT
 TGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGACACATTGATCTGGATTTTCTGTTTGGCACATCC
 CTGGACTCAGTTGCTTATTTGTGTAATGGATGTGGTCCCTCTAAAGCCCCCTATTGTTTTTGATTGCCTTCTATAG
 GTGATGTGGACACTGTGCATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATC
 AGGTTTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGTGGCCGGGCG
 CGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTCACAAGGTCAGGAGTTCAAGACC
 AGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAATACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGT
 AATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGAT
 CACACCACTGCACTCCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 12

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELVREYRKEHQAYVFLFCG
AYLYKQGFAIPGSSFLNVLGALFGPWLGLLCCVLTSVGATCCYLLSSIFGKQLVVSYPDKVALLQRKVEENR
NSLFFFLFLRLFPMTNPNWFLNLSAPILNIPVQFFSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKL
LAIAMVALIPGTLIKFSQKHLQLNETSTANHIHSRKDT

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 13

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACCGTGTGAG
GGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTCCTTACACTTCGCCA
TGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCA
TGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACTGGA
AAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTCATGGTGCCTTTTTTACATTGGCTATTTTATTGTGAGCA
ATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGA
AACTAGGAGATCCCTTTCCCATTTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTG
GTGTGATTGGAGTGACTCTCATGGCTCTTCTTTCTGGATTGGTGCTGTCAACTGCCCATACACTTACATGTCTT
ACTTCTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGATCA
TAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACAAACCATCAG
GTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGGAAGTGAAAATCTTACTCTTATTCAACAGGAAG
TGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAG
AATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGAAAA
TTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTACAAAGAGGCATTGAGATCA
CTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATTTCTTTCATTCTTGTGGAATAA
TCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTT
CCAATGTCATTTGTCTGCTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGA
GTATGCCCTTTAGAATAACCGACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGT
TTGATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCAGAGA
AGCAAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAAATTTAGATATAAGAGG
GGGGAAAAATGGAACCAGGGCCTGACATTTTATAAACAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGC
ATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGGAGAACTAACTCAA
GACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAAAG
GTGAAAAATACACTGGAACCTGAGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTTA
AGGTTACATGGAAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATTTAAATCAGAGACTGTAACAAAAA
AAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGCTTGCCGCCATGGCCCACTTGTTTATTG
CAGCTTATAATG

FIGURE 14

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEILGVLNSSSRYPHW
KMNL CVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFFWKLGDPPILSPKHGILSIEQLISRV
GVIGVTL MALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPS
GFWGMIKSVTTSASGSENLT LIQQEVDAL EELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWK
IFMATINIVFDRVGKTD PVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKS
SNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLV SALSSILFLYLAHKQAPE
KQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, 425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 15

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCGGGACATGCGGCCC
CAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGCTGCTGCCGCCGCCCGTGCCTGCC
CACAGCGCCACGCGCTTCGACCCACCTGGGAGTCCCTGGACGCCCGCCAGCTGCCCGCGTGGTTCGACAGGCC
AAGTTTCGGCATCTTCATCCACTGGGGAGTGTTTTCCGTGCCCAGCTTCGGTAGCGAGTGGTTCGTTGGTATTGG
CAAAAGGAAAAGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTTCAAATATGAAGATTTT
GGACCACATATTACAGCAAAATTTTTAATGCCAACAGTGGGCAGATATTTTTTCAGGCCTCTGGTGCCAAATAC
ATTGCTTAACTTCCAAACATCATGAAGGCTTTACCCTGTGGGGGTGAGAATATTCGTGGAAGTGAATGCCATA
GATGAGGGGGCCCAAGAGGGACATTGTCAAGGAACCTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTGGA
CTGTACTATTCCTTTTTGAATGGTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAA
TTTCAGTTTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGGTCCGAT
GGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTTATATAATGAAAGCCAGTT
CGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCATCTGTAAGCATGGTGGCTTCTATACCTGCAGT
GATCGTTATAACCCAGGACATCTTTGCCACATAAATGGGAAAACATGCATGACAATAGACAACTGTCTGGGGC
TATAGGAGGGAAGCTGGAATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCA
TGTGGAGGAAATCTTTGATGAATATTGGGGCCACACTAGATGGCACCATTCTGTAGTTTTTGAGGAGCGACTG
AGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTATACCTGGCGATCCCGAATGAC
ACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAGAAAAATTAGTCTATGCCATTTTTCTTAAATGGCCC
ACATCAGGACAGCTGTTCTTGGCCATCCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGA
CAGCCACTTAACTGGATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTTCATCAGATG
CCGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTGATGCTGCAAGTT
ATGCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGAAAGCAATGTAACTGGATAAGAAAA
TTATTTGGCAGTTTCAGCCCTTTCCCTTTTTCCCACTAAATTTTTCTTAAATTAACCATGTAACCATTTTAACTCT
CCAGTGCACCTTTGCCATTAAAGTCTCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCA
CATTATAGTAGCAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATGAT
TATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAATTTTTTTTTTGTGCCAA
CATCATAGAGTGATTTACAAAATCCTAGATGGCATAGCCTACTACACACCTAATGTGTATGGTATAGACTGTTG
CTCCTAGGCTACAGACATATACAGCATGTTACTGAATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAA
ACATATGGAAACATAGAGAAGGTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCAC
GAATGGAGCTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTATTGAA
CACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAGTTTTTCTTTCTTCAATT
ATAAATTAACATAAGTGTAAGTTTACAAACGTTTTAATTTTTTAAACCTTTTTGGCTCTTTTGTATAAAC
ACTTAGCTTAAACATAAACTCATTTGTGCAAAATGTAA

FIGURE 16

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPWTWESLDRQLPAWFDQAKFGIFIHWGVFSVPSFGSEWFW
WYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQASGAKYIVLTSKHHEGFTLWGSEYSWNW
NAIDEGPKRDIVKELEVAIRNRDRLRFGLYYSLFEWFHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVL
WSDGDGGAPDQYWNSTGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKL
SWGYYREAGISDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYTWRS
QNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWISLEQNGIMVELPQLTI
HQMPCCKWGWALALTNVI

Signal sequence:
amino acids 1-28

N-glycosylation site.
amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.
amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319, 375-375

Tyrosine kinase phosphorylation site.
amino acids 361-369, 389-397

N-myristoylation site.
amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.
amino acids 410-432

Alpha-L-fucosidase putative active site.
amino acids 283-295

FIGURE 17

[illegible]

FIGURE 18

MKFLLDIILLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKL
VLWDINKHGLEETAACKGGLGAKVHTFVVDSCNREDIYSSAKKVKAIEIGDVSILVNNAGVVYT
SDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVFPFLAYCSSK
FAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMHGILT
EQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 19

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGTGGCCTAGAGAT
 GCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGTAG
 CGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGGCCG
 TGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCCTCGG
 ATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTATAAAG
 TCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCTGCAGGA
 GGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAAAAGTTCA
 TTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGAGGAGAAAC
 AAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATATCACAATTTA
 GGAACCTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATGTACCATCAGC
 CATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGACCGGTGCAACA
 TGAAGAACAATTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTTCTAGAGAAGCTG
 AAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAGGAAGAAGATGCCA
 AAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACATCCTAATCCCCAGCA
 TTCCCCTTCTCCTCCTCCTTGTGGTCAACACAGTTGTATGTTGGGTTTGGATCTGTAGAAAAA
 GAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATCTGGCCCTCTCCTCACC
 AGGGAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAAACAAAGCGAAGCTGACTTAG
 CTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTTTCGGGAGAAGCCACTCCCG
 ATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCAGAAAGTGGGTTTGTGACTC
 TGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGAGTTCTCCCCAGACCAATGG
 GGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATGGTTATTAGGACATATAAAAAA
 CTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATCCTCTTATTTTCTATAAGGAAAA
 TACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGTGGATGAGCATGTGGTCCCCACGA
 CCTCCTGTTGGACCCCCACGTTTTTGGCTGTATCCTTTATCCAGCCAGTCATCCAGCTCGACC
 TTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTAGAGTCTCAATAAATGTCACTTGGTT
 GGTGTATCTAACTTTTAAGGGACAGAGCTTTACCTGGCAGTGATAAAGATGGGCTGTGGAGC
 TTGGAAAACACCTCTGTTTTCTTGTCTATACAGCAGCACATATTATCATAACAGACAGAAA
 ATCCAGAATCTTTTCAAAGCCCACATATGGTAGCACAGGTTGGCCTGTGCATCGGCAATTCTC
 ATATCTGTTTTTTTTCAAAGAATAAAATCAAATAAAGAGCAGGAAAAA

FIGURE 20

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLLDLRGQPVCRRGGTQRPCYKVIYFHDTSRRLN
FEEAKEACRRDGGQLVSI ESEDEQKLIKFIENLLPSDGD F WIGLRRREEKQSNSTACQDLYA
WTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE
KPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLLVTTV
VCWWICRKRKREQPD PSTKKQHTIWPSPHQGN SPDLEVYNVIRKQSEADLAETRPDLKNISF
RVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKESGWVENE
IYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 21

AGGCTCCCGCGCGGGCTGAGTGCAGGACTGGAGTGGGAACCCGGGTCCCGCGCTTAGAGAACACGCGATGACCA
CGTGAGCCTCCGGCGGAGGCCGCGCCGACGCTGGGACTCCTGCTGCTGGTCTGCTTTGGGCTTCCTGGTGCTCC
GCAGGCTGGACTGGAGCACCTTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGCCCTGTGGCTTGAACACCCCTCACCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCTGTATGGCCGAGAGATCG
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCCCACTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTACCAGAAGCAGTGGACCTTTATTTTGACCACC
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG
GTTCCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCTGGCATTTGTGGAAGTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTTGCCAGGGAGTCTTGGCCACCATCAACTTGCAGT
CAACACAGAGCTGCAGCTACTGACCACCTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT
ACTGGACGGGGTGGTTTGACTCGTGGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTGGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG
GAGCCATGCACCTTCCATGACTACAAGTCAGATGTACCAGCTATGACTATGATGTGTGCTGACAGAAGCCGGCG
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTTCAGAGGTTTCGGCCTGGACAAATGGNGTTCCCTCCAGAAACACCCACATTACCTGCTTTCTTCTTGG
GTAGCTTGTCCATCAGCTCCACGCCTTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTGTATTCA
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCCAAGAGCGCTTACCTCCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTCATCGTTTTTGGAGGAGACGATGGCGGGCCCTGCATTACAGTTACCGAAACCCCC
ACCTGGGCAGGAACCACTACATTAAGTGAAGCGGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTC
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGGCTACAGTCTGCCCTGTCTCAGCTCAAACCCCTAAGCCTGCAGGGAAGGTGGGATGGCTCTGGGGC
TGGCTTTGTTGATGATGGCTTTCCACAGCCCTGCTCTTGTGCCGAGGCTGTGGGGCTGTCTTAGGGTGGGAGC
AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGCTGAAACGTGCCCTTGACCCGACGTACAGCCC
TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTGTCTGTTTCTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTACCAAGTGTAGAGGGTGGGGAAGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCTTCAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACCTCGGCGTGAGAAACATGTGACTTCCCCTT
TCCCTTCCCACTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG
ACAGAAGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCAAGCCGAAACAGCAGGGGCAGAGCAGCCCTCCTTC
GAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTGTA
GTTGCAGTAAAGCTATAACCTTGAATCAAA

FIGURE 22

MTTWSLRRRPPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFWI
FGGSIHYFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDGSGNLDLEAFVLMMAE
IGLWVILRPGPYICSEMDLGGLPSWLLQDPMRLRTTYKGFTEAVDLYFDHLMSRVVPLQYKR
GGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKGDLGSKGIVQGVLATINLQ
STHELQLLTTFLFNVOGTQPKMVMYWTGWFDGWGGPHNILDSEVLKTVSAIVDAGSSINLY
MFHGGTNGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIPLPPPPD
LLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYIYETSITSSG
ILSGHVHDRGQVFVNTVSIQFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGENIDDQRKGL
IGNLYLNDSPKKNFRIYSLDMKKSFFQRFGLDKWXSLEPETPTLPAFFLGSLSSISSTPCDTFLK
LEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPALQFTETPHLG
RNQYIK

Signal sequence:
amino acids 1-27

Casein kinase II phosphorylation site.
amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.
amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 24

MNSSKSSETQCTERGCFFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPENF
TELSCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQEF
LSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCAITMRDSSNPR
QNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 25

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACCC
 TGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGGGG
 AGCAAAGCCGGGCTCGGCCCCGAGGCCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATCCGA
 CACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCCAAGA
 AGCTGTCTGCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCAGGCAG
 AACTCGGTTCGTTAGTGGATAGGGGTCTGACCGGTTTCTCTAGACGGGGCCCCGTTCC
 GCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGACCGGCTTT
 TGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACACCACGAGC
 CACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGAATGAGGCAG
 CTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAGTGGGAGATGG
 GGGGTCTCCCATCTGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTCAGATCCAGACT
 TCCTTGCCGCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATCCATGGCTTTATC
 ACAATGGGGGCAACATCATTAGCATTGAGGTGGAGAATGAATATGGTAGCTACAGAGCCTGTG
 ACTTCAGCTACATGAGGCACCTGGCTGGGCTCTTCGCTGCACTGCTAGGAGAAAAGATCTTGC
 TCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGGGACTCTATACCACTG
 TAGATTTTGGCCAGCTGACAACATGACCAAAATCTTTACCCTGCTTCGGAAGTATGAACCCC
 ATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTACTGGGGCCAGAATCACT
 CCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGCTCAAGTTGGGAGCCAGTG
 TGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGGAATGGTGCCGATAAGAAGG
 GACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACCTATATCTGAAGCAGGGGACC
 CCACACCTAAGCTTTTTTGCTCTTCGAGATGTATCAGCAAGTTCAGGAAGTTCCTTTGGGAC
 CTTTACCTCCCCGAGCCCCAAGATGATGCTTGACCTGTGACTCTGCACCTGGTTGGGCATT
 TACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCATTCAATTCAATCTTGCCAATGACCT
 TTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACCGAACCTATATGACCCATACCATTT
 TTGAGCCAACACCATTTCTGGGTGCCAAATAATGGAGTCCATGACCGTGCCTATGTGATGGTGG
 ATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAGAGACAACTATTTTTTGACGGGGAAAC
 TGGGGTCCAAACTGGATATCTTGGTGGAGAACATGGGGAGGCTCAGCTTTGGGTCTAACAGCA
 GTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTGGGGCAAACAATCCTTACCCAGTGGATGA
 TGTTCCTCTGAAAATTGATAACCTTGTGAAGTGGTGGTTTCCCCTCCAGTTGCCAAAATGGC
 CATATCCTCAAGCTCCTTCTGGCCCCACATTCTACTCCAAAACATTTCCAATTTTAGGCTCAG
 TTGGGGACACATTTCTATATCTACCTGGATGGACCAAGGGCCAAGTCTGGATCAATGGGTTTA
 ACTTGGGGCCGGTACTGGACAAAGCAGGGGCCACAACAGACCCTCTACGTGCCAAGATTCCTGC
 TGTTCCTAGGGGAGCCCTCAACAAAATTACATTGCTGGAAC TAGAAGATGTACCTCTCCAGC
 CCAAGTCCAATTTTTTGATAAGCCTATCCTCAATAGCACTAGTACTTTGCACAGGACACATA
 TCAATTCCCTTTTCAGCTGATACACTGAGTGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAA
 AGGTAGGCCGGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTG
 GATTACCTGAGGTGAGGACTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTA
 AAAATACAAAATTAGCCGGGCGTGATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTG
 AGGGCAGGAGAATTGCTTGAATCCAGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTG
 CACTCCAGCCTGGCTGACAGTGAGACACTCCATCTCAAAAAAAAAAAAA

FIGURE 26

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRGHRFLLDGAPFRYVSGSLHYFRVPRVLW
ADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYICA
EWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENEYGS
YRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKI FTLLR
KYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMYPFHGGTNFGYWNG
ADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMMLGPVTLH
LVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPNNGVHDRA
YVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNS SDFKGLLKPPILGQ TIL
TQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGD TFLYLPGWTKGQVW
INGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLDKPILNSTSTL
HRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 27

[illegible]

FIGURE 28

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQG
ASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQDKE
HDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQVCA
EQAAVVASFQQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPRHRRL
HRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDRCDAGW
LADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303,
307-313

FIGURE 29

GCAAGCGGCGAAATGCGGCCCTCCGGGAGTCTTGACAGTTCCCCTGGCAGTCCTGGTGCTGTTG
 CTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTGCGGTCATCACGGACGAGAAC
 TGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCTTGT
 CAAAATCTTCAACCGGAATGGGAAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTAAATATT
 GCGAAAGTAGATGTACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTCTTCCT
 ACTATTTATCATTTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAGAAGGAC
 TTCATAAACTTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCCGTTTCATCATGGTTTGGT
 CCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGATCAGGACG
 TGCCATAACTACTTTTATTGAAGACCTTGGAATTGCCAGTGTGGGGATCATATACTGTTTTTGCT
 TTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGCAGATTGCCTT
 TGTCCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCTTCAAAAAAATTATTATCAGAA
 TCTGCACAACCTTTGAAAAAAGTGAGGAGGAACAAGAGGCGGATGAAGAAGATGTTTCAGAA
 GAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGCCATAAGACAACGC
 TCTCTGGGTCCATCATTGGCCACAGATAAATCC**TAG**TTAAATTTTATAGTTATCTTAATATTA
 TGATTTTGATAAAAACAGAAGATTGATCATTTTGTGTTGGTTTGAAGTGAAGTGTGACTTTTTT
 GAATATTGCAGGGTTCAGTCTAGATTGTCTAATAATTGAAGAGTCTACATTCAGAACATAAAA
 GCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATGGTTTAAATAGTTCTCTA
 ATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGTTTAAATAATAACCTATTTTC
 AAGTCTGAGTTTTGAAAAATTACATTTCCCAAGTATTGCATTATTGAGGTATTTAAGAAGATT
 ATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTTCTCTGTTTCACTGTGTGAAAAAAG
 AAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAGAAATGTGTATTTCACTGACAA
 TTTCTGTGCTCTTTTTAGAGGTATATTCAAAAATTTCTTGTATTTTTAGGTTATGCAACTAAT
 AAAAAGTACCTTACATTAATTAATTACAGTTTTCTACACATGGTAATACAGGATATGCTACTG
 ATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTCCAACAAAGTTTGATTTTCTCTTGT
 ATTTTTCTTACTTACTATGGGTACATTTTTTATTTTTCAAAATTGGATGATAATTTCTTGGA
 ACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTTGTTTCAAAGTGAAGTTTACTGAGAGA
 TCCATCAAATTGAACAATCTGTTGTAATTTAAATTTTGGCCACTTTTTTCAGATTTTACATC
 ATTCTTGCTGAACTTCAACTTGAAATGTTTTTTTTTTCTTTTTGGATGTGAAGGTGAACATT
 CCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTATTTTACATTTTGAAAATTCAAAGAAGCTT
 AATATAAAAGTTTGCATTCTACTCAGGAAAAAGCATCTTCTTGATATGTCTTAAATGTATTT
 TTGTCCTCATATACAGAAAGTTCTTAATTGATTTTACAGTCTGTAATGCTTGATGTTTTAAAA
 TAATAACATTTTTATATTTTTTAAAGACAACTTCATATTATCCTGTGTTCTTTCCTGACTG
 GTAATATTGTGTGGGATTTACAGGTAAAAGTCAGTAGGATGGAACATTTTAGTGTATTTTTTA
 CTCCTTAAAGAGCTAGAATACATAGTTTTACCTTAAAGAAGGGGGAAAATCATAAATACAA
 TGAATCAACTGACCATTACGTAGTAGACAATTTCTGTAATGTCCCCTTCTTCTAGGCTCTGT
 TGCTGTGTGAATCCATTAGATTTACAGTATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCC
 TTTAGAATTTAAATATTGTACCATTAAAGAGTTTGGATGTGTAACCTTGTGATGCCCTTAGAAA
 AATATCCTAAGCACAAAATAAACCTTTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAA
 AAA

FIGURE 30

MAPSGSLAVPLAVLVLLLVWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNLQ
PEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFINF
ISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFALATL
FSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSEEEAE
SKEGTNKDFPQNAIQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 31

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTCACGATGGC
TCGCCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAAAC
TGCCGCCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTGACT
GGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGATCCA
TCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAATTCTTT
TCTTCCGCTTGGATATTTCGCATGGGCCCTACTTTACATCACACTCTGCATAGTGTTTCTGATGA
CGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAAACCATTG
ATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAATTGGTCTA
ATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAACGTGTACAGGGC
TAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTACAAAGTGAGCA
CATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAAGGAGGCAATGC
GGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTGAGGAGAATGTGA
TCCGAGAATTTAACTTAAATGAGCTATAACCAGCGGGCCAAGAACTATCAAAGGCTGGAGACA
ATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGATGGGGAAAACAAGA
AGGATAAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATTCCAGGCTCTTTCCAT
AACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGGCTGNGACTGGNTGGGG
CAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAGGCACCCTACAGGAAGGC
CTGCCATGCTGTGGCCAACCTGTTTCACTGGAGCAAGAAAGAGATCTCATAGGACGGAGGGGGA
AATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATCAGCTATTCAGACATCTCCA
TGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAGTTGACCTGCACAGCTTGGTT
AGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAACGCTAAGAATTTTCCCCCAAG
GACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTCTTCATTAAAAGTATAAGCCTAA
CTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAGTTTTTATCATTGAAGACAATATT
GAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAATAGAGGCTTGAGACTTTCCTTTGT
GTGGTAGGACTTGAGGAGAGAAATCCCCTGGACTTTCACTAACCCTCTGACATACTCCCCACAC
CCAGTTGATGGCTTTCGTAATAAAAAGATTGGGATTTTCCTTTTG

FIGURE 32

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFDW
REVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFLMT
CKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPYADLSLKYNCTGL
NFGKVDVGRYTDVSTRYKVSTSPSTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSEENV
REFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 33

CGGACGCGTG GGGGTGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGCG
GCAGCGGCGGCGGCGGCGCCTCCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGGCA
CTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGAGAG
GTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCTAGCTACTGAATCCC
AACAGGCAGACCATTATTTTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTTAGTTGCTG
AATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAAGGAAGA
TACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGTCTTGGTC
CCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGGAGATTGAA
GTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAAGGGAACACA
GAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGACCAGTCAGCTG
ATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGGAGCACCTTGCG
GTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCTCAAGTGCACATT
CAGATGACTTATCCTCTACAAGGCTTAACCCGGAAGGGGACGCGCTTGAGTTAACATGTGAA
GCCATCGGGAAGCCCCAGCCTGTGATGGTAACCTTGGGTGAGAGTCGATGATGAAATGCCTCAA
CACGCCGTACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAAACAGATAATGGTACA
TACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTATATGCTGTATGTATAC
GATCCCCCACAACCTATCCCTCCTCCCACAACAACCACCACCACCACCACCACCACCACCACC
ACCATCCTTACCATCATCACAGATTCCTGAGCAGGTGAAGAAGGCTCGATCAGGGCAGTGGAT
CATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCATGCTGTGCTTGCTCATCATT
CTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTCATGAAGCCAAAGGAGCCGAT
GACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGAGGACAGAACAACTCCGAAGAA
AAGAAAGAGTACTTCATCTAGATCAGCCTTTTTGTTTCAATGAGGTGTCCAACCTGGCCCTATT
TAGATGATAAAGAGACAGTGATATTGG

FIGURE 34

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQ
VNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLNFSSSELKVSLTNVSISDEGRYFCQLYT
DPPQESYTTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSE
VEEWSDMYTVTSQMLMLKVHKEDDGVPIVCQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQ
GLTREGDALELTCEAIGKPQPMVTWVRVDDMPQHAVLSGPNLFINNLNKTDNGTYRCEASN
IVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAIVIGGV
VAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
```

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310, 430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408, 411-417, 427-433, 428-432

FIGURE 35

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTGTGTCAGGAGGAGACAGCCTCCCGCCCCGGGGAG
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCTGCGCTCAGCTGCCGGCCG
AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGG
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGTAATCGCAAAACCCATTTTGGAGCAGGAATCCAATCA
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAAACTCCAGGCAGGAACACCTTTTGCTGTG
ATGGCCGCGTCATGATGGCCCGGCAAAAGGGCATTCTTCTACCTGACCCTTTTCTCATCTCTGGGGACATGTACAC
TCTTCTTCGCCCTTTGAGTGCCGCTACCTGGCTGTTACAGTGTCTCTGCCATCCCTGTATTTGCTGCCATGCTCT
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCCTCGGGCGCTACCAGATG
AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACACCAGCCTCGTA
TCAAGAATTTCCAGATAAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCCGGCCTCCCC
GGGCTCCCATTGCAGCATCTGTGACAACCTGTGTGAGCGCTTCGACCATCACTGCCCTGGGTGGGGAATGTG
TTGGAAAGAGGAACTACCGCTACTTCTACCTCTTCATCCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCT
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAATTTGGCTTCTTGGAGACATTGAAAGAACTCCTGGAAGCTG
TTCTAGAAGTCTCATTTGCTTCTTTACACTCTGGTCCGTGCGTGGGACTGACTGGATTTTCATACTTTCTCGTGG
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGGCCCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGT
TTTTGCCACTGGAGGAAAGTGAAGTCGACCTCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC
CAGCCCCACAGAACACCTGAACTCAAATGAGATGCCGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
AGCCCCCAGAGCCACCACAGGAGCGAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTTTGTGTT
TAATTAGGGCTATGAGAGATTTCAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT
GTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTCTTCTGCTGCAAGCTTTTTTAAATTTCTGAACT
CAAGGCAGTGGCAGAAAGATGTGAGTCACTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
CCATGGCCTCAGCCACAGGGTCCCCCTGGACCCCCCTCTTCTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTCA
TGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG
TGGGGTCAGAAGATTTCTCTGGCCACCAAGTGCCAGCATTGCCCCACAAATCCTTTTAGGAATGGGACAGGTACCT
TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNTTGTTTTCTTTTGACTCCTGCTCCCATTAGGAG
CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTTCATTTCTTTTCTCAGAGGAAGCCGAGTGCTCACTTAAAC
ACTATCCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAAAAAAAATGCTAACCAGTTCTTCCATTAAGCCT
CGGCTGAGTGAGGGAAAGCCAGCACTGCTGCCCTCTCGGGTAACTCACCCTAAGGCCTCGGCCCACCTCTGGCT
ATGGTAACCACTAGGGGGCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCAGAGCCACTT
CACCCTGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTTCAAGGAAGAAGATTTATGT
ATTATATGTGGCTATATTTCTTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT
GCGGTGGGGGAGTGTAACCGGAACCTTTTCATCTATTTGAAGGCGATTAACTGTGTCTAATGCA

FIGURE 36

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAVQ
LSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPPRI
KNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGNCVGKRNRYFYLFIL
SLSLTLTIYVFAFNIVYVALKSLKIGFLET LKETPGTVLEVLI CFFTLWSVVGLTG FHTFLVAL
NQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSRPPSTQ
ETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEAEK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

FIGURE 37

GGCGGAGCAGCCCTAGCCGCCACCGTCTCGCAGCTCTCGTCCGCACTGCCACCGCCGCCCGCTCACTGCG
TCCTGGCTCCGGCTCCCGCGCCCTCCCGGCCGCCATG CAGCCCCCGCGCGCCAGGCGCCCGGTGCGCAGCTGC
TGCCCCGCGCTGGCCCTGCTGCTGCTGCTCGGAGCGGGGCCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCG
CCGCGCCCTTGTCTGCGCCCGGCCGTGCGCCGCGCAGCCCTGCCGGAATGGGGGTGTGTGCACCTCGCGCCCTG
AGCCGGACCCGAGCACC CGCCCCCGCGCGAGCCTGGCTACAGCTGCACCTGCCCGCCGGGATCTCCGGCG
CCAACTGCCAGCTTGTGTGCAGATCCTTGTGCCAGCAACCCCTTGTACCATGGCAACTGCAGCAGCAGCAGCA
GCAGCAGCGATGGCTACCTCTGCATTTGCAATGAAGGCTATGAAGGTCCCAACTGTGAACAGGCACTTCCCAGTC
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTCTGTCTACTCAGGAGCCTGACA
AAATCCTGCCCTCGCTCTCAGGCAACGGTGACACTGCCCTACCTGGCAGCCGAAAACAGGGCAGAAAGTTGTAGAAA
TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCCTGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGGCC
GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTGCGCAAGATGCCACTGCCTCACTGATTTTGC
TCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTCAGGCTT
CAGGGGGACTGGTCTCTCTGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTTGGTTTGTGAATGATTCTG
TGACTAAGTCTATTTGTGGCTTTGCGCTTAACCTGTTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACG
CAAATGACTTGGAGTGTT CAGGAAAAGGAAAATGCACCACGAAGCCGT CAGAGGCAACTTTTCTGTACCTGTG
AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAACGCGAGCT
GTATTTGATGCAAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCCCTGTTTATACTGGAGAGCTTT
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGT
GCCAGAACAACGGCACCTGCTATGTGGACGGGGTACACTTTACCTGCAACTGCAGCCCCGGGCTTCACAGGGCCGA
CCTGTGCCAGCTTATTTGACTTCTGTGCCCTCAGCCCCCTGTGCTCATGGCACGTGCCGACGCTGGGCACAGCT
ACAAATGCCCTCTGTGATCCAGGTTACCATGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT
GCCTGAAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGTGCCCTGGCAGAATACAAAGGAACAC
ACTGTGAATTTGTACAAGGATCCCTGCGCTAACGT CAGCTGTCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA
ATGGCACGTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGCACATTGACATAAATGAATGTGACAGTAACC
CCTGCCACCATGGTGGGAGCTGCCTGGACCAGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG
CAAACCTGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCAACATGCCACGGCACTCCC
TCTACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTTGCCGCA
TCAGCCGCATTGAATACCAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAACCTGCCGACATCGACAGCG
AGTT CAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAAAGAAATCCCGGCCTGCAATGTATGATGTGA
GCCCCATCGCCTATGAAGATTACAGTCTCTGATGACAAACCCCTGGTCCACTGATTAAAACTAAAGATTTGTAAT
CTTTTTTTGGATTATTTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTAAAGAAAATAAAAAGCTTAA
GAAATTTAAATGCTAGCTGCTCAAGAGTTTTTCAGTAGAATATTTAAGAACTAATTTTCTGCAGCTTTTAGTTTG
GAAAAAATATTTTAAAAACAAAATTTGTGAAACCTATAGACGATGTTTAAATGTACCTTCAGCTCTCTAAACTGT
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAATTTCTGTGGTTGTTACA
GAATAAGTCTAATCAAGGAGAAGTTTCTGTTTGACGTTTGAGTGCCGGCTTCTGAGTAGAGTTAGGAAAACCAC
GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAGTCTGAAATGTTTCGTTTTGTGAAA
AGAACTAGTTAAATTTACTATTCTTAACCCGAATGAAATTAGCCTTTGCCTTATTCTGTGCATGGGTAAAGTAAC
TTATTTCTGCACTGTTTTGTTGAACTTTGTGGAACATTCTTTTCAGTTTGTTTTGTCAATTTTCGTAACAGTCG
TCGAACTAGGCCTCAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAAATCTGATTGATTTGAATCTATATTT
TTCTTTAAAAAGTCAAGGGTTCTATATTGTGAGTAAATTAATTTACATTTGAGTTGTTTGTGCTAAGAGGTAG
TAAATGTAAGAGAGTACTGGTTCCTTCAGTAGTGAGTATTTCTCATAGTGACGCTTTATTTATCTCCAGGATGTT
TTTGTGGCTGTATTTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC
AAGTCA

FIGURE 38

><subunit 1 of 1, 737 aa, 1 stop
><MW: 78475, pI: 5.09, NX(S/T): 11
MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSRP
EPDPQHPAPAGEPGYSCTCPAGISGANQQLVADPCASNPCHHGNCSSSSSSSSSDGYLCICNEG
YEGPNCEQALPSLPATGWTESMAPRQLQVPATQEPDKILPRSQATVTLPTWQPKTGQKVVEM
KWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRODATASLILLWKVTATGFGQCSL
IDGRSVTPLQASGGLVLLEEMLALGNNHFIGFVND SVTKSIVALRLTLVVKVSTCVPGESHAN
DLECSGKGKCTTKPSEATFSCTCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQDGSNFTC
VCLPGYTGELCQSKIDYCIDPCRNGATCISSLGFTQCCEGYFGSACEEKVDP CASSPCQN
NGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPGYHGLYCEE
EYNECLSAPCLNAATCRDLVNGYECVCLAEYKGTHCELYKDPCANVSC LNGATCDSDGLNGTC
ICAPGFTGEECDIDINECDSNPCHHGGSCLDQPNGYNCHCPHGWVGANCEIHLQWKSGHMAES
LTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYNCRSIDSEFSNA
IASIRHARFGKKS RPAMYDVSP IAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 39

[illegible]

FIGURE 40

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979
><subunit 1 of 1, 204 aa, 1 stop
><MW: 22147, pI: 8.37, NX(S/T): 3
MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALVG
LIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQRNL
NCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVVGIGLFFSFTEILGVWLTYR
YRNQKDPRANPSAFL
```

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

FIGURE 41

CAGTCACCA**ATGA**AGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTGC
TCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGTCT
GCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCTTCC
AGGTCAAGGCCTACACTTTTCAGTGAACCCCTCCACCTGATTGTGTCCTATGACTGGCTGATCC
TCCAAGGTCCAGCCAAGCCAGTTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGCCTGGC
AAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCCCGGGC
CTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCACTGCAGTG
GCATCTTCCAGAGCCCTGGTCTGGGATCCCAGAAACAGCATCTGTTGTGGCTATCACAGTCC
AAGAACTGTTTTCCAGCGCCAATTCTCAGAGCTGTACCCCTCAGCTGAACCCCAAGCAGGAAGCC
CCATGACCCTGAGTTGTCAGACAAAGTTGCCCTGCAGAGGTGAGCTGCCCGCCTCCTCTTCT
CCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATTCAGATCCCCA
CAGCTTCAGAAGATCACTCCGGGTCACTAGTGGTGTGAGGCAGCCACTGAGGACAACCAAGTTT
GGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCTGCTGCACCTCCCA
CATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCTGAGGAGGCCCTGGGC
CTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTTCTCCTCTGGGGATGC
CAGATCCTCATCTGTATCACAGATGGGCCTTCTTCTCAAACACATGCAGGATGTGAGAGTCC
TCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCAGAAGCCTGGGACCACAA
AGGCTACTGCTGAAT**AGA**AGTAAACAGTTCATCCATGATCTCACTTAACCAACCCCAATAAATC
TGATTCTTTATTTTCTCTTCTGTCCTGCACATATGCATAAGTACTTTTACAAGTTGTCCCAG
TGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTTATATAAAGTGAGAATTAGAG
TTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTCTGCTGTCTAGATCAGGAATTT
CTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAACTAATGGAAGTGGATTGAATAC
AGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACATTGGGCAATGTTTGGAGACATTT
TGGTCATTATACTTGGGGGGTGGGGGATGGTGGGATGTGTGTCTACTGGCATCCAGTAAATA
GAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAGGGCAGTACCCCAACAACGAAAAATAA
TCTGGCCCCAAAATGTCAGTTGTACTGAGTTTGAGAAACCCAGCCTAATGAAACCCTAGGTGT
TGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTATTATCTCTTTCCAGCCTCATTAGCTAT
TCTTACTGACATACCAGTCTTTAGCTGGTGCTATGGTCTGTTCTTTAGTTCTAGTTTGTATCC
CCTCAAAAGCCATTATGTTGAAATCCTAATCCCCAAGGTGATGGCATTAAAGAAGTGGGCCTTT
GGGAAGTGATTAGATCAGGAGTGCAGAGCCCTCATGATTAGGATTAGTGCCCTTATTTAAAAA
GGCCCCAGAGAGCTAACTCACCCCTCCACCATATGAGGACGTGGCAAGAAGATGACATGTATG
AGAACCAAAAAACAGCTGTGCCCCAACCCGACTCTGTCGTTGCCTTGATCTTGAACCTCCAG
CCTCCAGAACTATGAGAAATAAAATCTGGTTGTTTGTAGCCTAA

FIGURE 42

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359 aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVK
AYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGPNR
EFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMT
LSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWKQ
SPQLEIRVQGASSAAPTTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSDPGFSSPLGMPDP
HLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE
```

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

FIGURE 43

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTAACTAATTCAACAAACGGGACCCTTC
TGTGTGCCAGAAACCGCAAGCAGTTGCTAACCAGTGGGACAGGCGGATTGGAAGAGCGGGAA
GGTCTTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGCATT
GCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCCTTACCTCTATTGGGCA
CATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATCCTTGT
GGAGGAAGCCAAGCTTTCCAAGATTAAAGAGCTGGGCCAACAAATGGAAGCCTTGACTAGCAA
GTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGGTGAAGCG
GCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCAGGTTTAT
CGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGGAGCTGCCAA
AGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCAGAGGGGAACT
TCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATGGGCCGCTCGGC
CTACAATGAAGGGGACTATTATCATACGGTGTTGTGGATGGAGCAGGTGCTAAAGCAGCTTGA
TGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCAGCTATGCTGTCTT
CCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTCTCCCTTGACCCAAG
CCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGAGGAAGAGAGAGAAAA
AACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCATCTATGAGAGGCCTGT
GGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGGGAGGGTGTCAAACCTGAC
ACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAACAGGGCCCCACAGCTGCT
CATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACATCGTCAGGTACTACGATGT
CATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAACCTAACTTGCACGAGCCAC
CGTTCGTGATCCCAAGACAGGAGTCTCACTGTGCGCCAGCTACCGGGTTTCCAAAAGCTCCTG
GCTAGAGGAAGATGATGACCTGTTGTGGCCCGAGTAAATCGTCGGATGCAGCATATCACAGG
GTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAATTATGGAGTGGGAGGACAGTATGA
ACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGGCCTCAAAACAGAGGGGAATAGGTT
AGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTGGTGGTGCCACCGTCTTCCCTGATCT
GGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTGTTCTGGTACAACCTCTTGCGGAGCGG
GGAAGGTGACTACCGAACAAGACATGCTGCCTGCCCTGTGCTTGTGGGCTGCAAGTGGGTCTC
CAATAAGTGGTTCCATGAACGAGGACAGGAGTTCTTGAGACCTTGTGGATCAACAGAAGTTGA
CTGACATCCTTTTCTGTCTTCCCTTCCCTGGTCTTCAGCCCATGTCAACGTGACAGACACC
TTTGTATGTTCTTTGTATGTTCTATCAGGCTGATTTTTGGAGAAATGAATGTTTGTCTGGA
GCAGAGGGAGACCATACTAGGGCGACTCCTGTGTGACTGAAGTCCCAGCCCTTCCATTACGCC
TGTGCCATCCCTGGCCCCAAGGCTAGGATCAAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGC
CTAGCAAGGTGCCTTTGTACCTCAGGTGTTTTAGGTGTGAGATGTTTCAGTGAACCAAAGTTC
TGATACCTTGTTTACATGTTTGTGTTTTATGGCATTTCTATCTATTGTGGCTTTACCAAAAAAT
AAAATGTCCCTACCAGAAAAA

FIGURE 44

MKLWVSALLMAWFGVLSVCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWAN
KMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFPTD
EDEIGAALKMRLQDTYRLDPGTISRGLPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTVLWM
EQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRLLSLDPSHERAGGNLRYFEQ
LLEEEEREKTLTNQTEAELATPEGIYERPVDYLPERDVYESLCRGEGVKLTPRRQKRLFCRYHH
GNRAPQLLIAPFKEEDEWDSPHIVRYDVMSEDEIERIKEIAKPKLARATVRDPKTGVLTVAS
YRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFSRRPFDSG
LKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGECDYRTRHAACPV
LVGCKWVS NKWFHERGQEF LRPCGST EVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 45

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGGG
CGGCGGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTCGCTCCAGCC
TGTCTGTGTCGTTTGGCGCCCCGCCTCCCCGCGGTGCGGGGTTCACACCGATCCTGGGC
TTCGCTCGATTTGCCGCCGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAGCGG
TCGTCTGTGTCCTCTCTCTCTGCGCCGCGCCGGGGATCCGAAGGGTGCGGGGCTCTGAGGA
GGTGACGCGCGGGGCCTCCCGCACCTGGCCTTGCCCGCATTCTCCCTCTCTCCAGGTGTGA
GCAGCCTATCAGTCACCATGTCCGCGAGCCTGGATCCCGGCTCTCGGCCCTCGGTGTGTGTCTGC
TGCTGCTGCCGGGGCCCCGCGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATGTTTTACCA
GAGGCTTGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCCCTCTTGAGG
AATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGGGCTGTGTCC
ACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACCTGGTCGAGAAA
ACTATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGATGGTCTGCTTCTT
TCACAGTAACTAAAGGCCAAAAGTAGTACACAGGAGGCCACAGGACAAGCAGTGTCCACAGCAC
ATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAAGTGGCAATAAAGATTGTA
AAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGCGCCGATTTAATTTAC
AGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACAGAAGGACCACATGTGG
GCCTTGTTCAAGCCAGTGAACATCCCAAATAGAATTTTACTTGAAAACTTTACATCAGCCA
AAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTAATTCCAATACAGGAAAAG
CCTTGAAGCATACTGCTCAGAAATTCCTCACGGTAGATGCTGGAGTAAGAAAAGGGATCCCCA
AAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACATCGAGGAAGCAGGCATTGTGG
CCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCAAGCCTATCCCTGAAGAACTGG
GGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGTGCGGAATAATGGCTTCTTCTCTT
ACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAAGCCTCTGGTACAGAAGCTGTGCA
CTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACTCAGTGAACATTGCCTTTCTAATTG
ATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTCATGCTTGAATTTGTTTCCAACATAG
CCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGATAGCTGCTGTACAGTTTACTTATGATC
AGCGCACGGAGTTCAGTTTCACTGACTATAGCACCAAAGAGAATGTCCTAGCTGTCATCAGAA
ACATCCGCTATATGAGTGGTGGAACAGCTACTGGTGATGCCATTTCTTCACTGTTAGAAATG
TGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAACTTCCTAGTAATTGTCACAGATGGGCAGT
CCTATGATGATGTCCAAGGCCCTGCAGCTGCTGCACATGATGCAGGAATCACTATCTTCTCTG
TTGGTGTGGCTTGGGCACCTCTGGATGACCTGAAAGATATGGCTTCTAAACCGAAGGAGTCTC
ACGCTTTCTTCACAAGAGAGTTCACAGGATTAGAACCAATTGTTTCTGATGTCATCAGAGGCA
TTTGTAGAGATTTCTTAGAATCCCAGCAATTAATGGTAACATTTTGACAACTGAAAGAAAAAGT
ACAAGGGGATCCAGTGTGTAAATTGTATTCTCATAATACTGAAATGCTTTAGCATACTAGAAT
CAGATACAAAATATTAAGTATGTCAACAGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCG
CTGCCCTTCTGGTTACAATTTACAGTGTACTTTGTTAAAAACACTGCTGAGGCTTCATAATCAT
GGCTCTTAGAACTCAGGAAAGAGGAGATAATGTGGATTAAACCTTAAGAGTTCTAACCATG
CCTACTAAATGTACAGATATGCAAATTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAA
AAAAA

FIGURE 46

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLLEFSVYG
NIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVTVTKG
KSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKNFVG
KVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKALKHTA
QKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELGMVQDV
TFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLIDGSSSV
GDSNFRMLLEFVSNIAKTTEISDIGAKIAAVQFTYDQRTFESFTDYSTKENVLAVIRNIRYMS
GGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITIFSVGVAVA
PLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 47

GCCCCGCGCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAG
 CCTGCTCCCTGCTCAGCTGCGCGTCTTGCCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCT
 GCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCCTTG
 GGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCT
 GGGTGTGTGAGGAGGGGGGCCGGGATCCCCACCGTCTTGACAGGGCCACATCGACTGTGGCTCCC
 TGCTTGGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTCTTT
 TCACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAGAATGGGT
 TTTGGTTCTTTAAGTTCCCTGATCCTGGTGGGCCTCACCGTGGGTGCCCTTCTACATCCCTGACG
 GCTCCTTTCACCAACATCTGGTTCTACTTCGGCGTCTGTTGGGCTCCTTCCTCTTCATCCTCATCC
 AGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGCAAGGCCGAGG
 AGTGCGATTCCCGTGCCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTTCTACTTGCTGT
 CGATCGCGGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCAGCGGTGCCACGAGGGCA
 AGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTTGCCCA
 AGGTCCAGGACGCCCAGCCCCAACTCGGGTCTGCTGCAGGCCTCGGTTCATCACCTCTACACCA
 TGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTTGCCAA
 CCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAGACCCAGTGGTGGGATG
 CCCCAGCATTTGTGGGCCTCATCATCTTCTCCTGTGCACCCTCTTCATCAGTCTGCGCTCCT
 CAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCA
 CACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCCTTTGACAACGAGCAGGACG
 GCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGTGGCCTCACTGCACGTCATGA
 TGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGATGATCAGCACGTGGACCGCCG
 TGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTCTACCTGTGGACCCTGGTAGCCC
 CACTCCTCCTGCGCAACCGCGACTTCAGTTGAGGCAGCCTCACAGCCTGCCATCTGGTGCCTC
 CTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTCCCCACACCAATCAGCC
 AGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTGCCCTGAGCCGGGCCTTCTAGTCGT
 AGTGCCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCACACCCAC
 ACGGTGGAGCTGCCTCTTCTTCCCCTCCTCCCTGTTGCCATACTCAGCATCTCGGATGAAA
 GGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCCACC
 ACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTTCTTGGTACGTCCCCCAGGGGACCCTGCC
 CCCTTCTGGACTTCGTGCCCTTACTGAGTCTCTAAGACTTTTTCTAATAAACAAGCCAGTGCG
 TGTA

FIGURE 48

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFFLGLVLSIIMLSPGVES
QLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPR
AAIQNGFWFFKFLILVGLTVGAFYIPDGSEFTNIWFYFGVVGSLFILIQLVLLIDFAHSWNQR
WLGKAEECDRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVS
IAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGY
ETQWWDAPSIIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRA
FDNEQDGVITYSYFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICASWAGLLLY
LWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 49

[illegible]

FIGURE 50

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSS
SCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKSRR
KRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQK
LRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL
KKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGA
SGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYL
DCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 51

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCCGGGAGCGGCAG
CAGTAGCCCCGGGCGGCGAGGGCTGGGGGTTCCTCGAGACTCTCAGAGGGCGCCTCCCATCGGCGCCACCACCC
CAACCTGTTTCCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCCAACATGGATTTTCTCCTGGCGCTGGT
GCTGGTATCCTCGCTCTACCTGCAGGCGGCGCCGAGTTCGACGGGAGGTGGCCCAGGCAAATAGTGTATCGAT
TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTGAGCC
TGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTGATCCTGGTTATGCTGG
AAAAACCTGTAAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGATGGTTTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACCTGTGATATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTGATAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTGATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTGTCTCGATGTTATAA
CGTACGTGGGTCTTACAAGTGCAAATGTAAAGAAGGATACAGGGGTGATGGACTGACTTGTGTGTATATCCCAA
AGTTATGATTGAACCTTCAGGTCCAATTGATGTACCAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCCTATCATTACCAA
CAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTCTTACTCCACCACCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACACCAGGACTGACAACCTATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTCAGAAACCCAGAGG
AGATGTGTTTCACTGTTCTGGTACACAGTTGTAATTTTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGCCGCTCATGCATTGAGGGACCTGTGCTGTCTATTGAGGCA
CAAGGTGACGGGGCTGCACTCTGGCAGCTCCAGGTGTTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGCGAGGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAGGGTTGGAAAAAAGATCTATGATGGAAAATTAAGGAACTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAACCATGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTG
TTCTCCATATGCACTAAGAATAGAACACAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAGG
GGCCATTGTTAGAATACTTCATAAAAAAAGAGTGTGAAAATCTCAGTATCTCTCTCTTTCTAAAAAATTAGA
TAAAAATTTGCTATTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTTCCCAA
AGATGTTTTGATCCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
CATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCAACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC
TTTTATTTGTTCAATGGATGATGTTTACAGATTTTTTTTTTTTTTAAGAGATCCTTCAAGGAACACAGTTCAGAGAG
ATTTTCATCGGGTGCACTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGCCCTGCCCC
ACACCGGCAGACCTTTCTTCACCTCATCAGTATGATTGATTTCTCTTATCAATTGGACTCTCCCAGGTTCCAC
AGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGTCTTCTGTCAATTAACCTGGTAAAGGCAGGGCTGG
AGGGGAAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAAATATATGGCTGTAGATCCATTTTAAATGGTTTCAAT
TCCTTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAAAATAAATGAAAATTTTACTTTTTCGATGCCAA
TGATACATTGCATAAAGCTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTATTATTTAATGTTTT
CTAAATAAAAAATGTTAGTGGTTTTTCAAATGGCTAATAAAAAACAATTATTTGTAAATAAAAAACTGTAGTAAT

FIGURE 52

MDFLLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQPR
CKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGS
CSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDVDECATGRASCPRFRQCVNT
FGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQGDGLT
CVYIPKVMIEPSGPIHVPKGNGTILKGDGTGNNNWIPDVGSTWWPPKTPYIPPIITNRPTSKPT
TRPTPKPTPIPTPPPPPLPTLRTPLPPTTTPERTTGLTTIAPAASTPPGGITVDNRVQTD
QKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVL
PLGRLMHSGDLCLFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIK
SESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 53

CGGGCCGCCCCGGCCCCATTTCGGGCCGGGCTCGCTGCGGCGGCGACTGAGCCAGGCTGGG
 CCGCGTCCCTGAGTCCCAGAGTCGGCGCGGGCGGGCAGGGCAGCCTTCCACCACGGGGAGCC
 CAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGTGCA
 TGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGGTCCC
 TGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCCCCTGA
 GCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACAGCTGGT
 GCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCCTCTTCCC
 GGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGGTGTGGCGGACGAGGG
 CAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTGAGCCTGCAGGTGGC
 CGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCCAACAAGGACCTGCGGCCAGGGGACAC
 GGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTCTGGCAGGATGG
 GCAGGGTGTCCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGAGCAGGGCTTGT
 TGATGTGCACAGCGTCCTGCGGGTGGTGTGGGTGCGAATGGCACCTACAGCTGCCTGGTGCG
 CAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCAACATCACAGGGCAGCCTATGACATT
 CCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCATTTGCACTGCTGGTGGC
 CCTGGCTTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGGAGAATGCAGGAGCTGA
 GGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCTCTGAAACACTCTGACAG
 CAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGGGAGCTGCTACCCCTCCCT
 ACAGCTCCTACCCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCCTGCCCCAACAGATGCATC
 CTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACACAGACCACTGTGCAGCCTTAT
 TTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTTTTCTTATAGACACAATGAACA
 GACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCTGCCTTATTTACAGTACATACA
 TTTCTTAGGGACACAGTACACTGACCACATCACCACCCTCTTCTTCCAGTGCTGCGTGGACCA
 TCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTTCAGACTGACTGACCCCTGCCTTATTT
 ACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTCTCCAATGGCCGTGATACACTAGTGA
 TCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTTTCTTCTCAGACAGGGACAGTGCGGCC
 TCAACATCTCCTGGAGTCTAGAAGCTGTTTCTTTCCCTCCTTCCCTGCCCCAAGTGAA
 GACAGGGCAGGGCCAGGAATGCTTTGGGGACACCGAGGGGACTGCCCCCACCACCATGG
 TGCTATTCTGGGGCTGGGGCAGTCTTTTCTGGCTTGCCTCTGGCCAGCTCCTGGCCTCTGGT
 AGAGTGAGACTTCAGACGTTCTGATGCCTTCCGGATGTCATCTCTCCCTGCCCCAGGAATGGA
 AGATGTGAGGACTTCTAATTTAAATGTGGGACTCGGAGGGATTTGTAAACTGGGGGTATATT
 TTGGGGAAAATAAATGTCTTTGTAAAAA

FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQL
NLIWQLTDTKQLVHSFAEGDQGSAYANRTALFPDLLAQGNASLRLQVRVVADEGSFTCFVSI
RDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDQGQGVPLTGN
VTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVNPNVLQQDAHXSVTITGQPMTFPPEALWVT
VGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGESESKTALQPLKHSDSKEDDGQEIA
```

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

FIGURE 55

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTG
GCTATGTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTT
CTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAG
TGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAACTGCATTT
CTTGAGCATAAAGAACAGTTTCAATTATTTATTCTCATAAACTGTGGAGCTAATGTAGACCTA
TTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGGCCAGTC
AATGTCGTCAATGTATACAACGATACCCAGATCAAATTAATCATTAAACAAGATGATGACCTT
GAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATTAGGAAAT
GACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATAGTGGAGCAA
ACCATGCGGAGGAGGAGCGCGGAGAGTGGGAGGCCCGGAGAAGAGACATCCTCTTTGACTAC
GAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGGCTTGGATGCTG
TCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGACCAGTGGGTGCAA
GACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGTCAGCGCCACGTTTCCCGC
CACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCACACGGATCTCCTTT
GAGTATGACCTCCGCTGGTGCTCTACCAGCACTGGTCCCTCCATGACAGCCTGTGCAACACC
AGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAAGCGGCTCCAGGAGTTC
CTTGCAGACATGGGTCTTCCCCTGAAGCAGGTGAAGCAGAAGTTCCAGGCCATGGACATCTCC
TTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAATAAATTTGGGATGAAGGACATG
CGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAAGCACAAGTTTCTGGCCAGCGACGTGGTC
TTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCTCAGGGACAGATCACTTCATC
CAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTGTACCATGGCCTGGAACCTCGCC
AAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGCCTTTGCACCAACCTCGTCATC
TCCCAGGGGCCTTTCCTGTACTGCTCTCTCATGGAGGGCACTCCAGATGTCATGCTGTTCTCT
AGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCAAGTCCTTTGTGTGTTTCGACAAAG
AACCGGCGCTGCAAACCTGCTGCCCCTGGTGATGGCTGCCCCCTGAGCATGGAGCATGGCACA
GTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTCGGACAGGAAGAACTTTTTTGGGAGG
GCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGATGCTGCACAACCATTTTGACCTCTCA
GTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTTCTGGACGCACTTATTTCCCTCCTGTCC
TAGGAAATTTGATTCTTCCAGAATGACCTTCTTATTTATGTAAGTGGCTTTCATTTAGATTGTA
AGTTATGGACATGATTTGAGATGTAGAAGCCATTTTTTTATTAAATAAAATGCTTATTTTAGGAAA

FIGURE 56

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAFLEHKEQFHYFILINCGANVDLLDILQPDEDITFFVCDSHRPVNVNVYNDTQIKLLIKQDDDLVPAYEDIFRDEEEDEEHSGNDSGSEPSEKRTLLEEEIVEQTMRRRQRREWEARRRDILFDYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRHVSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKRLQEFLEADMGLPLKQVKQKFQAMDISLKENLREMIIEESANKFGMKDMRVQTFSIHFGFKHKFLASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQOTIASCLCTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAPLSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFLDALISLLS

FIGURE 57

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCCGC
CCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTCGCCTTGCTGACGGCGTCGAG
CCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTG
GCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAACCCT
TCTGTGGGGCTCAATTTTGGAAATCTTGGAAAGTACTTCAACTCCAGCAACTACATCTGCTCCT
TCAAGTGGTTTTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTAGGAGGA
ACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCTGCAA
GGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCCTTCTCCAGA
CCTCCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAAGGAATCAGA
GATGCTACCACCTACCCGCCTGGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGGCA
CGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGCCTCAGCCTCTG
AGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTTGGGGCCAGCTGGCCTCGATGTACGTACGC
ACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCTGAACGTGTACGCG
CCGGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTC
ATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCCGCGAGAAAGTGGTGCTG
GTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTTGAGCACGACGACAGCCACGCGCGC
GGGAACTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGCAGGAGAACATCGCAGCC
TTCGGGGGAGACCCAGGAAATGTGACCCTGTTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCA
GGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCAGAGTGGCACC
GCGTTATTCAGACTTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGGTTGCCACCTG
GCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACC
AAGGTGATGCGTGTGTCCAACAAGATGAGATTCTCCAACTGAACTTCAGAGAGACCCGGAA
GAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGGTATCCAGATGACCCTTTGGTG
CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAACCTGGAATTC
AATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGAGTACCTG
GACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGAT
GCCACTTTTCGTGTATGCCACACTGCAGACTGCTCACTACCACCGAGAAACCCCAATGATGGGA
ATCTGCCCTGCTGGCCACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAA
GAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTTGGATGAGTCTGTACCAGTCTCAAA
GACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTTGC
CCCCACCATCCAGGCCCTGGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA
CCCCAGTTTGAAGCTGCAGGAGCTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGT
TGTGTGGGACCTGCACTGCCCTTTCAGCCTGACATCCCATGATGCCCCCTCTACTTCACTGTT
GACATCCAGTTAGGCCAGGCCCTGTCAACACCACACTGTGCTCAGCTCTCCAGCCTCAGGACA
ACCTCTTTTTTTCCCTTCTTCAAATCCTCCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTA
TGGGAGGTGACCCAGACTGCCACTGCCCTGTCACTGCACCCAGCTTGGCATTATACCATCCA
TCCTGCTCAACCTTGTTCCTGTCTGTTACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACAT
GGAGCAAACCTTTTGGTAGTTTGGGATCTTCTCTCCACCCACACTTATCTCCCCAGGGCCAC
TCCAAAGTCTATACACAGGGGTGGTCTCTTCAATAAAGAAGTGTGATTAGAAAAA

FIGURE 58

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
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GTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPFSSRPPLG
ILRFAPPEPPEPWKGI RDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLSVWG
YRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLVYAPARAPGDPQLPVMVWFPGGAFIVGA
ASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGD
PGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLACN
HNSTQILVNCLRALSGTKVMRVS NKMRFQLNFRDPEEIIWSMSPVVDGVVIPDDPLVLLTQ
GKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATFV
YATLQTAHYHRET PMMGICPAGHATTRMKSTCSWILPQEWA
```

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

FIGURE 59

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGGTCCCGAGCGTCCCGCGCCCTC
 GCCCCGCCATGCTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGCAGG
 AAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAGTCA
 GACTGTTGCAGAGGCTGAAAACCAACCTTTGATGACAGAATTCTCAGTGAAGTCTACCATCA
 TTTCCCGTTATGCCTTCACTACGGTTTCCTGCAGAATGCTGAACAGAGCTTCTGAAGACCAGG
 ACATTGAGTTCAGATGCAGATTCAGCTGCAGCTTTCATCACCAACTTCACTATGCTTATTG
 GAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGGGTAAAAG
 AGAAAAGGAATAAAACACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTCAGAGCTTCTG
 CAGTGATTCCAGCAAGGACAAAGCCGCTTTTTCTGAGTTATGAGGAGCTTCTGCAGAGGC
 GCCTGGGCAAGTACGAGCACAGCATCAGCGTGC GGCCCCAGCAGCTGTCCGGGAGGCTGAGCG
 TGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCCGCTTCACAACA
 GCAGGCAGAGGGGCAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCATCTACTGTCATTA
 ACCAAAATGAAACATTTGCCAACATAATTTTAAACCTACTGTAGTACAACAAGCCAGGATTG
 CCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAGAGAACAGAGCATTG
 GGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTAAAGACCTTCCTCCTT
 TACCCAAGAATGTGGTATTTCGTGCTTGACAGCAGTGCTTCTATGGTGGGAACCAAACCTCCGGC
 AGACCAAGGATGCCCTCTTCACAATTCTCCATGACCTCCGACCCAGGACCGTTTTCAGTATCA
 TTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCATTGATATCAGTCACTCCAGACAGCA
 TCAGGGATGGGAAAGTGTACATTACCATATGTACCCACTGGAGGCACAGACATCAACGGGG
 CCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCACAGTGGCATTGGAGACCGGA
 GCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCACGGTCGGGGAGACGCACACCCCTCA
 AGATCCTCAACAACACCCGAGAGGCCGCCGAGGCCAAGTCTGCATCTTCACCATTTGGCATCG
 GCAACGACGTGGACTTCAGGCTGCTGGAGAACTGTGCTGGAGAACTGTGGCCTCACACGGC
 GCGTGCACGAGGAGGAGGACGCAGGCTCGCAGCTCATCGGGTCTACGATGAAATCAGGACCC
 CGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGCTCAGTGGTGCAGGCCACCAAGACCC
 TGTTCCCCAACTACTTCAACGGCTCGGAGATCATCATTCGGGGGAAGCTGGTGGACAGGAAGC
 TGGATCACCTGCACGTGGAGGTACCGCCAGCAACAGTAAGAAATTCATCATCCTGAAGACAG
 ATGTGCCTGTGCGGCCTCAGAAGGCAGGGAAAGATGTACAGGAAGCCCCAGGCCCTGGAGGCG
 ATGGAGAGGGGGACACCAACCACATCGAGCGTCTCTGGAGCTACCTCACCACAAAGGAGCTGC
 TGAGCTCCTGGCTGCAAAGTGACGATGAACCGGAGAAGGAGCGGCTGCGGCAGCGGGCCAGG
 CCCTGGCTGTGAGCTACCGCTTCTCACTCCCTTCACCTCCATGAAGCTGAGGGGGCCGGTCC
 CACGCATGGATGGCCTGGAGGAGGCCACGGCATGTGCGCTGCCATGGGACCCGAACCGGTGG
 TGCAGAGCGTGCAGGAGCTGGCACGCAGCCAGGACCTTTGCTCAAGAAGCCAAACTCCGTCA
 AAAAAAACAAAAACAAAAACAAAAAAGACATGGGAGAGATGGTGTTTTTCTCTCCACCACC
 TGGGGATACGATGAGAGATGGCCACCTGCAAGCCAGGAAGACGGCCCTCACCAGACACCATG
 TCTGCTGGCACCTTGATCTTGGACCTCCCAGCCTCCAGAACTGTGAGAAATAAATGTGTTTTG
 TTTAAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 60

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192
<subunit 1 of 1, 694 aa, 1 stop
<MW: 77400, pI: 9.54, NX(S/T): 6
MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLRKTPLMTEFSVKSTIISR
YAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKEKR
NKTTEENGEGKTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLSVDV
NILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQARIAQN
GILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTKLRQTK
DALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTDINGALQ
RAIRLLNKYVAHSGIGDRSVSLIVFLTLDGKPTVGETHTLKI LNNTREAARGQVCIFTIGIGND
VDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVVQATKTLFP
NYFNGSEIIIIAGKLVDRLDHLHVEVTASNSKKFII LKTDVPVRPQKAGKDVGTGSPRPGDGE
GDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTSMKLRGPVPRM
DGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLKKPNSVKKKQNKTKKRHRGRDGVFPLHHLGIR
```

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 61

CAGGAACCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAACC
ACGAAGGGACGATACCAGAAAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTGGC
TGACTTTGGCTATAGAAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTTTGGAAAGCTAAGTC
TTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAATTGAGT
AAAGTACGCTCCGGTCACCATGGTGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTCCTGCT
CTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGCCAGCGG
CTGCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAGCCTCTTC
CTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTACATTAATATCACCATCCTGAAGGG
TGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGGTCCCCAAGG
GGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCGGCGCCCCGTG
CCAGAAGCGCTTCTTCGCCTTCTCAGTGGGCGCAAGACGGCCCTGCACAGCGGCGAGGACTT
CCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGACATGGCGACCGG
CCAGTTTGCTGCTCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGCACAGCTGGAATTA
CAAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTCTATCCTGTACGCGCAGCC
CAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGCCTACGGGACCCGCT
CTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCAACGACTTCGACACCTA
CATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGACTGAGGGCCTCTGGGCCACCCCTCC
CGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAGTTTGCACCTGCTGTGAAGC
AGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATCTGGGGAGACCCTGCTTCTATCTTGGCT
GCCATCATCCCTCCAGCCTATTTCTGCTCCTCTCTTCTCTCTTGGACCTATTTTAAAGAGCT
TGCTAACCTAAATATTCTAGAACTTTCCAGCCTCGTAGCCAGCACTTCTCAAACCTTGGAAA
TGCTATGGAATCACCCGGGGTTCGTGTTAAATGCAGATTCTGACTCAGCAGGTCTGAGTGGGT
CCAGGATTCTGTGTTTTCTCATATGTTCTCTGGGTGATGCTGATGGGGTCAGTCTATGAACCACA
CTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAGTACTTTCTGAACATTCTGGAATCC
TCCCCACATTCTAGAATTCTCCCAACATTTTTTTTTTCTTGAGACAGAGTCTTGCTCTGTTGCC
CAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCAGTCAACCTCTGCCTCCCGGGTCAAGCGA
TTCTTCTGCTCAGCTCCCTAGTGGCTGGGATTACAGGCGCCTGCTACCATGCCTGGCTAAT
TTTTGTATTTTTAGTAGAGATGGGGTTTCACCATATTGGCCAGGCTGGTCTTGAACCTCTGAC
TTCAGGTGACCCACCCGCTCGGCCTCTCAAATGCTGGGATTACAGGTGTGAGCCACCGTGC
CTGGCCAATTCCAACATTCTTAAATTCTCTCATCCCTCCAGGGCTCCCGTGCTATGTTCTCT
TTACCCCTTCCCCCTCTTCTCTTGCTCAGGCCTGCACCACTGCAGCCACCGTTTCATTTATTCA
TTCATTAAACACTGAGCACTCACTCTGTGCTGGGTCCCGGGAAGGGTGAGGGGGTCAGACACA
GGCCCTGCCCCCTGCCCTCAGTGACTGGCCAGTCCAGCCCAGGCGGGAGAGATGTGTACATAG
GTTTTAAAGCAGACCCAGAGCTCATGGGGGCTGTGTTCTGGGTGTTCAAGGTGCTGCTGGTCC
TCCATTACCCACTGCTCCCCAAGGCTGGTGGGACGGGGTCCCGGTGGCAGGGGCAGGTATCTC
CTTCCCGTTCCTCATCCACCTGCCAGTGCTCATCGTTACAGCAAACCCAGGGGGCCTTGGC
CAGGTCAAGGGTCTGTGAGGAGAGGACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGC
CCCCGAAGAATGGAACCCACACCCATAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAG
ACCTGCCCTCCTCACTGGGATCCCCTTCTGCCCTCCAGGGCTCTGCCAGGGCCTTGCTC
AGTCCCTTCCACCAAAGTCATCTGAACCTCCGTTTCCCCAGGGCCTCCAGCTGCCCTCAGACA
CTGATGTCTGTCCCAGGTGCTCTCTGCCCTCATGCCCTCTCACCGGCCAGTGCCCCGAC
TCTCCAGGCTTTATCAAGGTGCTAAGGCCCGGGTGGGCAGCTCCTCGTCTCAGAGCCCTCCTC
CGGCCTGGTGCTGCCTTTACAAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGA
GCCCTCAGCAGGTCTGGGGAGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCGTTTCTTCTTCC
AGGGTGGGGTGGCCTGGTGTTCCTTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAG
AGGGAGGCGGCCTCCGCCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGGT
GATCTCTGGTGCTCACAGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAACAGGGTCT
GACCAAGTGCCAGGAAGACCTGTGCTATAAACACCCCTGCCTGATCCTGCCCTGCCTGACCC
CGCCACGCCCTGCCGTCCAGCATGATTAAAGAATGCTGTCTCTCTTGGAAAAA

FIGURE 62

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGRPHA
LPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPGAPCQKRFFA
FSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKETVH
IMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITFSGH
LIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

C1q domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 63

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGAC
TCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCACCA
TGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTTGGCCTTG
ATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTGTCAC
TGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGCACTGG
CCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCTTTAAGT
GTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGACGAGTACC
GCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTCGTGGAAGA
CCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAACTGGGTTTCC
CAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTCCGGGAGGAGT
TTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCACTCAGTATATG
TGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAGTGCACAGCCTGTGGTCATAGAA
GGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAGTGGCCCTGGCAGG
CCAGCCTTCAGTTCAGGGCTACCACCTGTGCGGGGGCTCTGTCATCACGCCCCCTGTGGATCA
TCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGACCATCCAGGTGGGT
TAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAGATTGTCTACCACAGCA
AGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCTGGCCGGGCCACTCACGT
TCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGAACTTCCCCGATGGAAAAG
TGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGACGCCTCCCCTGTCTGAACC
ACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAGGGACGTGTACGGTGGCATCA
TCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCGTGGACAGCTGCCAGGGGGACA
GCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACCAGCTTTG
GCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACACCCGTGTCACCTCCTTCCTGGACT
GGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTTGAAGAGGAAGGGGACAAGTAGCCACCT
GAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCTGGACTCCCGTGTAGGAACCTGCACA
CGAGCAGACACCCTTGAGGCTCTGAGTTCGGGCACCAGTAGCAGGCCCGAAAGAGGCACCCTT
CCATCTGATTCAGCACACCTTCAAGCTGCTTTTTTGTGTTTTTTGTTTTTTTGGAGTGGAGTCT
CGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAATCCCTGCTCACTGCAGCCTCCGCTTCCC
TGGTTCAAGCGATTCTCTTGCCCTCAGCTTCCCCAGTAGCTGGGACCACAGGTGCCCGCCACCA
CACCCAATAATTTTTTGTATTTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGGCTGCTCT
CAAACCCCTGACCTCAAATGATGTGCCTGCTTCAGCCTCCACAGTGCTGGGATTACAGGCAT
GGGCCACCACGCCTAGCCTCACGCTCCTTTCTGATCTTCACTAAGAACAAAAGAAGCAGCAAC
TTGCAAGGGCGGCCTTTCCCACTGGTCCATCTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCT
GACGAGATAAGCAGTTATGTGACCTCACGTGCAAAGCCACCAACAGCCACTCAGAAAAGACGC
ACCAGCCCAGAAGTGCAGAACTGCAGTCACTGCACGTTTTTCATCTCTAGGGACCAGAACCAAA
CCCACCCTTTCTACTTCCAAGACTTATTTTCACATGTGGGGAGGTTAATCTAGGAATGACTCG
TTTAAGGCCATTTTTTCATGATTTCTTTGTAGCATTTGGTGCTTGACGTATTATTGTCCTTTGA
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CAAAATCATCCACTGAAA

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234
><subunit 1 of 1, 453 aa, 1 stop
><MW: 49334, pI: 6.32, NX(S/T): 1
MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILAL
AIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAASWK
TMCSDDWKGYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV TALHHSVY
VREGCASGHVVT LQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWI
ITAAHCVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHISKYKPKRLGNDIALMKL AGLT
FNEMI QPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHA AVPLISNKICNHRDVYGGI
ISPSMLCAGYLTGGVDSCQGDSSGGLVCQERRLWKLVGATSF GIGCAEVNKP G VYTRVTSFLD
WIHEQMERDLKT
```

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

FIGURE 65

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCACCCGTTAAGGTGTCTTCTCTTTAGGGATGGT
GAGGTTGGAAAAAGACTCCTGTAACCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAG
AACGCTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCC
ACACAACCTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTC
AGGAGGACTTTTCTGTTTGTTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATA
GAGTTAAATGTGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTAC
TATTCTTCATATTTTGATATATTTCTTCTGGCAGTTTTTTCGATTTAAAGTGTTAATACTTGCA
TATGCTGTGTGCAGACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCC
TTTTTACTAGCAAAAGTGATCCTTTTCAAGCTTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTG
CCCATCATTTTCATTCATCCTTGCCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCT
CAAGAAGCAGAAGAAGAAAACAGACTCCTGATAGTTTCAGGATGCTTCAGAGAGGGGCAGCACTT
ATACCTGGTGGTCTTTTCTGATGGTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAA
GAAGCTGAAGAAAAACAGGACAGTGAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTA
AATGTGAAAAACCCTCACAGAAAGTCATCGAGGCCAAAAGAGGCAGGCAGTGGAGTCTCCCTG
TCGACAGTAAAGTTGAAATGGTGACGTCCACTGCTGGCTTTATTGAACAGCTAATAAAGATTT
ATTTATTGTAATACCTCACAAACGTTGTACCATATCCATGCACATTTAGTTGCCTGCCTGTGG
CTGGTAAGGTAATGTCATGATTCATCCTCTCTTCAGTGAGACTGAGCCTGATGTGTTAACAAA
TAGGTGAAGAAAGTCTTGTGCTGTATTCTTAATCAAAAGACTTAATATATTGAAGTAACACTT
TTTTAGTAAGCAAGATACCTTTTTTATTTCAATTACAGAAATGGAATTTTTTTGTTTCATGTCT
CAGATTTATTTTGTATTTCTTTTTTAACACTCTACATTTCCCTTGTTTTTTAACTCATGCACA
TGTGCTCTTTGTACAGTTTTTAAAAAGTGTAATAAAATCTGACATGTCAATGTGGCTAGTTTTTA
TTTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTTGGACTTGCAAAAGGGGAAGAAAGG
AATTGCGAATACATGTAAAATGTCACCAGACATTTGTATTATTTTTATCATGAAATCATGTTT
TTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGCACAAAATGACTTAAACC
ATTCATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAAATGAACATAAATTAATAA

FIGURE 66

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDL
LFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAI
ALTTAVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLPQEAEENRLLIV
QDASERAALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 67

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCATC
CAACCATTCCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCCTCTCCCGTAGCCCAACCGACT
AACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCAC
GGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTACAGTACCTGC
CACCCCTCAACGTCCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGCTACAC
AGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGA
GATGTTCTCAGTTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTTCAAGACCGCGT
GGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGTGATGCTGAGAAACGTGCAGCCGGA
GGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGCCCATGGCAA
GATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGGCCGTGATTGT
GGGTGCCTCCGTCGGGGGCTTCTGGCTGTGCTCATCTTGGTGCTGATGGTGGTCAAGTGTGT
GAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGAGGAGGGCAAGAC
GGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCCCTGCAGCCTCCCG
TGTCCCGTCTCTCCCTCTCCGCCCTGTACAGTGACCTGCCTGCTCGCTCTTGGTGTGCTT
CCCGTGACCTAGGACCCAGGGCCACCTGGGGCCTCTGAACCCCCGACTTCGTATCTCCCA
CCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCATGCTCTGGGACGTGTG
GGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGGGGGGAGGCAGGAGGCAC
ATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGAGGAGGGGCCGCTGTCACC
TGCCCAAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGGGGAGGGAGGGCTTTCTCTGT
GCTGACAGCGCTCCCTCAGGAGGGCTTGGCCTGGCACGGCTGTGCTCCTCCCTGCTCCCAG
CCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTTGAACCTTGAGGGGGCATGTTAAA
GGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGGCTGCAGGCAAAGCTGGACATGT
GCCCTGGCCCAGGAGGCCATGTTGGGGCCCTCGTTTCCATTGCTAGTGGCCTCCTTGGGGCTCC
TGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAGACTGGAAGAGCAGCTCCAGGTAGG
GGGCCATGTTTCCCAGCGGGACCCACCAACAGAGGCCAGTTTCAAAGTCAGCTGAGGGGCTG
AGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAGGCTCTGCCTTCTCCATGGGGTAACCA
CCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAATGAGGAGGCCATGCACAGGGTGGGGCAG
CTTTCTTTGGGGCTTCAGTGAGAACTCTCCCAGTTGCCCTTGGTGGGGTTTTCCACCTGGCTTT
TGGCTACAGAGAGGGAAGGGAAGCCTGAGGCCGGCATAAGGGGAGGCCTTGGAACCTGAGCT
GCCAATGCCAGCCCTGTCCATCTGCGGCCACGCTACTCGCTCCTCTCCCAACAACCTCCCTTC
GTGGGGACAAAAGTGACAATTGTAGGCCAGGCACAGTGGCTCACGCCTGTAATCCCAGCACTT
TGGGAGGCCAAGGCGGGTGGATTACCTCCATCTGTTTGTAGTAGAAATGGGCAAAACCCCATCTC
TACTAAAAATACAAGAATTAGCTGGGCGTGGTGGCGTGTGCCTGTAATCCCAGCTATTTGGGA
GGCTGAGGCAGGAGAATCGCTTGAGCCCGGGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGAT
AGTGCCACTGCAATTCAGCCTGGGTGACATAGAGAGACTCCATCTCAAAAAAAA

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

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SLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGIYN
CYIMNPPDRHRGHGKIHQLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRKKEQ
KLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

FIGURE 69

GCGCCTGGTTCTGCGCTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCGCCAGCCTCCGCGCCGAGCCTC
 GTTCGTGTCCCCGCCCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA
 GCAGCTCCCTTCCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGC
 CGCAGAGGCGGAGGCTCGCGTATTCCTGCAGTCAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTC
 GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCCGTCCGGTTTGGCT
 CACCTCTCCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGAGATTTTCTGGGGAA
 ATCCTGAGGTCATTCAATATGAAGTGTACCGCGCGGGAGTGGCTCAGAGTAACACAGTGCTGTTTCATGGCTAGA
 GCAATTCCAGCCATGGTGGTTCCTCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT
 GAGTGGTGGATAGCCAAACAACGAGGGAAAAAGGCCATCAGACAAATGACATGCAGAGTATTTTGGACCTTCAT
 AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
 TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT
 TTGGGAGCACACTGGGGAAGATATAGGCCCCCGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAAGACTTT
 AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTACAGGTGTTCTGGCCCTGTATGTACACATTATACA
 CAGGTCGTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTACATAACATGAACATCTGGGGGCAG
 ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCCTTACAAA
 CATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG
 TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
 CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATTGTTTCT
 TGTGAAGTAAGATTAAAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCCTGCTGGCTGTTTGGAT
 AGTAAAGCTAAAGTTATTTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
 ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTCATCAAGTCCAATAGA
 AATGGTATTCAAACAATTGGCAAAATATCAGTCTGCTAATTCCTTCACAGTCTCTAAAGTAACAGTTCAGGCTGTG
 ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTTCATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCCT
 CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATTGGAACCTCGAGTTTATTCTGATCTGTCCAGTATC
 TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA
 AAGACCTACATTGCTTCTTTTCAGAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATTC
 AGAGTGTTTGCTGTGTGTGAACCTGAATACTTGGAAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA
 ATTTTGTATAAACTGTAACTTACTGTACAGAGTACATCAACTATTTTCAGCCCCAAAAGGTGCCAAATGCATA
 TAAATCTTGATAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG
 TTTTAGAAATCCTGTGTAAATATTTGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT
 GTTCTACGTTTCATATATTATATGGTGTCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG
 GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAAACTGAAAGAAACCTTATCACATTTTCCCC
 AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTC
 TGTTAATTTAGGCATATAGAATATTAAATCTGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC
 CAAATGAATCTGTTAAATGTTTGAATTCCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT
 ATGAAAACATTCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA
 AAATTGAGGTCACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT
 GAACAAAGATGAACTAATGTATTACATTACCATTGCCACTGATTTTTTTTTAAATGGTAAATGACCTTGATATAA
 ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGTATTGTGCTTTGATACTAAA
 AATCTGTAAAAATGTAGTTTGGTAATTTTTTTTCTGCTGGTGGATTTACATATTAAATTTTTTCTGCTGGTGGTA
 TAAACATTAAAAATTAATCATGTTTTCAAAAAAAAAAAAA

FIGURE 70

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417
<subunit 1 of 1, 500 aa, 1 stop
<MW: 56888, pI: 8.53, NX(S/T): 2
MKCTAREWLRVTTVLFMARAI PAMVVPNA TLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDMQ
SILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHWGR
YRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGCAINLCHNM
NIWGQIWPKAVYLV CNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENL CYKEGSDRYYP PR
EEETNEIERQQSQVHDTHVRTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNRYECPA
GCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKH YFIKSNRNGIQTIGKY
QSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIGTRVYSDL
SSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRVFAVV
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Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

FIGURE 71

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGGC
 TGGGCGCGCCCCCGGGCCCCGCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCT
 CTGCTGGCCCACTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCC
 CTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCC
 GAGCGCCACGCGGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGGCGCC
 GCCAACCTTCTTGCCATGGTAGACAACCTGCAGGGGACTCTGGCCGCGGCTACTACCTGGAG
 ATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTT
 GCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACA
 TACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTT
 GGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACT
 ATTTTGAATCAGAGAATTTCTTTTGGCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT
 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAA
 GCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCT
 GGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATC
 TGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAATTGGA
 GGCCAAAGCCTTAATCTGGAAGTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGC
 ACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCA
 TCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAAT
 TCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGC
 AGGTCATTCCGTATCACAAATCCTGCCTCAGCTTTACATTACAGCCCATGATGGGGGCCGGCCTG
 AATTATGAATGTTACCGATTCCGCATTTCCCATCCACAAATGCGCTGGTGATCGGTGCCACG
 GTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC
 CCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTCTCAACAGAGGAT
 GTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTAT
 GCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTT
 CGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTGTCATGATGAGTCCTCTCTGGTCAGACAT
 CGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCA
 CATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTTCAAT
 CTCTGTTCTGCTCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTT
 CAAATCCTCCCTACTTCCAAGAAAAATAATTAACAAAAAACTTCATTCTAA

FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pI: 5.08, NX(S/T): 2
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LEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYI
DTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENFLLP
GIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLG
GIEPSLYKGDIIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLLRLPQKV
FDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSRSFRITILPQ
LYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAETAGAAV
SEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLIIVLLLLPFRQRRPRDPE
VVNDESSLVRHRWK
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

FIGURE 73

GCCGCGGCGAGAGCGCGCCAGCCCCGCGCGATGCCCCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCCGGC
CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGGCGGCGGGCGCTGGGGCGCCCGGGCCCCAGG
AGGCGGCGGGCGGGCGGGCGGACGGGCCCCCGCGCGAGACGGCGAGGACGGACAGGACCCCGACAGCAAGCACC
TGTACACGGCCGACATGTTACGCACGGGATCCAGAGCGCGCGCACTTCGTCACTGTTCTTCGCGCCCTGGTGTG
GACACTGCCAGCGGCTGCAGCCGACTTGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT
ATGTGGCTAAAGTGGACTGCACGGCCACTCCGACGTGTGCTCCGCCCAGGGGGTGCAGAGGATACCCACCTTAA
AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCCTCGGGACTTCCAGACACTGGAAAAGTGGATGC
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGAACCGCCAGTGGCCCCGAGCTCAAGCAAG
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC
CGTGGTGTGGTCACTGCAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCGGAAGT
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTCTGCTCCGGAACAGGTTCTGGCTATCCCACTC
TTCTCTGGTTCCGAGATGGGAAAAGGTGGATCAGTACAAGGGAAGCGGATTTGGAGTCACTGAGGGAGTACG
TGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCGGCTGCTGGCAG
CTGAGCCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTCAGAAAGGAA
TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCACTGTAAGACTCTGGCTCCTACTGGGAGGAACCTCTA
AAAAGGAATTCCTGGTCTGGCGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA
AGTATTCGGTACGAGGCTACCCACGTTATGCTTTTCCGAGGAGGAAGAAAGTCACTGAGCACAGTGGAGGCA
GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAGCGAAAGACGAACCTTTAGGAACACAGTTGGAGGTCAC
CTCTCCTGCCAGCTCCCGCACCCCTGCGTTTAGGAGTTCACTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT
GTTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTGTTTCCAAGCCAACACACTCTACAG
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TATCCCCCTTTGACCTTCTTTGATGAAATTTACATGTTTCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAA
TTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGC
CCACGAGTTCGGAAGGTGGCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTCACAGTTGACTCAATAC
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTCACGGCCGCTGC
TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC
GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTCGATACTTGTCAAATCAGTTACTGTTTCAAGGGAT
CCTTCTGTTTCTCACGGGTGAAACATGTCTTTAGTTCTCATGTTAACACGAAGCCAGAGCCACATGAACGTGT
TGGATGTCTTCTTAGAAAGGGTAGGCATGGAAAATTCACGAGGCTCATTCTCAGTATCTCATTAACTCATTGA
AAGATTCAGTTGTATTTGTACCTGGGGTGACAAGACCAGACAGGCTTTCCAGGCCCTGGGTATCCAGGGAGGC
TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCTTTTAGAGG
CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC
CAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA
ACTCATGCTGTCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA
GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCATAATAACCACTTTGCATCCAACACTCTTCACCCACCT
CCCATACGAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACACTTATA
CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCAGC
TATGGTTTACAGATAATTCTTTTTTAAAAAACCCAACTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA
CACAACCTCAGCTTTGCATCACGAGTCTTGATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTTTACACTAT
GATACTTTCTAAATAAACTCTTTTTTTTTAA

FIGURE 74

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
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VCSAQGVRGYPTLKLFPKPGQEAVKYQGPRDFQTLNWMQLTLNEEPVTPEPEVEPPSAPELKQ
GLYELASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCTQHYE
LCSGNQVRGYPTLLWFRDGGKKVDQYKGKRDLESLEYVESQLQRTETGATETVTPSEAPVLAA
EPEADKGTVLALTENNFDFTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLAGVKIAE
VDCTAERNICKYSVRGYPTLLLFRRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL
```

Signal sequence:

amino acids 1-32

FIGURE 75A

CGGACGCGTGGGCGGACGCGTGGGCAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG
 CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG
 TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT
 GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCGCGCTGGTGAAGTGTGCGGGAGATTGGCAAACGCCTAGG
 AAAGGACTGGGAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG
 TCTGATCAGAGCCAGACGCGACGCTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA
 TCCCGCCGCCCTCCGTACCAGCACTCCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA
 AAAGTTCTGTCCACTGTGATTCTCAATTCTTGTGTTTCTTCCAGAGAACTTTTGGGTGGAGATATTA
 ACTTTTTCTTTTTTTTTTCTTGGTGAAGCTGCTCTAGGGAGGGGGAGGAGGAGGAGAAAGTGAATGTGC
 TGGAGAAGAGCGAGCCCTCTTGTCTTCCGGAGTCCCATTCAATTAAGCCATCACTTCTGGAAGATTAAAGTTGT
 CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTACCCTCTGTTGGGTGCATG
 TGTGCGCCCGCAGCGGCGCGGGGCGGTGTTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA
 GGGGCTGTGCGGGGCATCCGCTCCGCTTCTCCACAGGCTGTGTCTGTCTGGAAAGATGCTAGCAATGGGGG
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 TCGAACACTACCGATCCATTATCAACATAAACAGGAGAGATATGCTGCCATGCTTCTGCTTAGATGAAGCAA
 TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACACAGCATTATCATTTACTCTTCAAGTAATG
 GTGGCCAGCCTACGGCAGGAGGAGTAAGTGGCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
 GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGAACAGTGTGTAAGGAACCTGTGCACATCACTG
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 GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGATAACATTGACCCCTATACACCAAGGC
 AAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
 GAAATGGTTACAGGAAATCCTGGCTACAGCGACTGGGTCCTCCCTCAGTCTTTCAGCAACCTGGGACCGAACC
 GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAGAGTGTATGGCTTTTCAACATCACAGCCGACCATATGA
 GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAA
 TGCAGTGCCGGTCAGGTATCCCCCAAAGACCCAGAAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG
 GTATAAGAGGAAACCAAGAAAAAGCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAAAGCAAAAAA
 GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
 GGCTTGTTTTCTGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCCACTGAAAACTGTCTGCTCAGTG
 CCAAGGTGCTACTCTTGCAAGCCCACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG
 GTGAGTCTGAGTTCCACTGTGTGCTTCACTCACTGACCAACACTGCTTTGAATTATAGGAGGAGAACATA
 ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAAACTACCTTTGATAAATTAC
 AGTCAAAGATTGTGTACCTCAAAGGCCCTGAAGAATATATTTTCTTGGTGAATTTTGTATGTCTGTCTATGA
 CACTTGGGTTTTTTAATTAAATCTATTTATATATATAAATATATGTTTCTTTCTGTGAAAAGCTGTTTTTCT
 CACATGTGAACAGCTTGCACTCATTTTACCATGCGTGAGGGAATGGCAAAATAAGAATGTTTGTAGCACACTGCC
 ACAATGAATGTAACATTTTCTAAACACTTTACTAGAAGAACATTTCAGTATAAAAAACCTAATTTATTTTACA
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 TAAAAACATCATTCAGAAAACCTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
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 GTATCATTGGTCTTAAAAATAAAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGTCTAACAACACAGTAA
 TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAAGATTTTCCCATATAATAACTAA
 TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCATTAAAAAGTAATAACCTTACTCTTATACAAAGT
 GGACACTGTGGGGAGATACAGAGAAATGGAAGATCAGGATCCTGCGGTGAGTAGGTAACCTTGTGGAAACCCC
 ACATGCAACGTGATGAGGAGAAATTAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTGATCAATGAGCATA
 GATTGGTGTGGATCCTGTAGACCCTGGTGTCTTTTGAAGTGCCCTCTCCTAATGCAGAGGCCTTGAAGCTTAC

FIGURE 75B

[illegible]

FIGURE 76

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEEGALLAQAGEKLEPSTTSTSQ
PHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAAEGVKLENYYVQPICTPSRSQFITGKYQIHTGLQHSIIRPTQP
NCLPLDNATLPQKLKEVGYSTHMGVKGWHLGFNRKECMPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCYDLYEN
DNAAWDYDNGIYSTQMYTQRVQQILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSC
DEAINNVTLALKTYGFYNNIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGVHSPLLKNKGTVCHEL
HITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPGQQAMGSGTLQSSQPSE
CSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFSTSQPTHMRGWTYLTGIQES
```

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

FIGURE 77

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCCTTTTGAAGAACAGTACTGTGGA
GCTATTTAAGAGATAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC
GCCGCTGTTACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGACGCGCCTGAAGCACAAAGCAGAT
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAACAACGGAGGAGCTCTGACTTCCCACTGTCCCATTCTAT
GGGCGAAGGAACCTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAAATGAT
TCCTGCGCGACTGCACCGGACTACAAAGGGCTTGCTCTGCTGGGAATCCTCCTGGGACTCTGTGGGAGACCGG
ATGCACCCAGATACGCTATTAGTTCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGCAGCTTTTCGCCCT
GAATCCGCGCAGCGGCAGCTTGGTCACGGCGGCGAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG
TCAATTAAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA
CGACAATGCGCCTTACTTTCTGTGAAAGTGAATTAGAAATAAAAAATTAGTGAAAATGCAGCCACTGAGATGCGGTT
CCCTCTACCCACGCTTGGGATCCGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCCTGGACCG
CGAAGAAAAGGCTGCTCACCACCTGGTCTTACGGCCTCCGACGGGGCGACCCGGTGCGCACAGGCACCGCGCG
CATCCGCGTGATGGTTCTGGATGCGAACGACAACGCACCGAGCGTTTGCTCAGCCCCGAGTACCGCGCGAGCGTTCC
GGAGAATCTGGCCTTGGGCACGCAGCTGCTTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGCGGAAGT
GAGGTATTCCTTCCGCTATGTGGACGACAAGGCGGCCAAGTTTTCAAACCTAGATTGTAATTCAGGGACAATATC
AACAATAGGGGAGTTGGACCACGAGGAGTCAGGATTCTACAGATGGAAGTGCAAGCAATGGATAATGCAGGATA
TTCTGCGCGAGCCAAAGTCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCTCACCTCTCT
CGCCAGCTCGGTTCCCGAAAATCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGACCAAGATTCTGA
GGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA
TAGTTTTAGTCACAGACATAGTCTTGGATAGGGAACAGGTTCTTAGCTACAACATCACAGTGACCGCCACTGACCG
GGGAACCCCGCCCTATCCACGGAACCTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCGGCTCTT
CCCTCAGGCCTCTATTCCGCTTATATCCAGAGAACAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA
CGACCCGACTGTGAAGAGAACGCCAGATCACTTATCCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC
GTCCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA
CTTGCAAGTGAAGTGATGGCGCGGGACAACGGGCACCCGCCCCCTCAGCAGCAACGTGTCTGTTAGCCTGTTCTGT
GCTGGACCAGAACGACAATGCGCCCGAGATCCTGTACCCCGCCCTCCCGACGGACGGTTCCACTGGCGTGGAGCT
GGCTCCCGCTCCGACAGAGCCCGGTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC
CTGGCTGTCTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG
CACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGTGGCCGTCCAGGACCACGGCCAGCC
CCCTCTCTCCGCCACTGTACGCTCACCGTGGCCGTGGCCGACAGCATCCCCCAAGTCTTGGCGGACCTCGGCAG
CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG
CGTCTTCTTGGCCTTCTGTCATCTTGCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCAACGCTGCTGCAGGC
TTCAGGAGGCGGCTTGACAGGAGCGCCGGCTGCACTTTGTGGGCGTGGACGGGGTGCAGGCTTTTCTGCAGAC
CTATTTCCACGAGGTTTTCCCTCACCACGGAAGTCACTGATCTTCCCCAGCCCAACTATGCAGA
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAGCGAGCCCCCTTTGCTGTCAGGTGATTCCGGTATTTTCTAAAGA
CAGTCATGGGTTAATTGAGGTGAGTTTATATCAAATCTTCTTTCTTTTAAATTGCTCTGTCTCCCAAGC
TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCCTCAAACCTCTAGGCTCAAGCAATTATCCACCTTTGCCT
CCGGTGTAAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCCTATCTATCTATCTATCTATCTATCTATCTAT
CTATCTATCTATCTATCTATTACTTTCTTGTACAGACGGGAGTCTCACGCCTGTAATCCAGTACTTTGGGAGGC
CGAGGCGGGTGGATCACCTGAGGTTGGGAGTTTGGAGACCAGCTGACCAACATGGAGAAACCCGCTTATACTAA
AAAAATACAAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT
TGCTTTAACCTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG
AACTCTATCTCA

FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306
><subunit 1 of 1, 916 aa, 1 stop
><MW: 100204, pI: 4.92, NX(S/T): 4
MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVPPELEKGSRVGDISRDLGLEPRELAERGVRIIPRGRTQLF
ALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVVEVVRDINDNAPYFRESELEIKISENAATEM
RFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGADGSKYPELVLRALDREEKAAHHLVLTASDGGDPVRTGT
ARIRVMVLDANDNAPAFAPQPEYRASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGT
ISTIGELDHEESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSASSVPENSPRGTLIALLVNDQD
SEENGQVICFIQGNLPFKLEKSYGNYSLVTDIVLDREQVPSYNITVTATDRGTPPLSTETHISLNVADTNDNPP
VFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTIQQASLSSYVSINSDTGVLYALSSFDEYQF
RDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDNAPEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQ
NAWLSYRLLKASEPGLFSVGLHTGEVTRARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIPQVLADL
GSLESPANSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLLQASGGGLTGAPASHFVGVDGVQAFL
QTYSHVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGLIEVSLYQIFFLFFFNCSVS
QAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDRCPPPTVCLSIYLSIYLSIYLSIYLLLSCTDGSILTPVIPVLW
EAEAGGSPEVGSRLPA
```

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

FIGURE 79

AGCCGCTGCCCCGGGCGGGCGCCCGGGCGGCACCAATGAGTCCCCGCTCGTGCCTGCGTTCGCTGCGCCTCCTC
 GTCTTCGCCGCTCTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCAAGCTGTCGTCGGTGGGGAGCATCTCA
 GAGGAGGAGACGTGCGAGAAACTCAAGGGCCTGATCCAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTC
 ATGGACTCGGTGCGCCGCGGTGCCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGAACCGGCGCTGGAAC
 TGCTCCACACTCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTGTAC
 GCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGCAGCAGTGGGGAGCTGGAGAAGTGCGGCTGT
 GACAGGACAGTGATGGGGTCAGCCACAGGGCTTCCAGTGGTCAGGATGCTCTGACAACATCGCCTACGGTGTG
 GCCTTCTCACAGTCGTTTGTGGATGTGCGGGAGAGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTC
 CACAACAATGAGGCCGGCAGGAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTCAAGC
 TCCTGTGAGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAGAAGTTT
 GATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACCACGCAACGCACAGTTCAAG
 CCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCGACTTCTGTGAGCAGGACATGCGCAGCGGCGTG
 CTGGGCACGAGGGGCCGACATGCAACAAGACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGC
 GGCTTCCACACGGCGCAGGTGGAGCTGGCTGAACGCTGCAGCTGCAAAATCCACTGGTGTGCTTCGTCAAGTGC
 CGGCAGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGAACCGCCTGCCTAGCCCTGCGCCGGCAACCACCTA
 GTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGAGATACTGGTTGTATTTTTTTGTT
 CTGGTTTGGTTTTTTGGGTCCTCATGTTATTTATTTGCCGAAACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGC
 CTCCCCAAAGCCTGGGCCTTTGTGGCTGCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTG
 GCTGCCACTGACCACTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGACAGACCTAAGGTGGAGTAACAAGGAGTA
 TTACCACCACATGGCTACTGACCGTGTATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATAGGTACCGACTTG
 ATGGAAGTCACACCCCTCTGGAAAAAAGAACTCTTAACCTCTCCAGCACACATACATGGAAGTCTGGCAGCTTGA
 GCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAAGGGAACAAGCAGATACCAGGTCAAGGGCACAGGTTTCATT
 TCAGCCCTTACATGGACAGCTAGAGGTTGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAG
 AGACGACTGAAGTCCCACCCTAGAACCAGCCTGCCCCAGCCTGCCCCTGGGAAGAGGAACTTAACCACTCCCC
 AGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTTTGCAGTCATGCCCCGA
 GTCACCTTTTACAGCGCTGTTCTCCATGAAACTGAAAAACACACACACACACACACACACACACACACACAC
 ACACACACACGACACACACACACACCTGCGAGAGAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAG
 TCACCTTTCACAGCACTGTTCTC

FIGURE 80

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
<subunit 1 of 1, 351 aa, 1 stop
<MW: 39052, pI: 8.97, NX(S/T): 2
MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLGKLIQRQVQMCKRNLEVMDSVRRGAQLAI
EECQYQFRNRRWNCSTLDSLPLVFGKVVTQGTREAAFVYAISSAGVAFVTRACSSGELEKCGCDRTVHGVSPQGF
QWSGCSNLIAYGVAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCRAVP
PFRQVGHALKEKFDGATEVEPRRVGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTS
KAIDGCELLCCGRGFHTAQVELAERCSCCKFHWCCFVKCRQCQRLVELHTCR
```

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 81

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
CTGATGGTGGGTCTGTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT
TGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTTAAATTAATGCCTGCAGTCT
GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCT
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCCTCCACCTGATCCCGGTGT
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCGTGTGACGGAGCCCCCTGTGA
CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCATGCC
CGCATCATTTTAAGCTGGTCTCAGTGCAATGTGTTTCATTGCCCCACGGAGACAGGTACCCACTGTATGTCATTCCCA
AAACAAAGCGACAGAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCA
TTAGTCACATGTCAAAGGATCCGGAGCCTCTTTCGAAAGCCCCCTTGAACCTCCTTGCTCTTTACCCAAATCACC
CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTCAGCTGCTGAGGGATA
TCTATCTAAAGAAACACAACTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA
GCCGGACCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCCAGATTTTGAAGTGAAGAAATTTATTCA
GGCAGCAGCAAGTGGCTGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAGAAACCACTATCTGGAAAAGGAGC
AGCGTCGTCAGTACCTTCTACGTTTGAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG
ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTCAGCT
TTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCATTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA
GGGAAAGACGGGAGAAGAAATTGTACTTCGGGTATTCTCTCCTGGGTGCCACCCCATCTGAACCAAAACCATCG
GCCGGATGCAGCGTGCCACCGAGGGCAGGAAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACCTGT
CACCAGTTCTCAGTGCCTTGCGCCTTTTCAGAAAGCCAGGTTCCCAAGGTTTGACGCCAGGTTGATCTTTGAGCTTT
GGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCGGGATTCTTTACAATGGCGTCGATGTCACATTCCACACCT
CTTTCTGCCAAGACCACCACAAGCGTTCTCCAAGCCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAAA
GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTAATTATGATGCATGTCACAGGGAAGGATTTCTAAAGG
TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTGTCTGTTAC
TAAGGGTAGAAGATTATTGCTTTTAAAGGCTAAATATTGTTTGTGGGAACCACAGATGGTTGGGGTTGAACAGT
AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCACAGAGGAATAGAAGGTACTT
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC
TCTTCTGGCCTGCCCCATGTTACTATGTGATGGAACCAGCACACCTCAACCAAAATTTTTTAACTCTAGACATT
TTTACCTTGTCCTTGTTAAGAATTTCTTGAAGTGATTTATCTAAATAAAGGTTGGCAAACTTTTTCTGTAAAGG
GCCAGATTGTAAATATTTAGACTGTGTGGACAAAAGGCCACATACAGTCTCTGTCTATAACTACTCAACTCTGT
TTCTGAAGCAGGAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAACA
GATGGTGACCAGACTTGGCCCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCTCAGTAACCTCTGCTAGAAAACA
CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA
AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTTAAGTATGTTCTAAATATTTGT
CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAAATATT
TTCTAAGACCAGTTTATAGTACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG
GAGGCTAGAAGATGAATTCAGGCACTTTCTTCCAATAAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA
ACTGGATTCAATTTTTAAACCATTTTCATCAGTTTCAAATGGTAAATTTCTGATTGATTTTTAAATGCGTTTTTGG
AGAACTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG
TGATTTCTGAACATAATGGTCTAATTCAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTATCGGCATTCC
AACTTTTTCTCTTTGTTTTTGTCCAGTGTGCAATTTGAATATGCTGTTTCTATAAAATAAATTTTTTAAGAATAA

FIGURE 82

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2
MLFRNRFLLLLALALAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDVTEPPVTDVPVYEALLYCNIPSVAE
RSMEGHAPHHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKPYPHPKLEAFISHMSKSGSGASFESPLNS
LPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLLKKHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDF
DWKKIYFRHQPSALFCSGSCYCPVRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMC
HFCHNVSPCTRNGCVDMEHFVKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELFALY
SAHDVTLSPLVLSALGLSEARFPRFAARLIFELWQDREKPSSEHSVRILYNGVDVTFHTSFCQDHHKRSPKPMCPLE
NLVRFVKRDMFVALGGSGTNYDACHREGF
```

Signal sequence:
amino acids 1-18

FIGURE 83

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGT
GACGTTGTGGAGATGGGGAGCGTCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAAGTGCC
CCGTGTTTGTCTATGCCGATGCTGTCTTAGTGGAAACAACCTCACTGTAAC TAGATTGATCTATGCACCTTTCTTG
CTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTGGATT
TGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTGGT
TTGGCTATGTTCTATCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTG
CACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGA
ACTTTTACAACCTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAAC TAGTCTTACTT
ATTGATTTTGCACATTCATGGAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACCTGAGATGTTGGTATGCA
GCTTGTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTCTGTTCTTTGTCTACTACACT
CATCCAGCCAGTTGTTTCAGAAAACAAGGCGTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGTCTCTGTAATG
TCTATACTGCCAAAAATCCAAGAATCACAACCAAGATCTGGTTTGTACAGTCTTCAGTAATTACAGTCTACACA
ATGTATTTGACATGGTCAGCTATGACCAATGAACCAAGAAACAATTTGCAACCCAAGTCTACTAAGCATAATTGGC
TACAATACAACAAGCACTGTCCCAAAGGAAGGGCAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTA
ATTCTCTTTTGTGTGTGATTTTATCCAGCATCCGTACTTCAAACAATAGTCAGGTAAATAAATGACTCTA
ACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATCACTGGAGGATGGGGACGATGTT
CACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACAGTTATTCTTCTTTCACTTCATGCTTTTCTCTGGCT
TCACTTTATATCATGATGACCCCTTACCAACTGGTCCAGGTATGAACCCCTCTCGTGAGATGAAAAGTCAGTGGACA
GCTGTCTGGGTGAAAAATCTCTTCCAGTTGGATTGGCATCGTGTGATGTTTGGACACTCGTGGCACCCTTGTT
CTTACAAATCGTGATTTTGACTGAGTGAGACTTCTAGCATGAAAGTCCCACCTTTGATTATTGCTTATTTGAAAAC
AGTATTTCCCAACTTTTGTAAAGTTGTGTATGTTTTTGTCTCCCATGTAACCTCTCCAGTGTCTGGCATGAATTA
GATTTTACTGCTTGTCTATTTTGTATTCTTACCAAGTGCATTGATATGTGAAGTAGAATGAATTGCAGAGGAA
AGTTTTATGAATATGGTGTAGTTAGTAAAGTGGCCATTATTGGGCTTATCTCTGCTCTATAGTTGTGAAAT
GAAGAGTAAAAACAATTTGTTTGAATTTTAAATTTATATTAGACCTTAAGCTGTTTTAGCAAGCATTAAGC
AAATGTATGGCTGCTTTTGAATATTTGATGTGTTGCTGGCAGGATAGTGAAGAACAATGTTTATTTTAA
ATTTATAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATAAGGTTTTACCCTTGATACGGAATTTACA
CAGGTAGGGAGTGTTTAGTGGACAATAGTGTAGGTTATGGATGGAGGTGTCCGCTACTAAATTTGAATAACGAGTAA
ATAATCTTACTTGGGTAGAGATGGCTTTGCCAACAAAGTGAACCTGTTTGGTTGTTTTAACTCATGAAGTATG
GGTTCACTGAGCAAGTCTGAACTCTGAAGGATTTAGACAAGGTTTGAAGAAGGATAATCATGGGTTAGAAGGAA
GTGTTTTGAAAGTCACTTTGAAAGTTAGTTTGGGCCCAGCACGGTAGCTCACCTTGGTAATCCAGCACTTTG
GGAGCTTAAGTGGGTAGATTACTTGAGCCCAGGAATTCAGACCAGCTTGGCACATGGTGAACCTGTTCTATAAAA
ATAATCTGGCTTTGAGCATATGCCCTGTGGTCCAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCAGAGCCAAAG
GTTGCAGTGAGCAAGTCACTGCACTCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATATTTGAAAT
CAAGGAGGCAAAATTTTGACAGGGAAGGAAGTAACTGCAAAACCCTAGGCTTTAGTAGGTACTTATATAAAATC
TAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATAGCTCAGATAGCTAATTAGGAA
ATTTCAAGTTGGCCAATAATAGCATTCTCTGACATTTAAAAATAATTTCTATTCAAAATACATGCATATTGAT
TTACACCTCATACTGTGATAATTAATGTGATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTCAGAAGA
ATGATGGAATGTTTGAATAAACTCCTGCTTATAGTATACTACACAGTTCAAAAGATGTTTAAATGCTTTTGT
ATTTACTGCCATGTAATGAAATATATAGATTATTGTAACCTTTCAACCTGAAAAATCAAGCAGTATGAGAGTTTA
GTTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTACAATTTCTTCTTTAAAAATATTTATTAAT
GTGAATGGAATATAACAATTCAGCTTAATCCCCAACCTTATTCTGTGTGTAGACATTGTATCCACAATTTTGA
ATGGCTGTGTTTTACCTCTAAATAAATGAATTCAGAGAAAAA

FIGURE 84

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQLNKIPGFCENE
KGVVPCNILEVGYKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFITT
VWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKMEEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPAS
CSENKAFISVNMLLCVGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIIGYNTT
STVPKEGQSVQWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVHRAV
DNERDGVITYSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNRDFD

FIGURE 85

AACAAAGTTCAGTGA CTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGAGCTGCTGGGCAGA
GAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCCTCGTGGGATGGATCACAGGTGCTGCT
GTGGCGGTCTGCTGCTGCTGCTGCTGCTGCTGGCCACCTGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGG
AACCGTACAGCTGCAGGGGGAACCGAGTCCGCCGGGCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGA
ATCTTTTACCATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCACCCC
CGCCACACCCCTCACCACCTCCACCACCACCACCACCCCAACCGCCACCATCCCCGCCACGCTCGCTGAGGCTGC
TGTCGCCGGTGCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTGTTCCAGGACAAGTGGACCCCATGTTTCC
ATGTGGAAGGATGCATCTCTGGGGTGAACGAGGGGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGTCATGGC
ATGCCCCAGTGTACTATGGCAGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAG
AGCAAGGGTGCTCTTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATGACAAGC
GTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTCATCAGGCTGCTGCAGGCCT
CTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAAATGTCCTTTTGGTTTGGGAGAAGGCAGTGTGAGGCTGCACAGT
CAATTCATCGGTGCCTTAGTCCAAGAAAATAAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

MLGLLGSTALVGWITGAAVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNVRRAPWPFRRRGHLGIFHHHRH
PGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

FIGURE 87

CCCACGCGTCCGTCTTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTATTGCAACGGTCAAGGCTGGCTTGT
GCCAGAACGGCGCGCGCGCGCACGCACGCACACACGGGGGAACTTTTTTAAAAATGAAAGGCTAGAAGA
GCTCAGCGGGCGCGCGCGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCGCGA
CGCCCCGGCCCCGGCTCGGCGCCCCGCGTGGGATGGTGACGCGCTCGCCGCCGGGCCCCGAGAGCTGCTGCACTGAAG
GCCGGCGACGATGGCAGCGCGCCCCGCTGCCCGTGTCCCCCGCCCGCCCTCCTGCTCGCCCTGGCCGGTGCTCT
GCTCGCGCCCTGCGAGGCCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTGAGTGCCTCTGT
TCGGAGTGGGGACCTCTGGATCCCACTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGCTGAATATTCGACT
ACAACGGGAAAGCAAAGAATGATCATAAATCTGGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAAC
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCAGTGTACTACCATGGACATGT
ACGGGGATATTTCTGATTACGACAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTTGTGTTTGAAGATGA
AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAACTCTTCCCAGCGAAGAAGCTGAAAAGCGT
CCGGGGATCATGTGGATCACATCACAAACACACCAAACTCGCTGCAAAGAATGTGTTTCCACCACCTCTCAGAC
ATGGGCAAGAAGGCATAAAAGAGAGACCTCAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGCGACACAACCG
AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAGAGTTAAGCAGCGATTAATAGAGATTGCTAATCACGTTGACAA
GTTTTACAGACCACTGAACATTCCGATCGTGTGGTAGGCGTGGAAGTGTGGAATGACATGGACAAATGCTCTGT
AAGTCAGGACCCATTACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA
TGACAATGCGCAGCTTGTGAGTGGGGTTTATTTCCAAAGGGACCAACCATCGGCATGGCCCCAATCATGAGCATGTG
CACGGCAGACCACTGCTGGGGGAATTTGTCATGGACCAATCAGACAATCCCCTTGGTGCAGCCGTGACCCTGGCACA
TGAGCTGGGCCACAATTTCCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
AGGAGGCTGCATCATGAACGCTTCCACCGGTTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT
GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCA
GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
CTGCAATGCCACCACCTGTACCTGAAGCCGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGCCC
TCACTGCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT
CTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGACCAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA
GAGAGTCAATTCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCCTTTGCCAAATGCGAGAT
GAGAGATGCTAAATGTGGAAGAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC
CATAGAAAACAAACATCCCTCTGCAGCAAGGAGGCCGGATTCTGTGCGCGGGGACCCACGTGTACTTGGGCGATGA
CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGAGATGGAAAAATCTGCCTGAATCGTCAATGTCA
AAATATTAGTGTCTTTGGGGTTTACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA
CTGCCACTGCGAGGCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC
CATCCGGCAAGCAGAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG
ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCACTG
CTGCTGCAGAGGAGGTACGCGTCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT
TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA
CAGTGCAAGGAAGGGCAGCGACTTCCTGGTTGAGCTTCTGCTAAACATGGACATGCTTCAGTGCTGCTCCTGAG
AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC
ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGGCCAGTGTCCCTTTCCCCAGTGACACCTCAGCCT
TGGCAGCCCTGATGACTGCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAAT
AGCAGGGTTTTAGTTTTTAATTTATCAGAGACCTGCCACCCATTCCATCTCCATCCAAGCAAATGAATGGCAA
TGAAACAAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACCTCTGGCTCTTTGCTGTGGACATGCGTGACCAAGC
AGTACTCAGGTTTGGAGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCACCAACCCCTTCATTTAAACAAGTAAGAA
TGTTAAAAAGTGAAAACAATGTAAGACCTAACTCCATCCCCGTTGGCCATTACTGCATAAAATAGAGTGCATTT
GAAAT

FIGURE 88

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
><subunit 1 of 1, 735 aa, 1 stop
><MW: 80177, pI: 7.08, NX(S/T): 5
MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVVSASVRSGLWIPVKSFDSKNHPEVLNIRLQRE
SKELIINLERNEGLIASSFTETHYLQDGTVDVSLARNYTGHCCYYHGHVVRGYSDSAVSLSTCSGLRGLIVFENESYV
LEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLAAKNVFPFPSQTWARRHKRETLKATKYVELVIVADNREFQ
RQKGDLEKVKQRLIEIANHVDKFFRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNA
QLVSGVYFQGTITIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFNMNHDTLDRGCSCQMAVEKGGC
IMNASTGYPPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFQQKCGNRFVEEGEEDCGEPEECMNRCNA
TTCTLKPDCAVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGASPHCPANVYLHDGHSCQDQDGYCYNGICQT
HEQQCVTLWGPGAKPAPGICFERVNSAGDPYGNCGKVSFSSFAKCEMRDAKCGKIQCGGASRPVIGTNAVSIET
NIPQQGGRIICRGTHVYLGDDMPDPGLVLAGTKCADGKICLNRQCQNI SVFGVHECAMQCHGRGVCNNRKNCHC
EAHWAPPFCDKFGFGGSTDSGPIRQAEARQEAESNRERGGQGEVPGSQEHASTASLTLI
```

Signal peptide:
amino acids 1-28

FIGURE 89

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAGTGAGGCGGGCCGG
CGCGGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTTCCTA
GAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTA
CTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCA
TACCATGCCTGTGGTGTATATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGT
GATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTT
GGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGA
ATTGCTGTATTTTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTTAAGTTTGGCCGCACTGAAGACTTA
TGGCAGTGAACACATCTGATTTCCACAGCACAAACAGCCCTGCATGGGTTTGTTTGTTTTTTTACTGCTCACTCC
CAACCTTTTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACTAAATC
ACGAGAACACCTAAACAACAACCAAAAATCTATTTGTGGTATGCACTTGATTAACTTATAAAATGTTAGAGGAAAC
TTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATTTGTAAAAATAAAAAGAAATTACAAAAGAAATT
ATGGATTTGTCAATGTAAGTATTTGTCTATCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGT
GTTTATTCAAATGTGGTCTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTTCC
GTGGTCAAAATTTCTTCCTCACTATAATTGGTATTTACTTTTACCAAAAATTCTGTGAACATGTAATGTAACCTGGC
TTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCATGGTCCAGCCACCAGGCTCCCTG
TGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATTCCAAGGGCAGGAAGATGTGACTCAGCCATGACACG
TGGTTCTGGTGGGATGCACAGTCACTCCACATCCACCACTG

FIGURE 90

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDAAVIYPTMKDFNHSYHACGVIATIAFLMINAVSN
GQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEKDIVYPGIAVFFQNAFIFFGGLVFKFG
RTEDLWQ

FIGURE 91

CGACGCCGGCGTGATGTGGCTTCCGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGGCCGTCCTCTGCAAAGTTTA
CTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTCAAACGGCCCCCAGCGCCCCCTGGTAAC
TGACAAGCAGGCCAGGAAGAAGGTTCTCAAACAAGCTTTTTCAGCCAACCAAGTGCCGGAGAAGCTGGATGTGGT
GGTAATTGGCAGTGGCTTTGGGGGCCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCCTGGTGCT
GGAAACAACATACCAAGGCAGGGGGCTGCTGTGCATACCTTTGGAAAGAATGGCCTTGAATTTGACACAGGAATCCA
TTACATTGGGCGTATGGAAGAGGGCAGCATTGGCCGTTTTATCTTGGACCAGATCACTGAAGGGCAGCTGGACTG
GGCTCCCCCTGTCTCTCCTTTTGACATCATGGTACTGGAAGGGCCCAATGGCCGAAAGGAGTACCCCATGTACAG
TGGAGAGAAAGCCTACATTAGGGCCTCAAGGAGAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAA
GCTGGTTAAGGTGGTATCCAGTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTGCCCCGTGGTTTCAGCT
CCTCGACAGGTGTGGGCTGCTGACTCGTTTTCTCTCCATTCTTCAAGCATCCACCCAGAGCCTGGCTGAGGTCTT
GCAGCAGCTGGGGGCCCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCACTTACGGTGTCACCCCAA
CCACAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTACATGAAAGGAGGCTTTTATCCCCGAGGGGGTTC
CAGTGAAATTGCCTTCCACACCATCCTGTGATTGAGCGGGCTGGGGGGCGCTGTCTCTACAAAGGCCACTGTGCA
GAGTGTGTTGCTGGACTCAGCTGGGAAAGCCTGTGGTGTGAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTA
TTGCCCCATCGTGGTCTCCAACGCAGGACTGTTCAACACTTATGAACACCTACTGCCGGGAACGCCCGCTGCCT
GCCAGGTGTGAAGCAGCAACTGGGGACGGTGGCGCCGGCTTAGGCATGACCTCTGTTTTCTATCTGCCTGCGAGG
CACCAAGGAAGACCTGCATCTGCCGTCCACCAACTACTATGTTTACTATGACACGGACATGGACCCAGGCGATGGA
GCGCTACGTCTCATGCCAGGGAAGAGGCTGCGGAACACATCCCTCTTCTCTTCTCGCTTTCCCATCAGCCAA
AGATCCGACCTGGGAGGACCGATTCCAGGCCGGTCCACCATGATCATGCTCATACCCACTGCCTACGAGTGGTT
TGAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGCAGTGACTATGAGACCTTCAAAAACCTCTTTGTGGAAAGC
CTCTATGTGAGTGGTCTGAAACTGTTCACAGCTGGAGGGGAAGGTGGAGAGTGTGACTGCAGGATCCCCACT
CACCAACCAGTTCATCTGGCTGCTCCCCAGGTGCCCTGCTACGGGGCTGACCATGACCTGGGCCCGCTGCACCC
TTGTGTGATGGCCTCCTTGAGGGCCAGAGCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTCACCTG
TGGACTGGTGGGGGCCCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCCTGAAGCGGAACCTGTACTCAGACCT
TAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAATTAGTTCATCAGGGAGGAGTCAAGGAATTTG
CCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTGCATTAGTTCTTTCACGTATAAAGCACT
CTAATTTGGTTCTGATGCCGTAAGAGAGGCCCTAGTTTAAATCACAATTCGGAATCTGGGGCAATGGAATCACTGC
TTCCAGCTGGGGCAGGTGAGATCTTTACGCCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATA
GCTTGATGTCTCATGACGAGCGGGCTCTGCATCCCTCACCCATGCCTCCTAACTCAGTGATCAAAGCGAATATT
CCATCTGTGGATAGAACCCTGGCAGTGTGTGAGCTCAACCTGGTGGGTTCAAGTTCTGTCTGAGGCTTCTGCT
CTCATTCATTTAGTGTACGCTGCACAGTTCTACACTGTCAAGGGAAAAGGGAGACTAATGAGGCTTAACCTAAA
ACCTGGGCGTGGTTTTGGTTGCCATTCCATAGGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCAAGTGCT
CTTCAGGGGACAGGAAATGCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGT
TAGTAGGGTGCATGTGATGATCATATCCAATTATATGGAAGTCCCGGTCTGTCTTCTTATCATCGGGGTG
GCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGCCTTATCCACCAATACACAGG
GAAGGGTGTGACAGGGAAGGGTGACATCAGGAGTCAGGGCATGGACTGGTAAGATGAATACTTTGCTGGGCTGAA
GCAGGCTGCAGGGCATTCCAGCCAAGGGCACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGAGGGAAGT
ACATCAGAAAAGGGAAAGCCACGGAATGTGTGTGAAGCCAGAAATGGCATTTCAGTTAATTAGCACATGTGAG
GGTTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGTCTTTGGTATCAGACAT
ACGAAAGGTCTCTTTGTAGTTCGTGTTAATGTAACATTAATAAATTTATTGATTCCATTGCTTTAAAAA

FIGURE 92

MWLPLVLLLLAVLLLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKEARKKVLKQAFSANQVPEKLDVVVIGS
GFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIGRMEEGSIGRFILDQITEGQLDWAPLS
SPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQEEAIDKYIKLVKVVSSGAPHAILLKFLPLPVVQLLDRC
GLLTRFSPFLQASTQSLAEVLQQLGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIA
FHTIPVIQRAGGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLPGVK
QQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYDMDQAMERYVSMPREEAAEHIPLLFFAFPSAKDPTW
EDRFPGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNSFVEASMSVVLKLPQLEGKVESVTAGSPLTNQF
YLAAPRGACYGADHDLGRLHPCVMASLRAQSPIPNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLD
SRIRAQKKKN

FIGURE 93

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCTGTGGCAGCAGTGGCGGCGATGTTTGTGGCTCGGGATGG
GTCCAGGATGTTACTCCTTCTTCTTTTGTGGGTCTGGGCAGGGGCCACAGCAAGTCGGGGCGGGTCAAACGTT
CGAGTACTTGAAACGGGAGCACTCGCTGTGGAAGCCCTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAA
TCTGATGGGCAATGCCATGGTGATGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTT
GTGGAACCGGGTGCCATGTTTCTTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAATCCATGGACAAGGAAAGAA
GAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGCCTGTGTTTGGAAACAT
GGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAATGAGGAGAAGCAGCAAGAGCGGGTATTCCC
CTACATCTCAGCCATGGTGAACAACGGCTCCCTCAGCTATGATCATGAGCGGGATGGGCGGCCCTACAGAGCTGGG
AGGCTGCACAGCCATTGTCCGCAATCTTCATTACGACACCTTCTTGGTGATTCTGCTACGTCAAGAGGCATTTGAC
GATAATGATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGAGTCCGCCTGCCCCGCGG
CTACTACTTCGGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCAATTTCTTGAAGTTGTTGA
ACTGACAGTGGAGAGAACCCAGAAAGAGGAAAAGCTCCATCGAGATGTGTTCTTGCCCTCAGTGGACAATATGAA
GCTTGCTGAGATGACAGCTCCAAGTCCCGCCCTGAGTGGCCTGGCCCTCTTCCCTCATCGTCTTTTCTCCCTGGT
GTTTTCTGTATTTGCCATAGTCATTGGTATCATACTCTACAACAATGGCAGGAACAGAGCCGAAAGCGCTTCTA
CTGAGCCCTCCTGCTGCCACCCTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCCTGGCCTGAGCA
TGCAGCCTGGAGAGTGTTCCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTGTCACTGGAGTTTGAATGCAGG
GACCCCGCATTTCCCATGGTTGTGCATGGGGACATCTAACTCTGGTCTGGGAAGCCACCCACCCAGGGCAATGCT
GCTGTGATGTGCCCTTCCCTGCAGTCCCTCCATGTGGGAGCAGAGGTGTGAAGAGAAATTTACGTGGTTGTGATGC
CAAAATCACAGAACAGAATTTATAGCCAGGCTGCCGTGTGTTTGAAGTCTCAGAAGGCCCTTCTACTTCAGTTTT
GAATCCACAAAGAATTAACCACTGGTAACACACAGGCTTTCTGACCATCCATTCGTTGGGTTTTGCATTTGACC
CAACCTCTGCTTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAACTTCTTCCCTGCCTTACCTTCTTTCA
CTCCATTCAATGTCCTCTCTGTGTGCAACCTGAGCTGGGAAAGGCATTTGGATGCCTCTCTGTTGGGGCTGGGG
CTGCAGAACACACCTGCGTTTCACTGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTG
TTCCCTAGCATGGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTGAA
GTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATGGATTAGCTGTGCAAC
TGACCAGCTCCAGGTTTGATCAAAACCAAAAGCAACATTTGTGATGTGGTCTGACCATGTGGAGATGTTTCTGGAC
TTGCTAGAGCCTGCTTAGCTGCATGTTTGTAGTTACGATTTTGGAAATCCCACTTTGAGTGTGAAAGTGTAAAG
GAAGCTTTCTTCTTACACCTTGGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTTCTTAATGGACAA
GAGACAGTTGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCTGGAAGAGTTCACTG
TCATTGAGCAGCACAGCCTGAGTGTGGCCTCTGTCAACCTTATTCCACTGCCTTATTGACAAGGGGTACAT
GCTGCTCACCTTACTGCCCCTGGGATTAAATCAGTTACAGGCCAGAGTCTCCTTGGAGGGCTGGAAGTCTGAGTC
CTCCTATGAACCTCTGTAGCCTAAATGAAATTTCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCG
GCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLSDGSRMLLLLLLLGSGQGPGQVAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLM
GNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFQKIHGQKKNLHGDGLAIWYTKDRMQPGPFVFGNMDK
FVGLGVFVDTPNEEKQQERVFPYISAMVNNGSLSYDHERDGRPTELGGCTAIVRNLYDFTFLVIRYVVRHLLTIM
MDIDGKHEWRDCIEVPGVRLPRGYFSGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLLPSVDNMKLP
EMTAPLPPLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY
```

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

FIGURE 95

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACACACATCCCCAAGA
ACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTCGCTTGTCATCTCCCTCCCGGGGGAG
CCGGCGCGCGCTCCCACCTTTGCCGCACACTCCGGCGAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGA
ACTCGGATTGCAGCTCTGAACCCCCATGGTGGTTTTTTTAAACACTTCTTTTCTTCTTCTCCTCGTTTTGATTGC
ACCGTTTTCCATCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTTGGCTTGCCATCGTCCA
TCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGGCTGGCAGAAGGGGGTG
ACGCTGGGCAGCGCGAGGAGCGCGCCGCTGCCTCTGGCGGGCTTTTCGGCTTGAGGGGCAAGGTGAAGAGCGCAC
CGGCCGTGGGGTTTACCGAGCTGGATTTGTATGTTGCACCATGCCCTTCTTGATCGGGGCTGTGATTCTTCCCT
CTTGGGGCTGCTGCTCTCCCTCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTA
CGGTGCCAAGGGATTTCAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTGTCTCTCA
GGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAACCTCGAATTTGAAAACCTTGT
GGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGGCATAAGAAATTTGACGAATTTTCCGAGAGCT
CCTGGAGAATGCAGAAAAGTCACTAAATGATATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAAATTCAGA
AGTCTTCCAGGACCTCTTCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAA
TGACTTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCTCAGTATCACTTCAGTGAAGACTACCT
GGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCCGAAACTGAAGATTTCAGGTTAC
CCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTGACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAA
GGTCAGCCCAACCCAGGGTGTATCCGTGCCCTCATGAAGATGCTGTACTGCCCATACTGTGCGGGGCTTCCCAC
TGTGAGGCCCCTGCAACAACACTACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGA
GTGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACATTGAGTCGGTCAT
GGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAAACAGCATGCAGGTGTCTGCAAAGGT
CTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCCCTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATAC
ACGTTTCAGGCCCTACAATCCTGAGGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGCTGGTTCACAGA
CATAAAAGAGAAATGAAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGCGT
GACAGCGGGCAGCTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTTGCTGAGATCATGAA
TGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACATCACTCGGCCTGACACTTTCATCAGACA
GCAGATTATGGCTCTCCGTGTGATGACCAACAACTAAAAAACGCTTACAATGGCAATGATGTCAATTTCCAGGA
CACAAGTGATGAATCCAGTGGCTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCCACGGAGTTTGAGTT
TGTCACCACAGAGGGCCCCCGCAGTGGATCCCCGACCGAGAGAGGTGGACTCTTCTGCAGCCAGCGTGGCCACTC
CCTGCTCTCCTGGTCTCTCACCTGCATTGTCTTGGCACTGCAGAGACTGTGCAGATTAATCTTGGGTTTTTGGTCA
GATGAAACTGCATTTTAGCTATCTGAATGGCCAACCTCACITCTTTTCTTACACTCTTGGACAATGGACCATGCCA
CAAAAACCTTACCGTTTTCTATGAGAAGAGAGCAGTAATGCAATCTGCCTCCCTTTTTTGTTCCTCCAAAGAGTACC
GGGTGCCAGACTGAACTGCTTCTCTTCTTTCAGCTATCTGTGGGGACCTTGTTTATTCTAGAGAGAATTCTTA
CTCAAATTTTTTCGTACCAGGAGATTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAATCTCACGTT
GTGAGGGTTTTTTTTTTCTCATTTAAAT

FIGURE 96

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLLSLPAGADV KARS CGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQEYTCCTTEMEDKL
SQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFRELL ENAEKSLNDMFVRTYGM LYMQNSEVFQDLFTELKRY Y
TGGNVNLEEMLNDFWARLLERMFQLINPQYHFSE DYLEC VSKYTDQLKPFGDVPRKLKIQVTRAFIAARTFVQGL
TVGREVANRVSKVSPTPGCIRALMKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAE
RLEGPFNIESVMDPIDVKISEAIMNMQENSMQVSAKVFGCGQPKPAPALRSARSAPENFNTFRFPYNPEERPTT
AAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDES VTAGTSNEEECWNGH SKARYLPEIMNDGLTNQINNPEVD
VDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSGSGSGCMDDVCPTFEFEFVTTEAPAVDPDRR
EVDSSAAQRGHSLLSWSLTCIVLALQRLCR
```

Signal peptide:
amino acids 1-23

FIGURE 97

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGATATTGACAAACTG
AAGCTTTCTGCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGACAGCTTTAGTGGCCGGCCGGCCGCTC
TCATCCCCCGTAAGGAGCAGAGTCCTTTGTACTGACCAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAA
TGGGAAGGTTTTATTGAAAACACAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTG
CAGAAATTTTATCCAACCTTTGTTTGAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTTCAT
AGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGCCATTCAAAGATGAATT
TCATTCACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCAAATGCTGGTTCTCATGATAATGGCAGCCA
GTTTTTCTTCACTGGGTCGAGCAGATGAACCTAACAAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATAC
AGTATATAACATGTTGCGACTGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAA
AAGCTGTGAGGTTTTGTTTAATCCTTTTGATGACATCATTTCCAAGGGAAATTAAGGCTGAAAAAGAGAAACC
AGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTTTCAATTTGGAGAGGAAGCTGA
GGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAGGGCAAAGCAAAAGTAGTCATGACTTGCTTAA
GGATGATCCACATCTCAGTTCTGTTCCAGTTGTAGAAAGTGAAAAGGTGATGCACCAGATTTAGTTGATGATGG
AGAAGATGAAAGTGACAGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAA
AAAATTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATCAGTCAGCCG
CAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAAAACGGGAACCTTTAGCAGCAAAACAAAAAAGTAGAAAA
TGCAGCAAAACAAGCAGAAAAAGAAGTGAAGAGGAAGAAGCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAG
AGAAAAGCAAAAGTATGAAGCTTTGAGGAAGCAACAGTCAAAGAAGGGAACTTCCCGGGAAGATCAGACCTTGC
ACTGCTGAACCAGTTTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCTGAAACAGA
AGTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGTGAAAGATGCAAG
CATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGAATAAAAGAAGGAGGGAAGAAAGCAA
AAAGCTGATGAGAGAGAAAAAAGAAAGAAGATATAAATGAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCT
ACAATGGCCTTGTAACAGCCATTGTTCCCAACAGCATCATTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTT
GTCTGGTTTTTGAACCAATTATCTTGTGTTTGCATTTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGGTA
CATGTGTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCTTCCACAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFIVQGGDPTGTGSGG
ESTYGAFFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELNNKHTIFGKVTGDTVYNMLRLSEVDID
DDERPHNPHKIKSCEVLFPNPFDDIIPREIKRLKKEKPEEEVKKLKPKGTKNFSLLSFGEEAESEEEVNRVSQSM
KGKSKSSHDLKDDPHLSSVPVVESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKS
GEGEVEKKSVSRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAEAPPDGAVAEYRREKQKYEALRKQ
KKGTSREDQTLALLNQFKSKLTQAIATPENDIPETEVEDDEGWMSHVLQFEDKSRKVKDASMQSDTFEYDPR
NPVNRKRREESKKLMREKKERR
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

FIGURE 99

CTTTTCTGAGGAACCACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTATCCTCCTGGTACTA
TTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTACCGCTGAAGTCTGTGCCACACACACA
ATTTCAACCAGGACCCAAAGGAGATGATGGTGAAAAAGGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGA
CGCATGGGGCCGAAAGGAATTAAAGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCC
ATTGGGAAGAAGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACTGTC
TGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCTCGGCTCAAGACATCTATGAAG
TTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAATTCTACTACATCGTGCAGGAAGAGAAGAAC
TACAGGGAATCCCTAACCCTGCAGGATTCCGGGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACA
CTCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTTCCGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGA
CAGTACATGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGACCCCTAT
GGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTACTTT
GTCTGTGAGTTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCTACGTATTGCTATTTTCCTGTGACCGTCATTA
CAGTTATTGTTATCCATCCTTTTTTTCCTGATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAAATGCTAA
ACTGAGGTATGGAGCCTCCATCATCAAAAAAAAAAAAAAAAAA

FIGURE 100

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPGEEGKHGKVGRMGPKGI
KGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGGRYRKFGVQLDISIARLKTSMKFVKNVIA
GIRETEEFYIYVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDN
TPLQNYSNWNEGEPSDPYGHEDCVEMLSGRWNDTECHLTMYFVCEFIKKKK
```

Signal peptide:
amino acids 1-25

FIGURE 101

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGACCCAGAGCTTCTCC
AGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCCTTAACCTTCCCTCCGCGGGGCCAGCCACCTTCGGGAGTCCGGGTT
GCCCACCTGCAAACCTCCGCCCTTCTGCACCTGCCACCCCTGAGCCAGCGCGGGCCCCCGAGCGAGTCA**ATG**GCCA
ACGCGGGGCTGCAGCTGTTGGGCTTCATTCTCGCCTTCCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGC
CCCAGTGGAGGATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGATGT
CCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGC
AAGCAACCCGTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCCTTGGCATGA
AGTGTATGAAGTGCTTGGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGTGCGATATTTCTTC
TTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAATCGTTCAAGAATTCATGACCCCTATGA
CCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCGCCTTCTGG
GAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCAAGGCCCTATCCAAAACCTG
CACCTTCCAGCGGGAAAGACTACGTG**TGA**CACAGAGGCCAAAAGGAGAAAAATCATGTTGAAACAAACCGAAAAATGG
ACATTGAGATACTATCATTAACATTAGGACCTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAAC
AAACAAACAAACAAAAAACCCATGTGTTAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTC
CTCAATATAGGAGGGAAGATTTTTCATTTGTATTACTGCTTCCCATTGAGTAATCATACTCAAATGGGGGAAGG
GGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAAATAGACAGTAAAATACTATTCT
CATTTATGTTGATACATAGCATACTTAAAATATCTCTAAAATAGGTAAATGTATTTAATTCATATTGATGAAGATG
TTTATTGGTATATTTTCTTTTTCGTCTTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGC
TTTGGGTGCCCTTGGCACAAGACCTAGCCTAATTTACCAAGGATGAATTCCTTCAATTCCTCATGCGTGCCCTTT
TCATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTATTTGTTTTGTGTT
TCATTGGTCTCTATCTCCTGAATCTAACACATTTTCATAGCCTACATTTTAGTTTCTAAAGCCAAGAAGAATTTAT
TACAAATCAGAACTTTGGAGGCAAATCTTCTGCATGACCAAAGTGATAAATTCCTGTTGACCTTCCCACACAAT
CCCTGTACTCTGACCCATAGCACTCTTGTGTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCC
CCAGGTGTGTAACACAACCTTATTGATTGAATTTTAAAGCTACTTATTCATAGTTTATATATCCCCCTAAACTAC
CTTTTTGTTCCCCATTCCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTATATCTTCCCTAATAAG
GTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATAATCTGGTGACAAATATTCTCTGTAGC
TGTAAGCAAGTCACTTAATCTTCTACCTCTTTTTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAG
AAGAGGTAGTGTGAATATTAATTAGTTTATATTACTCTTATTTCTTTGAACATGAACATATGCCTATGTAGTGTCTT
TATTTGCTCAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACTACACACGTACCTTCATGTGATTCACTG
CCTTCTCTCTCTTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCATGTGGTTCAAGTGCCTTCCT
CTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATACCTTCATGTGGCTCAGTGCCTTCTCTCTCTA
CCAGTCTATTTCCATTCTTTTCCAGCTGTGTCTGACATGTTTGTGCTCTGTTCCATTTTAACTGCTCTTACTTT
TCCAGTCTGTACAGAATGCTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAG
ACCTGGATTTGAGTCTTGGTGTATCAATCACCGTCTGTGTTTGAAGCAAGGCATTTGGCTGCTGTAAGCTTATTG
CTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATGTTGTGGGGATCCAGTGAGATA
GAATACATGTAAGTGTGGTTTTGTAAATTTAAAAGTGCTATACTAAGGGAAAGAATTGAGGAATTAACTGCATAC
GTTTTGGTGTGCTTTTCAAATGTTTGAAAAATAAAAAAATGTTAAG

FIGURE 102

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFI LAF LGWIGAIVSTALPQWRIYSYAGDNIVTAQAMY EGLWMSCVSQSTGQIQCKVFDSLNLSS
TLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDEDEVQKMRMAVIGGAI FLLAGLAILVATAWYGNRIVQEFYD
PMTFVNARYEFGQALFTGWAAASLCLLGALLCCSCPRKTTSYPTPRPYPKPAPSSGKDYV
```

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

FIGURE 103

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCCAGCCTGCAGGGCTGATAAGCGAGG
 CATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGCGCGCAGTAGAGCAGCAGCACAGGCGC
 GGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATGTTGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACC
 GCGCGCCGCGCGCTGGCTGTGCGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTTCTCCTCGGCTTCTCTTCTC
 GGGTGGTTTTATAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTCCTGGATGAA
 TTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGCAGGAACAGAACAAAAC
 TTTTCAGCTTGCAAAGCAAATTCAATCCAGTGGAAAGAATTTGGCCTGGATTCTGTTGAGCTAGCTCATTATGAT
 GTCCTGTTGTCTACCCAAATAAGACTCATCCCACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTC
 AACACATCATTATTTGAACCACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTTCAGTGCCTTC
 TCTCCTCAAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAAATTGGAA
 CGGGACATGAAAATCAATTGCTCTGGGAAAATTTGTAATTGCCAGATATGGGAAAGTTTCAGAGGAAATAAGGTT
 AAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCCGACCCTGCTGACTACTTTGCTCCTGGGGTG
 AAGTCTATCCAGACGGTTGGAATCTTCTGGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGTG
 GGAGACCTCTCACACCAGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAAATTGCAGAGGCTGTTGGTCTT
 CCAAGTATTCCTGTTTCATCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAGCACCA
 CCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTACTGGAACTTTTCTACA
 CAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGACGAGAATTTACAATGTGATAGGTAATCTCAGAGGA
 GCAGTGGAAACCAGACAGATATGTCATTCTGGGAGGTCACCGGACTCATGGGTGTTTGGTGGTATTGACCCCTCAG
 AGTGGAGCAGCTGTTGTTTCATGAAATTTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGA
 ACAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTCTACTGAGTGGGCAGAGGAGAATTCA
 AGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTATAGAAGGAACTACACTCTGAGAGTT
 GATTGTACACCGCTGATGTACAGCTTGGTACACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAA
 GGCAAATCTCTTTATGAAAGTTGGACTAAAAAAAGTCTTCCCCAGAGTTTCAGTGGCATGCCAGGATAAGCAA
 TTGGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAAATGCTTCAGGCAGAGCACGGTATACTAAA
 AATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATATGAGTTGGTGGAAAAG
 TTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTCCAGGAGGGATGGTGTGTTGAGCTAGCCAAT
 TCCATAGTGTCTCCCTTTTGATTGTGAGATTATGCTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATT
 TCTATGAAACATCCACAGGAAATGAAGACATACAGTGTATCATTGATTCACTTTTCTGTCAGTAAAGAATTTT
 ACAGAAATGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCAATAGTATTAAGAATGATG
 AATGATCAACTCATGTTTCTGGAAAGAGCATTTATTGATCCATTAGGGTTACCAGACAGGCCCTTTTATAGGCAT
 GTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTCATTCCCAGGAATTTATGATGCTCTGTTTGAT
 ATTGAAAGCAAAGTGGACCTTCCAAGGCCCTGGGAGAGAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTG
 CAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCTTAAGAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGGTA
 TGTCACCTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAAAATTGGTATATTTGAAATAAAGTTGAATATT
 ATATATAA

FIGURE 104

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756
><subunit 1 of 1, 750 aa, 1 stop
><MW: 84305, pI: 6.93, NX(S/T): 10
MWNLLHETDSAVATARRPRWLCAGALVLAGGFLLGFLFGWFIKSSNEATNITPKHNMKAFLDELKAENIKKFLH
NFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEP PPPG
YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSCGKIVARYGKVFRGNKVKNQLAGAKGV
ILYSDPADYFAPGVKSYPDGWNLPGGGVQGRNINLNLGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYY
DAQKLLLEKMGGSAAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKMHISTNEVTRIYNVIGTLRGAVEPDRYVILG
GHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSRLQERGVAI
NADSSIEGNYTLRVDCTPLMYSLVHNLTKEKSPDEGFEGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFF
QRLGASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFE LANSIVLPFDCRDY
AVVLRKYADKIYISMKHPQEMKTYSVSFDLSFAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAF
IDPLGLPDRPFYRHVIYAPSSH NKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA
```

Signal sequence:
amino acids 1-40

N-glycosylation sites.
amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340, 459-463,
476-480, 638-642

Tyrosine kinase phosphorylation sites.
amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.
amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341, 360-366,
427-433, 529-535, 707-713

FIGURE 105

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAGTGTATTTACTGCTGCGTTTTATGTTGGGAATT
CCTCTCCTATGGCCTTGCTCTTGGAGCAACAGAAAACCTCTCAAACAAAGAAAGTCAAGCAGCCAGTGCGATCTCAT
TTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTTTTTGTACCAGAGGAAATGAATACGACTAGTCATCACATC
GGCCAGCTAAGATCTGATTTAGACAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGT
ACTTTTATCATTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTCTAC
ATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGAGTTTGTTCATCAAAGTT
TCGATATCAATGACAAATGAACCAAAATTCCTAGATGAACCTTATGAGGCCATTGTACCAGAGATGTCTCCAGAA
GGAACATTAGTTATCCAGGTGACAGCAAGTGATGCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTAC
AGCTTACTTCAAGGCCAGCCATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGAT
AGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTGTCTGGA
ACAACAAGTGATTAAATTAACCTTTCAGATGTTAATGACAATAAGCCTATATTTAAAGAAAGTTTATACCGCTTG
ACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAAT
GCAGAAATGGATTACAGCATTGAAGAGGATGATTCGCAAAACATTTGACATTATTACTTAATCATGAAACTCAAGAA
GGAATAGTTATATTAAGAAAGAAAGTGGATTTTGTAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAGAAC
CATCATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAAGATCCAGGTGGAAGAT
GTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGAAGAAACCCACAGGGATCATT
GTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAATCTCCTATCAGGTATTCTATTACTAGGAGCAAAGTG
TTCAATATCAATGATAATGGTACAATCACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTA
AGTATTACAGCCACAGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATC
AATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCTGGTCAGGTAATT
CAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTTTACTTTAATCTATCTGTAGAAGAC
ACTAACAATTCAGTTTTTACAATCATAGATAATCAAGATAACACAGCTGTCATTTTGACTAATAGAACTGGTTTTT
AACCTTCAAGAAGAACCTGTCTTCTACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACA
AACACCCTTACCATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTGTG
CTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATATTTGGGTTTTATTTTT
TTGACTTTGGGTTTTAAACAACCGGAGAAAACAGATTCTATTTCTTGAGAAAAGTGAAGATTTTCAAGAGAGAATATA
TTCCAATATGATGATGAAGGGGGTGGAGAAGAAGATACAGAGGCCCTTTGATATAGCAGAGCTGAGGAGTAGTACC
ATAATGCGGGAACGCAAGACTCGGAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTT
GGCCCCGACAGTGCCATATTCAAGAAATTCATTCTGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTGCCCT
CCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCCCTGAGCTCCTTAGAATCA
GCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTTGGGACCTCGCTTTAAAGATTAGCATGCATG
TTTGGTTCTGCAGTGCAGTCAAAATAATTAGGGCTTTTTACCATCAAAATTTTTAAAGTGCTAATGTGTATTTCGA
ACCCAATGGTAGTCTTAAAGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGA
TTTCCCTGGAGTAAATACTCCATGGTTATTTTAAGCTACCTACATGCTGTCATTGAACAGAGATGTGGGGAGAAA
TGTAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATGTAGGAAGATATTAAGTAGA
TGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATATCATTATTTACTTAGGAAAAGAGTAAAAATACCAA
CGAGAAAATTTAAAGGAGCAAAAATTTGCAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTAT
CATATTGACATGAAAATTGAAAATGTATAGTCAGAGAAAATTTTCATGAATTATTCATGAAGTATTGTTTCTTT
ATTTAAA

FIGURE 106

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNN
SFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSDINDNEPKFLD
EPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQ
AKDMIGQPGALSGTTSVLIKLSDVNDNKPFIKESLYRLTVSESAPTGTSSIGTIMAYDNDIGENAEMDYSIEEDDS
QTFDIITNHETQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPY
VFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISAWYNLSITATEKYNIEQ
ISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESEIEHHFYFNLSVEDTNNSSFTIIDNQ
DNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIA
ILICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTS
AEIRSLYRQSLQVGPDSAI FRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESASVSDQDESYDYL
NELGPRFKRLACMFGSAVQSNN
```

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518, 516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 107

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCACATGATTTGACTCAGAGATT
 CTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCCCAAATGCTATATCTATTAGGGGCTC
 TCAAGAACAATGGAATATCATCCTGATTTAGAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCT
 CAAAGCAATACCAGGATAGCTGTTGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCT
 GTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCCAGC
 CCTTGTCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTAGCATGTCACTAAATTCCTGGGATGGA
 AGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAGACAGCTCAAATGAATTGGGATTTATAGTA
 AAACAAGTGTCTTCCCAACCTGATAATTCATTTTGGATAGGCCCTTCTCGGCCCCAGACTGAGGTACCATGGCTC
 TGGGAGGATGGATCAACATTCTCTTAACCTATTTTCTAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCA
 AATTGTGTATGGATTACAGTGTGAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGTGAGAAG
 AAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAAATATGTGAGGTAGTAAGGAGGACAGAAAACAGAA
 CAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATGTTTAGAGAGCTTGGCCAACTGTAATCTTAACC
 AAGAAATTGAAGGGAGAGGCTGTGATTTCTGTATTTGTGACCTACAGGTAGGCTAGTATTATTTTTCTAGTTAG
 TAGATCCCTAGACATGGAATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTTTTGTAGATAGG
 GTCTCACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGCCTCAGCCCC
 TCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTGTTTTTTGTAGAGACTGGGTTTT
 GCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAGTGATCTGCCCCGCTTGGCCTCCCAAAGTGTGGGA
 TTACAGATGTGAGCCACCACACCTGGCCCCAAGCTTGAATTTTCACTCTGCCATTGACTTGGCATTTACCTTGGG
 TAAGCCATAAGCGAATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGG
 TGTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAAGTGAAGGTGAAATATATTTCTGAAT
 AGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTTATTATTTTTCATCAGTATGATCATAA
 TTATGATTATCATCTTAGTAAAAAGCAGGAACCTCACTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATC
 TGCCATATCTCTAATAGAATCTTTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTCGCTCTTGTTGCCAGGCTG
 GAGTGCAACGGCACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCCTCTGCCTCAGCCTCC
 CAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGTAGAGACAGGGTTTCT
 CCATGTGGTTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGCCTGCCTCGGCCTCCCAAGTGTGGGATT
 ACAGGCGTGAGCCACTGCACCCAGCCTAGAATCTGTATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAA
 GTTTTCTGCTTTTTAAATACAAAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACC
 TCATTGGAACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTGTGATGTACTGTTTTACAATTTTTACCAT
 TTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATGTGCTGATTTGCTTATTT
 TTTTCATACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATATTTCTGTATTACTAGGGAGGCATTTACAGTC
 CTCTAATGTTGATTAATATGTGAAAAGAAATTTGTAACCAATTTTACTAAATTATGCAGTTTAAATGGATGATTTT
 ATGTTATGTGGATTTCAATTTCAATAAAAAAACTCTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 108

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
<subunit 1 of 1, 201 aa, 1 stop
<MW: 22563, pI: 4.87, NX(S/T): 1
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAVVLGTMGVLSSPCP
PNWIIYEKSCYLFMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQVSSQPDNSFWIGLSRPQTEVPWLWED
GSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQLCSVPSYSICEKKFSM
```

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

FIGURE 109

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCACA
ATATCTTAACCTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAGAC
CTACCTACCCGTACGCATACATACATATGTGTATATATATGTAACTAGACAAAGATCGCAGATCATAAAGCAAG
CTCTGCTTTAGTTTCCAAGAAGATTACAAAGAATTTAGAGATGTATTTGTCAAGATCCCTGTGATTCATGCCCT
TTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCCTTTGGTTTGGGGACATTATGATTTGTGTAAGACTCAGAT
TTACACGGAAGAAGGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAATATCTGAA
AGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCCTCCTGAGACGTTCTGTGCAATGGGCAATCCCTACAT
GTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGATTTTGAAGGAAG
ACATCCCTCCACATTTTGGCAGTCTGCCACTTGGGAAGGAGTATCCCAAGCCTCTCCAGGTTAACATCACTCTGTC
TTGGAGCAAAACCATTTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACCAAATGATCCT
GGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTAGATGCTTTTCA
CATGGATCCTAAATCCGTGAAGGATTTATCACAGCATAACGGTCTTAGAAATCATTGACAGAAGAGTACTCAAC
AGGGTATACAACAAATAGCAAAATAATCCACTTTTGAATCAAAGACAGGTTGCGCTTTTGTGGACCTCGCCT
ACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAAACTCAGAGATTTCTTTACAGTCACAGACCT
GAGGATAAGGCTGTTAAGACCAGCCGTGGGGAAATATTTGTAGATGAGCTACACTTGGCACGCTACTTTTACGC
GATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCTCCATGCCACTGTATGTGTGTATGACAACAGCAA
ATTGACATGCGAATGTGAGCACAACTACAGGTCCAGACTGTGGGAAATGCAAGAAGAATTATCAGGGCCGACC
TTGGAGTCCAGCTCCTATCTCCCCATCCCCAAAGGCACTGCAAATACCTGTATCCCCAGTATTTCCAGTATTGG
TACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGACGTGCCACAACAACGTGCGCTGCCTGTG
CCCGGCCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGCAGCTGCGGCTCCGACTCTGG
CCAGGGCGCGCCCCCGACGGCACCCACGCGCTGCTGCTGCTGACCACGCTGCTGGGAACCGCCAGCCCCCTGGT
GTTCTAGGTGTACCTCCAGCCACACCCGACGGGCTGTGCGGTGGGAAGCAGACACAACCCAAACATTTGCTA
CTAACATAGGAAACACACACATACAGACACCCCACTCAGACAGTGTACAAACTAAGAAGGCCCTAACTGAACATA
GCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTCTGACTCCAGAGGAGTTGGCAGCTG
TTGATATTATCACTGCAAATCACATTGCCAGCTGCAGAGCATATTGTGGATTGGAAAGGCTGCGACAGCCCCCA
AACAGGAAAGACAAAAACAAACAAATCAACCGACCTAAAAACATTGGCTACTCTAGCGTGGTGCGCCCTAGTAC
GACTCCGCCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTGAGGTGCATTGTGGGCATAAGGAAATCTGT
TACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAACCTGTGCTTTAGTGAACGTTGCTCTGTAA
CCCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACATGTGTAAACAGCCCCCTCTAAAAGCGCAAG
CCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCAGACACACCCACTATACAAGAGTGGCTATA
GGAAAAAGAAAGTGTATCTATCCTTTTGTATTCAAATGAAGTTATTTTCTTGAACACTGTGAATATGTAGATT
TTTTGTATTATTGCCAATTTGTGTTACCAGACAATCTGTTAATGTATCTAATTCGAATCAGCAAAGACTGACATT
TTATTTTGTCCCTCTTTCTGTTCTGTTTCACTGTGCAGAGATTTCTCTGTAAGGGCAACGAACGTGCTGGCA
TCAAAGAATATCAGTTTACATATATAACAAGTGTAAATAAGATTCCACCAAAGGACATTCTAAATGTTTCTTGT
GCTTTAACTGGAAGATTTAAAGAATAAAAACTCCTGCATAAACGATTTTCAAGAAATTTGTATTGCAATTTCTTA
AGATGAAAGGAACAGCCACCAAGCAGTTTCACTCACTTTACTGATTTCTGTGTGGACTGAGTACATTCACTG
ACGAATTTAGTTCCAGGAAGATGGATTGATGTTCACTAGCTTGGACAACCTCTGCAAAATATGAGACTATTTCC
ACTTGGGAAAAATTACAACAGCAAAAAA

FIGURE 110

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLVKLDPPDITCGDP
PETFCAMGNPYMCNNECDASTPELAHPPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI
TFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLHQHTVLEIICTEYSTGYTTNSKIIHFEI
KDRFALFAGPRLRNMASLYGQLDTTKKLRDFFTVDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCN
LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPKPGTANTCIPSISSIGTNVCDNELLHCQN
GGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQAPPHGTPALLLTLLGTASPLVF

FIGURE 111

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCTGCGCCTGCACCGCGTAGACCGAC
CCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCCGACCGGTCCCGCCTTTTTGTAAAACT
TAAAGCGGGCGCAGCATTAACGCTTCCCCGCCCCGGTGACCTCTCAGGGGTCTCCCGCCAAAGGTGCTCCGCGCG
TAAGGAACATGGCGAAGGTGGAGCAGGTCTGAGCCTCGAGCCGACGACGAGCTCAAATTCGAGGTCCCTTCA
CCGATGTTGTCAACACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTACAG
CACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATTAATGTATCTGTGATGT
TACAGCCTTTTCGATTATGATCCCAATGAGAAAAAGTAAACACAAGTTTATGGTTTCAGTCTATGTTTGCTCCAACGT
ACACTTCAGATATGGAAGCAGTATGGAAGGAGGCAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGT
TTGAATTGCCAGCAGAGAATGATAAACACATGATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAAGA
CAGAAACACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGGAAGAAT
GTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAAACAAGCAGTTCAAGGAAGAAGATGGACTGCGGA
TGAGGAAGACAGTGCAGAGCAACAGCCCCATTTAGCATTAGCCCCAACTGGGAAGGAAGAAGGCCTTAGCACCC
GGCTCTTGGCTCTTGGTGTGTTTTGTTCTTTATCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATG
CACAGGATGGTAAATTTGGATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGA
AATTAATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACACAGATACACA
CACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTGATTGAGGGGGAAAAAGAATGAT
CTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAATGGCATATTGTAATGTCAATTTTAAACATTGGTAGG
CCTTGGTACATGATGCTGGATTACCTCTCTTAAATGACACCCCTCCCTCGCCTGTTGGTGTCTGGCCCTTGGGGAG
CTGGAGCCCAGCATGCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCT
GCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAA
TTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGA
AATAAATGGCAGTGCTTTGTTCACCTTAAAGGGACCAAGCTAAATTTGTATTGGTTTCATGTAGTGAAGTCAAAGT
TTATTCAGAGATGTTTAAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGT
ACAGTTAATGCTGCGTGCTGCTGAACCTCTGTTGGGTGAACCTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCTGT
CTCTGGAGAGTCTGGTCATGTGGAGGTGGGTTTATTGGGATGCTGGAGAAGAGCTGCCAGGAAGTGTTTTTCT
GGGTCAGTAAATAACAACCTGTCATAGGGAGGGAAATTTCTAGTAGTGACAGTCAACTCTAGGTTACCTTTTTTAA
TGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATACCACCTCTCAACCATTACTCACACTTCAGCGCCAGGTCC
AAGTCTGAGCCTGACCTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAA
GCGAGGGCACCAAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTACTAGTT
GAGAGTTTGAAGTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAA
AGAAAAATTATAATAAAGCCCCAAAATTAAGAAAA

FIGURE 112

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFTDVVTNLKLGNPTRNVCFKVKTTAPRRYCVRPNNGIIDAGASINVSVMLOP
FDYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRVCFELPAENDKPHDVEINKIISTTASKTET
PIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREENKQFKEEDGLRMRKTVQSNSPISALAPTGKEEGLSTRLL
ALVVLFFIVGVIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

FIGURE 113

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCCGGCTAAGATTGCTGAGGAGGCGGCGGGTAGCTGGCA
 GCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCCTCATGACTTCTCTTGTGGACCATGTCCTCGTGATCTT
 TTTTGCCGTGCGTGGTACGGGTAAGGGATGGACTGCCCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTT
 TTTGGAATGGAGGAGACGGCTCAAGAGTTTAGCCTTGCGACTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGG
 TTGTGACTTTAGTATACATTTTTCTTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCACG
 AGCCATGGCCTTCTGCTTCCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCCATGACACTACCTGCATTGGCCT
 AGCCTCCAGGCCATACGCTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATTTTAACTATGTAAG
 TTCCTCTCAGATGGAGTGCAGCTTGGAATAATTCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCT
 GGAGGACACAGATGTGGCAATGGGGTGATGAATGGTCACACACCGATGCACCTGGAGCCTGCTCCTAATTTCCG
 AATGGAACCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCTCATTCCG
 AGGAGTTACCTTGACAGAACATTTCTTACAGGATCCAAGGAGCTGGTTCTGCTGGTTGGACCAAACCTCGTGAGC
 CAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCATCCGGGAGCAGTGATGTCAAACCTCTGCTGCTG
 GGGAAATCTCATCAGCAGGGAGCCTGTGGAAGGGCATGTGAGTGAATCTGGGAATGGCTGGATTTCGGAACA
 TCTGCCCATGTGTATTGATGGCAGAGCTGTTGCCACAAAGCGCCTTTTATTTAGGGTAAAAATTAACAAATCCATT
 CTATTCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTTACATTTATATGATTCTGGGGTTGCTTCAGAA
 GTGTTATTTTATGAATCATTATATGATTTGATCCCCAGGATTCTATTTTGTTTAATGGGCTTTTCTACTAAAA
 GCATAAAATACAGGCTGATTTAGTCAGGGCAAAACCATTTACTTTACATATTCGTTTTCAATACCTTGCTGTTC
 ATGTTACACAAGCTTCTTACGGTTTTCTTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAAACAAAC
 TCAGTAGTACAACCTAACTTGTATAAAAGTGTGTAATAATGTATAGCCATTTATATCCTATGTATAAATTAAT
 GAGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAATAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 114

MSVIFFACVVRVVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHFSSFGDVACMAICS
CQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKWHFNYVSSSQMECSLEKIQEELKLQPP
AVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPV TALGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

FIGURE 115

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGACCCGACCTTAAAG
 AGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAAACGAGGCGGGTGGTGCCTGCCCTTTAAGGGCGGGGCGTCC
 GGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTCTGTGCGAGGCTGCGAGGAAAGGCCCCTAGGCTGGGT
 TGGGTGCTTGGCGGGCGGCGGCTTCCTCCCCGCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCT
 GAGCAGAGTATGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAG
 TGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTCAAGAAGCCT
 GCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGCGCTCGAGCTGTGCACCTTTACCCTG
 GCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCCTCGG
 AACTACTACATCCAGTGGCTCAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTG
 TCCCTCATCTTCCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAGGGTGTC
 CTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCTAGGTATGGTGTGGGTGGCA
 TCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCTATGACTTTTGGGAGTACTATCTCCCTACCT
 TACTCATGCATCTCCTTCTTGGGGTTCTGCTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCC
 GTCACTGGGAAGCTGCTAGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAG
 GAGGCAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTGCTACACAGA
 CAGGTCTGGCTCTGCGAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGCTTCAGCCTGGCAACGGAACCTG
 GGCTACCCCTGGCTATGCTGTGCTTGTGCTGCTGACGGGCCTGTCTGTGCTCATTGTGGCCATCCACATCCTG
 GAGCTGCTCATCGATGAGGCTGCCATGCCCCGAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAG
 CTGGGCTCCTTTGGTGCCGTATTGAGGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTTCTAT
 AGCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATTGGGAAGTGTGTC
 TGTCTCCTGGTCCTAAGCTCAGCACTTCTGTCTTCTCTGAACCTTGGGGCTCACTCGCTTTGACCTGCTGGGT
 GACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACATTGTGTTCTCTACAACGCAGCCTTTGCAGGCCCTCACC
 AACTCTGTCTGGTGAAGACCTTCACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCTTTGGGCTGGACAGACTG
 CCGCTGCCCCGTCTCCGGTTTTCCCCAGGCATCTAGGAAGACCCAGCACCAGTGAACCTCCAGCTGGGGGTGGGAAG
 GAAAAAAGTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGGACCTCAGGACCTGGA
 ATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATTGCATAATCTGAGCCAGAGTTTGGGACCA
 GGACCTCCTGCTTTTCCATACTTAACTGTGGCCTCAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGAT
 CCCAAATCTGTTTACACATCAATCTGCCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGA
 TGTGCAATAGGGTGGGGTAGGGGAGGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCCCTTGC
 CTCTGGCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGCTTTGGACCACCTGAAAGACCAAGGGGATAGG
 GAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGAAAAAA

FIGURE 116

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNKIALELCTFTLAIA
LGAVLLLPPFSIIISNEVLLSLPRNYIQWLNGSLIHGLWNLVFLFPNLSLIFLMPFAYFFTESEGFAGSRKGVLR
VYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTG
KLLVKPRILLEDLEEQLYCSAFEEAALTRRICNPTSCWLPLDMELLRQVLALQTQRVLLEKRRKASAWQRNLGYP
LAMLCLLVLTGLSVLIVAIHILELLIDEAAMPQGMQGTSLGQVSFSLGSGFAGAVIQVVLIFYIMVSSVVGIFYSSP
LFRSLRPRWHDAMTQIIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCL
LVKTFTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

FIGURE 117

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCTGCTGTCTCGCTG
CTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTG
TGCATCTCTGTGCCCTGCTCTTCTCCTACCCCGACAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG
TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGAGAGGTGGAAATGAGC
ACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC TGCTCCTTGGTGATCAGAGACGCGCAGATG
CAGGATGAGTCACAGTACTTCTTTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTTTCATGAACGATGGGTTC
TTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCAGGACCACAACACCGACCTCACCTGCCATGTGGAC
TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTTATC
AGCATTTACGTGACAACACGCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCCAAAA
GGCCAGTTCTGTGCCCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCAGAACAGA
GTCCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCA
GGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTGCAGTATCCT
CCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAAACAGGACAGTCTTGGAACCTTGGGAACGGCACGCTCTCTC
CCAGTACTGGAGGGCCAAAGCCTGTGCCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACC
CAGAGGGGACAGGTTCTGAGCCCTCCCAGCCCTCAGACCCCGGGTCTGGAGCTGCCTCGGGTTCAAGTGGAG
CACGAAGGAGAGTTTACCTGCCACGCTCGGCACCCACTGGGCTCCAGCACGCTCTCTCTCAGCCTCTCCGTGCAC
TATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTC
CTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCAGGTTTC
TCCCGGCACAGCACGATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAG
AAAGCCACACCAACAGTCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCAGAATCAAAGAAGAACCAGAAA
AAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCCAGGAGAGCCAAGAG
GAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCTGAGGCCCCGATGCCCAAGGGCACCCAG
GCGGATTATGCAGAAGTCAAGTTCCAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGG
TAGAGTAAGAGGTTGAAGATAACAGAGTGCAAAGTTTCCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT
CTCTTTCTCTCTCTTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATCCAGCACTTTGGGAG
GTTGAGGTGGGCAGATCGCCTGAGGTGCGGAGTTCGAGACCAGCCTGGCCAACCTGGTGAAACCCCGTCTCTACT
AAAAATACAAAAATTAGCTGGGCATGGTGGCAGGCGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAA
TCACTTGAACCTGGGAGACGAGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCG
AGACTCCATCTCAAAAAAAAAATCCTCCAATGGGTGGGTGTCTGTAATCCCAGCACTTTGGGAGGCTAAGGTG
GGTGGATTGCTTGAGCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCCATCTCTACAAAAATACA
AAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCAGCTGTGAGACATTTAAACCAGAGCAACTCCATCTGG
AATAGGAGCTGAATAAAATGAGGCTGAGACCTACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAG
GATGAGACAGGAGGTCCGTACAAGATACAGGTATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAACCA
ACCAAATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTCTCACTGCTACACTCTTGACAGCAC
CATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCAAAAGGGGGAGGAATGAATAAT
CCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAAGTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGT
CTATGGAGTAGCCATTCTTTTGTTCCTTTACTTTCTTAATAAACTTGCTTTACCTTAAAAAAA

FIGURE 118

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFYSYPRQDWTGSTPAYGYWFKAVTETTTKGAPVAT
NHQSREVEEMSTRGRFQLTGDPKAGNCSLVIRDAQMQUESQYFFRVERGSYVTYNFMNDGFFLKVTVLSFTPRPQD
HNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPP
ATLSWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV
LENLGNGTSLPVLLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGS
QHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPT
AGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPR
PEARMPKGTQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

FIGURE 119

CTCGCGCAGGGATCGTCCCATGCGCCGGGGCTCGGAGCCGCGACCCCTGGGGGGCCTCCGGGATTGCTACCTTTT
TGCTCCCTGCTCGTCAACTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCGCAA
GGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCAGCAGGCAGAAATCGCACTGGAGGCCTCTTCGCTTG
CCCCTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA
GGAGAACCAAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCCCTGGGGGCAAGATTGTTACCTGTGCACACCGATA
TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTGCCTGCTTTGTGCTCAGCCAGGA
CCTGGCCATCCGGGATGAGTTGGATGGTGGGAATGGAAGTTCTGTGAGGGACGCCCCCAAGGCCATGAACAATT
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCTTCTCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGGCACACCTGGACGACGG
TCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCCGGTCCCTGCCAACAGCTACTTTGGCTT
CTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAACCA
CAAGGGTGTGTGGTCACTCTGCCAAGGACAGCGCCAGTGCCTGGTGCCCGAGGTTATGCTGTCTGGGGAGCG
CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTGGTGGCCAGACCTGATAGTGGG
TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGTGCTGTGTATGTGTACTTGAACCAGGGGGGTCACTG
GGCTGGGATCTCCCCCTCTCCGGCTCTGCGGCTCCCCGACTCCATGTTTCGGGATCAGCCTGGCTGTCTGGGGGA
CCTCAACCAAGATGGCTTTCCAGATATTGCAAGTGGGTGCCCCCTTTGATGGTGTGGGAAAGTCTTCATCTACCA
TGGGAGCAGCCTGGGGTGTGCGCCAAACCTTCAAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG
CTACTCCCTGTGAGCAGCTTGGATATGGATGGGAACCAATACCTGACCTGCTGGTGGGCTCCCTGGCTGACAC
CGCAGTGCTCTTCAGGGCCAGACCCATCCCTATGCTCCCATGAGGTCTCTATTGTCCACGAAGCATCGACCT
GGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCC
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGT
TCCCCGTGTGACGTTCTGTGAGCCGTAACCTGGAAGAACCAAGCACCAGGCCTCGGGCACCCTGTGGCTGAAGCA
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGGCATTGT
AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCCAGCAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGC
CCCCATCTCAATGCCACCAGCCAGCACCCAGCGGGCAGAGATCCACTTCTTGAAGCAAGGCTGTGGTGAAGA
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCGCTTCTGTACCCGGGTGACGACACGGAATTCCAACC
TCTGCCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCAGTGTGGGAGCCAGTCAATTGGCCTGGAGCTGAT
GGTCACCAACCTGCCATCGGACCCAGCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCAGCTCCTGGT
CATGCTTCTGACTCACTGACTACTCAGGGGTCCGGGCCCTGGACCCCTGCGGAGAAGCCACTCTGCCTGTCCAA
TGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTCACTTCTACCTCAT
CCTTAGCACCTCCGGGATCAGCATTGAGACCAGGAACCTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGTGCA
GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTCAATTGAGCTGCCACTGTCCATTGAGGAATGGCCATTCC
CCAGCAACTCTTCTTCTCTGGTGTGGTGGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGT
CAAGTATGAGGTACGGTTTCCAACCAAGGCCAGTGCCTCAGAACCTGGGCTCTGCCTTCTCAACATCATGTG
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCCCTGG
GCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCTCCACCTGGATGTGGACAGTAGGGATAGGAGGGCGGCGGGA
GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGGCGGCAGGAGCCAGCATGTCTGTTGGCCAGTGTCTCTGCTG
TGAGAAGAAGAAAAACATCACCTGGACTGCGCCCGGGGCAGGCCAACTGTGTGGTGTTCAGCTGCCACTCTA
CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCGCTCTTGGAACAGCACCTTTCTGGAGGAGTACTCAGC
TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCCCTCCATAAAGAACTTGATGCTCCGAGA
TGCCCTCCACAGTGATCCAGTGATGGTATACTTGGACCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGT
CATCCTCCTGGCTGTACTGGCTGGGCTGCTGGTGTCTAGCACTGCTGGTGTCTCTGTGGAAGATGGGATTCTT
CAAACGGGGCAAGCACCCCGAGGCCACCGTGCCTCAGTACCATGCGGTGAAGATTCTCGGGAAGACCGACAGCA
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAGCCCCCGGCGGGAGGGGCCCGGATGCACA
CCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCGGATGGGCATCCAGGGCCAGGCACCGCCTAGGTTC
CATGTCCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT
GGGCTGCTGGTGTGCGCATCAAGATTTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAAC
TCCTCCACCCAACTTCCCCTTAGAGTGTGTGAGATGAGAGTGGGTAATCAGGGACAGGGCCATGGGGTAGGG
TGAGAAGGGCAGGGGTGTCTGATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGT
GTAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCTTAACCTAGAGGGTGGGGAGGAGGTTGTGTCACTGA
CTCAGGCTGTCTTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGGCTGCCATCAGTCTAGTGGTTTCGTGGT
TTCGTCTATTTATTAATAAATATTTGAGAACAATAAAAAAAAAAAAAAAAAAAAA

FIGURE 120

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737
><subunit 1 of 1, 1141 aa, 1 stop
><MW: 124671, pI: 5.82, NX(S/T): 5
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QALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWLGVSVRSQGGKIVTCAHRYEARQRV
DQILETRDMIGRCFVLSQDLAIRDELGGGEWKFCGRPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKG
ARVELCAQGSADLAHLDDGPYEAGGEKEQDPRILIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVI
LRKDSASRLVPEVMLSGERLTSGFGYSLAVADLNSDGDWPD LIVGAPYFFERQEELGGAVYVYLNQGGHWAGISPL
RLCGSPDSMFGISLAVLGDNLNQGDFPDIAVGAPFDGDGKVFIYHGSSLGVVAKPSQVLEGEAVGIKSFYSLSGS
LDMDGNQYPDLLVGLADTAVLFRARPILHVSHEVSIAPRSIDLEQPN CAGGHSVCVDLRVCFSYIAVPSSYSPT
VALDYVLDADTDRLRLRGQVPRVTFLSRNLEEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTL SYS
LQTPRLRRQAPGQGLPPVAPILNAHQPSQRAEIHFLKQCGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVD
GTTALFALSGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLH YSGVRALDPAEKPLCLSNENASHV
ECELGNPMKRGAQVTFFYLILSTSGISIIETTELEVLELLATISEQELHPVSARARVFIELPLSIAGMAIPQQLFFS
GVVGERAMQSERDVGSKVKEYEVTVSNQGQSLRTLGS AFLNIMWPHEIANGKWLLYPMQVELEGGQGPQKGLCS
PRPNILHLDVDSDRRRRRELEPPEQQEPGERQEPSMSWVPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDR AA
VLHVWGRLWNSTFLEEYSAVKSLEIVRANITVKSSIKNLMLRDASTVIPVMVYLDPM AVVAEGVPWWVILLAVL
AGLLVLALLVLLLVKMGFFKRAKHPEATVPQYHAVKIPREDRQQFK EECTGTILRNNWGS PRREGPD AHPILAAD
GHPELGPDPGHPGPGTA
```

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

FIGURE 121

GGCACGAGGCGGCGGGGCAGTCGCGGGATGCGCCCGGAGGCCACAGCCTGAGGCCCTCAGGTCTCTGCAGGTGTC
GTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCAGCAGCTTTAGCCCATGAGGAGGATGT
GACCGGGACTGAGTCAGGAGCCCTCTGGAAGCATGGGAGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCA
TCTTCTGGCTTCGTTTGCAGCCTTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGC
GCTATGATTCTAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAACTGG
ACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATCGAAGATGCCTCGGGTC
TCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACTCTGACAGAGAAGCTTGTTGCCATGACAATGGGCT
CTGGGGCCAAGATGAAGACTTCAGCCAGTGTGACGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGG
ATGATGTTGTGAAGTCGATGTACCCCTCCGTTGGACCCCAAACCTCTGGACGCACGGACGACTGCCCTGCTCCTGT
CTGTCAGTCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACCAGTCTC
TGTCGGCTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAGCCAGATAAAGGCCCTCCAG
GCCCTGAAGGCTTCTCTGCAGGAGCAGTCTGCAATTTTAGTGCCTACAGGCCAGCAGCTAGCCATGAAGGCCCTGC
CGCCATCCCTGGATGGCTCAGCTTAGCCTTCTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTT
CAGCTGTGTGTGCATAGTAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACTGTGGCTGGT
GAGTGGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACCTCTCTGCAAGAGGAGTATTGAAAACCTGGTGGAC
TGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCTAAGAAATCAAGAGGTTTCACAT
TAAAATTAGAATTTCTGGCCTCTCTCGATCGGTCAGAATGTGTGGCAATTCTGATCTGCATTTTCAGAAGAGGAC
AATCAATTGAAACTAAGTAGGGGTTTTCTCTTTTGGCAAGACTTGTAATCTCTCACCTGGCTGTTTCATTTATT
TGTATTATCTGCCTGGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAGGTTTGGGTTTGAAGCTGAGGAAC
TACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTGGATAGTAAATTT
ATACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 122

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSELELDDVVITNPHE
AILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSASVSDIIVVAKRISPRVDDVVKSMYPPL
DPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWIDQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

FIGURE 123

CCCTTACATCCTCCTAGGACCCGGTCGGTAGTCGTCGCCCCAGCCCCGGGGGGCGCAGCGCCCCAGCCGCGGGCC
CTCGAGACGGGACCGAGAGCATCATGGGCAGCACTGTCCCGCGCTCCGCCCTCCGTGCTGCTTCTGCTGCTGCTCC
TGCGCCGGGGCCGAGCAGCCCTGCGGGGGCCGAGCTCACCTTCGAGCTGCCGGACAACGCCAAGCAGTGCTTCCACG
AGGAGGTGGAGCAGGGCGTGAAGTTCTCCCTGGATTACCAGGTCATCACTGGAGGCCACTACGATGTTGACTGCT
ATGTAGAGGACCCCCAGGGGAACACCATCTACAGAGAAACGAAGAAGCAGTACGACAGCTTCACGTACCGGGCTG
AAGTCAAGGGCGTTTATCAGTTTTGCTTCAGTAATGAGTTTTCCACCTTCTCTCACAAGACCGTCTACTTTGACT
TTCAAGTGGGCGATGAGCCTCCCATTTCTCCAGACATGGGGAACAGGGTCACAGCTCTCACCCAGATGGAGTCCG
CCTGCGTGACCATCCATGAGGCTCTGAAAACGGTGATTGACTCCCAGACGCATTACCGGCTGCGGGAGGCCCAGG
ACCGGGCCCGAGCGGAAGACCTTAATAGCCGAGTCTCTTACTGGTCTGTTGGCGAGACGATTGCCCTGTTCTGTG
TCAGCTTCAGTCAGGTGCTACTGTTGAAAAGCTTCTTTCACAGAAAAACGACCCATCAGCAGGGCAGTCCACTCCT
AGCCCCGGCATCCTGCTCTAGGGCCCCCTCATGCCCCAGGCTGGAGCAGCTCTCCTAGGTACAGCCTGCTGGGCT
GGGTGCGTAGCCAGGGTGGAGGCAGAACGATGCTGCTGTGGTAGCCCTTTGCCTTTTCATGCCCATGCTTGATT
CTTGACCTCAGCAGCTGAAGGTCTCAGAGACCAGTAATCAGAAGGCATCCGACTGCATTAAGTGTGACGCGCTG
AAAAGACATTTACAAC TAGGCCAGGGATTAGCCACTGTGGGAGGGTGGACAGGCAATGGTTTCAGTGGCCTGGCTG
TTGGCAGGAACTCCAAGTGCCCAGGCCTCTTGGGCAGCTTAGGGCCCTGCCTCTGTTTCATGATGCATGGGTCAT
TTGTCTTGGGTGTCCTATCCCATATGGAGAAGAAAGGGGCTCTAAGTTCTGGCTCTTCTTTCTTTGGGGTTCTCT
GTACCTGAGGAAACAGGCCCTGGGTGACTTTGCAGATCTGCTCACCTTCGGTGAGCAACAGTGTGAGCCATGCA
AGCAGGACAGAATGGTGACTGGGTGCCCTTGGTGAGCTGTGTATTTCTAGGAGGTAGAAAACTGTGGGAAACTG
TGGCTAATAAAAACTAAGTGTGAGCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 124

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56052
<subunit 1 of 1, 217 aa, 1 stop
<MW: 24777, pI: 5.55, NX(S/T): 0
MGSTVPRSASVLLLLLLRRAEQPCGAELTFELPDNAKQCFHEEVEQGVKFSLDYQVITG
GHYDVDCYVEDPQGNTIYRETKKQYDSFTYRAEVKGVYQFCFSNEFSTFSHKTVYFDFQV
GDEPPILPDMGNRVLTALQMESACVTIHEALKTVIDSQTHYRLREAQDRARAEDLNSRVS
YWSVGETIALFVVSFSQVLLLLKSFFTEKRPIsRAVHS

Important features:

Signal peptide:

amino acids: 1-23

Transmembrane domain:

amino acids: 187-201

N-myristoylation sites:

amino acids: 26-32,48-54,131-137

Tyrosine kinase phosphorylation site:

amino acids: 82-91

Glycosyl hydrolases family 25 proteins:

amino acids: 53-61

FIGURE 125

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTTCAGCCCATTGGCCCCGACGCCTCTGT
TCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTGCAAGATGGAGGAAGGCGGGAACCTAG
GAGGCCTGATTAAAGATGGTCCATCTACTGGTCTTGTCAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCT
CAGGCTTCCTGCTTTTCCGAAGCCTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTCTTCCCCTTCTACT
TCCACATCTCCATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCACAT
TCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAACGCCCCGCTGGCTGGAAC
CCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGAGCGAGGCCTGGGTGGGAGGTACCAGGCA
GCCACCAGGGTCCCGATCCCTACCGCCAGCTGCGAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCT
TCCGCTACCATGGGCTGTCTCTCTTTGCAATCTGGGCTGCGTCTGAGCAATGGGCTCTGTCTCGCTGGCCTTG
CCCTGGAAATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAAAAAAAA
AAAAAA

FIGURE 126

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGN LGGLIKMVHLLVLSCAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISMGC AFINLCILASQ

HAWAQLTFWEASQYLFLSLTLATVNARWLEPRTTAAMWALQTVEKERGLGGEVPGSHQGPDPYRQLREKDPKY

SALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 127

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGC
CATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGATTTGGAGTGTTTTTCCTGTTCTTTGG
AATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTTAGCCGGCTTGGCTTTTGTAAAT
TGGTTTAGAAAGAACATTCAGATTCTTCTTCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGT
ATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAGGGG
CTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAATTTACCTGGAATTAG
ATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACAAGTGAATTTGAAGACTCATTTAAAATA
TTGTGTTATTTATAAAGTCATTTGAAGAATATTCAGCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTT
TACAGGAGTTTAAAACGTATAGCCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAAACAGGCTTCTA
CTCAAGTGAAC TAAGAAGAAGTCAGCAAGCAAACTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAAACTC
TTGAAGGCTATTTGTTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAACTGTGGTGCCTGTTTCT
TTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCTTTT TAGAAGTGTCCTGCAATGGCAAAAA
TATTTCCAGTTGCACTGTATCTCTGGAAGTGATGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAAC
CAAGGAAACCCCAATTTTGATGTATGGAATTACTTTTTTTTGNCGNCAGGGCC

FIGURE 128

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQKHMKATGFFLGGV
FVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRRVPLGSLNLPGIRSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 129

AATTCAGATTTTAAGCCCATTCTGCAGTGGAAATTCATGAAC TAGCAAGAGGACACCATCTTCTTGATTATACA
AGAAAGGAGTGACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGGCCTCCTAATCCTCTGTGGTT
TTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTGATAAGTACATTTTTATCACTGGATGTGACT
CGGGCTTTGGAACTTGGCAGCCAGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAAT
CAGGATCAACAGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGA
ATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTG
GTGTTCCCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAACCTGT
TTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCA
GTGTTGGAGGTGCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAAGGTTTCAATGACA
GCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAAACTTGG
CAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATG
GAGAAGGTTACATTGAAAAAGTCTAGACAAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGG
TGGTAGAGTGCATGGACCAGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTATTGTTGAAACAGAAAGCAGAGCTGG
CTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGATTTCAAGAAC
ACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGATCGTGCTTATTTGGATTGCAAA
AGGGAGTCCCAACCATCGCTGGTGGTATCCCAGGGTCCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGT
ACATCACATAGGCAAGTCCTGCCCTGTATTTAGGCTTTGCCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTT
GCCCATTCAAAATGATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCAGCATTTACAGTAACTTGTGAATGT
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AAAAAAA

FIGURE 130

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
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RLRTVLLDVTDPENVKRTAQWVKQVGEKGLWGLINNAGVPGVLAPTDWLTLEDYREPIEVNLFGLISVTLNMLP
LVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDLRRDMKAFGVHVSCEPGLFKTNLADPVKVEKKLA
IWEQLSPDIKQQYGEGYIEKSLDKLKGNSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAA
LQDFLLLKQKAELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 131

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAAGCCATGAACATCA
 TCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGAGTCGTTGGTGAAGTTTTTCATTCCCTC
 AGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCATTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTT
 ATGAATTTGCAAAACGACAGAGCATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTG
 AGTGCCGAAAAC TAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCTCTC
 TAAATCAGGTGAAGAAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACAGTATATCCAGCCGATC
 TTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAACATCCTAGGACATTTTTGGATCACAAAAG
 CACTTCTTCCATCGATGATGGAGAGAAATCATGGCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGA
 TTCCTTACCTCATCCCATATTGTTCCAGCAAATTTGCCGCTGTTGGCTTTTCACAGAGGTCTGACATCAGAACTTC
 AGGCCTTGGGAAAAAC'TGGTATCAAAACCTCATGTCTCTGCCCAGTTTTTTGTGAATACTGGGTTACCCAAAATC
 CAAGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATAGATGGAATACTTACCAATA
 AGAAAATGATTTTTTGTTCATCGTATATCAATATCTTTCTGAGACTACAGAAGTTTCTTCTGAACGCGCCTCAG
 CGATTTTAAATCGTATGCAGAATATTCAATTTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAATA
 AGCTCCAGCCAGAGATGTATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTTACAT
 TTTTTCAGTCCTGATAATATTA AAAACATTTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTAATTACCTGT
 CTTCTGTTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCTTTTCATGCCTCTTAAAAACTTCTG
 TGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATATTTTATTTTTCCATTTAAAGGTGGACAAAAGCTACC
 TCCCTAAAAGTAAATACAAAGAGAACTTATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTG
 TAGCCATGCCACAGAATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTT
 TATCTCAACCTGGACATATTTTAAGATTCAGCATTTGAAAGATTTCCCTAGCCTCTTCTTTTTTCATTAGCCCAA
 AACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTATAACTCTGAAGTCCACCAAAAGTGGA
 CCCTCTATATTTCTCCTTTTATAGTCTTATAAGATACATTATGAAAGGTGACCGACTCTATTTTAAATCTCA
 GAATTTTAAGTTCTAGCCCCATGATAACCTTTTTCTTTGTAATTTATGCTTTTCATATATCCTTGGTCCCAGAGAT
 GTTTAGACAATTTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAACA
 ATGGACCCAAGAGAAGAA

FIGURE 132

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409
<subunit 1 of 1, 300 aa, 1 stop
<MW: 33655, pI: 9.31, NX(S/T): 1
MNIIIEIILLITIIYSYLESIVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSILVLWDINKRGVEE
TAAECRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDTVIVVNNAGTVYPADLLSTKDEEITKTFEVNILGHFW
ITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYCSSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGF
TKNPSTRLWPVLETDEVVRSLIDGILTNNKMIFVPSYINIFLRQLQKFLPERASAILNRMQNIQFEAVVGHKIKMK
```

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

FIGURE 133

CTGAGGCGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCGCACTCGCTTT
CCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAAGGTGAAGCCAAGAACAGCAT
TACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGACATTCAGAAATATATTCCATGCTATCAGCT
TTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAA
TGTGGTAGGTTGGTACAAATCCGTCGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAA
CTTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACACCAAGTATAATAACAGAAAGCTGCTC
TACTCATCGACTGGAACATTCCCTTATATAAACCTCAAAAAGGACTTTTTTCACAGGGTACCTTTTAGTGGTTGCCAA
TCTGGGCATGTCTGAACAACCTGGGTATATAAACTGTATCAGGTTCCCTGTATGTCCACTGGTTTTAGCCGAGCAGT
ACAAACACACAGCTCTAAATTTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGC
TTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACTAGTAAA
GGATGTAAACAGATTAAAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGGCAGCAAGAGAGAAGAACAT
CCAAAAGACCTCAGGAGAACATTTTTCTTTGTCAGGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCA
TTCATGTGTATGTCTTTAAAAAATAGACATGTTTTCTAAAAGTAGCTGTAACCTACAACCACCATCTCGATGTAGT
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTA
GCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTAGATACACAAGACAAACGATC
TAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCCAGAAACAGATGAAGAAATGA
AAAGATGAAGGGTTTTTGGTGAATATTCACGGTCTCCTACATTTTGAATCCTTTTAAACCTTACAAGGAGATTTTTTT
ATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTTTACTATGTTGAGCTACTTGACAGTAAGTTTCAATTTGTT
TTTACTATGTTTCACTGTTTGCAGTAATACACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTTTCAA
CATCAGATGCTTTTATTTCCAAACCTTTTTTTTCACTTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAGACACA
TTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACTTAGGGGAAGACAAGTC
AGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATTGAGACCATGTCTATAAAAAATAAA
ATGAAAAGCAAGAATAGCCTTATTTTCAAATATGGAAAGAAATTTATATGAAAATTTATCTGAGTCATTAAAA
TTCTCCTTAAGTGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAAT
AAATTTGCAAAACATCATCTAAATTTAAAAAATAAAAAAAAAAAAAA

FIGURE 134

MEGESTSAVLSGFFVLGALAFQHLNTSDTEGFLLGGEVKGEAKNSITDSQMDDVEVVYTIDIQYIPCYQLFSFYN
SSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRRERLLHKNLQEHFSNODLVFLLLTPSIITESCSTHRLE
HSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEE
LKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS
LKNRHVSKSSCNYNHHLDVVDNLTLMVEHTDIPASPASTPQIIKHKALDLDLDRWQFKRSRLDQTQDKRSKANTG
SSNQDKASKMSSPETDEEIEKMKGFGEYSRSTF

FIGURE 135

GGCACAGCCGCGCGGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCC
CAAGCAGCGCGCAGCGAACGCCCCGCGCGCCACACCCCTCTGCGGTCCCCGCGGCGCCTGCCACCCCTCCCTCC
TTCCCCGCGTCCCCGCTCGCGGGCCAGTCAGCTTGCCGGGTTCGCTGCCCGCGAAACCCCGAGGTACCAGCC
CGCGCTCTGCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGGCGCGCCTGGCACCGGGG
ACCGTTGCCCTGACGCGAGGCCAGCTCTACTTTTCGCCCCGCGTCTCCTCCGCTGCTCGCCTCTTCCACCAACT
CCAACCTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAGCGCCGC
TTCCCGTCCGGTCCCAAAGGTGGGAACGCGTCCGCCCGCGCCCGCACCATGGCACGGTTCCGGCTTGCCCGCGCTT
CTCTGCACCCCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCGA
CGTCTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATC
TGTCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAA
AGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTACGTTACAAGAAGTTTGATGAATTTCTTC
AAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAA
AATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAA
ATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGTACCACCTTACAGAT
GAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCTCGCAAATGAAGCTC
CAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTGCTCAAGGCTTAGCGGTTGCGGGAGATGTGCTGAGCAAG
GTCTCCGTGGTAAACCCACAGCCCAAGTATCCCATGCCCTGTTGAAGATGATCTACTGCTCCCACTGCCGGGT
CTCGTGACTGTGAAGCCATGTTACAACCTACTGCTCAAACATCATGAGAGGCTGTTTGGCCAACCAAGGGGATCTC
GATTTTGAATGGAACAATTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGAGGGTCTTTTCAACATTGAA
TCGGTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGATAATAGTGTTCAGTGTCT
CAGAAGGTTTTCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATTTCTCGTTCCATCTCTGAAAGT
GCCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACCACAGCAGCTGGCACTAGTTTGGACCGA
CTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGGTCTCCCTTCCGAGCAACGTTTGCAAC
GATGAGAGGATGGCTGCAGGAACCGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTACCTGTTT
GCAGTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAAACCAGACATA
CTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCA
GAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCTC
GGGGCACAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGGTTATGCAGAGAGAGTGGAGATTATTCTCA
AACTCTGAGAAAAAGTGTTTCATCAAAAAGTTAAAAGGCACCAAGTTATCACTTTTCTACCATCCTAGTGACTTTGC
TTTTTAAATGAATGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAGAAGTGCTGACTTTGTTTTT
TCATTTCAGTTTTTGGGAGGAAAAGGACTGTGCATTGAGTTGGTTTCTGCTCCCCCAAACCATGTTAAACGTGGCT
AACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTTGTTTGTATGTTTTT
TTCTCATTTTCGTTTGTGGTTTTTTTTTCCAACGTGATCTCGCCTTGTTCCTTACAAGCAAACAGGGTCCCTT
CTTGGCACGTAACATGTACGTA'TTCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTTATCATGTTATC
TTATTTAAAGAAAAAGCCCAAAAAGC

FIGURE 136

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGSTCCSQEMEKEY
SLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGHLYMQNSELFKDLFVELKRY
VVGNVNLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGL
AVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAE
RLEGPFNIESVMDPIDVKISDAIMNMQDNSVQVSQKVFQGC GPPKPLPAGRISRSISESAFSARFRPHHPEERPT
TAAGTSLDRLVTDVKEKLKQAKKFWSSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNEV
QVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISESSGEGSGSGCEYQQCPSEFDYNATDHAGKSANE
KADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 137

GCGGGCTGTTGACGGCGCTGCGATGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTTCTCTCAGTCGGA
 CTTCTGACGCCGCCAGTGGCGGGGCCCCCTTGGGCCGTCGCCACCACTGTAGTCATGTACCCACCGCCGCC
 GCCGCTCATCGGGACTTCATCTCGGTGACGCTGAGCTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGCG
 GCGCTCGTGCTGGAGGAAATGGAAGCAACTGTGAGATTGCAGCGGAATATGATTCTCTTCTCTCTGCTTTCT
 GCTTTTCTGTGGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAGCTCTGGCTTTTCAAGCTAGAGGAAGA
 GCAGAAGATGAGGCCAGAAATGCTGGGTAAAACAGCAAATCCACCCGCTTACCAGCTCCTCAGAAGGCGGA
 CACCGACCTGAGAACTTACCTGAGATTTGCTCACAGAAGACACAAAGACACATCCAGCGGGGACCACCTCACCT
 GCAGATTAGACCCCCAAGCCAAGACCTGAAGGATGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCTGT
 GGATCCCCGCCCCGAAGGAGATCCGAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCTGAGCAGGG
 CACCGAGCTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGGCACACC
 AGTGCACTGAACTATCGCCAGAAGGGCGTGATTGACGTCTTCTGCATGCATGGAAGGATACCGCAAGTTTGC
 ATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCCTTCACTGAGTGGTTTGGCCTCGGTCTCACACTGATCGA
 CGCGCTGGACACCATGTGGATCTTGGGTCTGAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTT
 ACCTTTGAAAAGGACGTGGACGTCAACCTGTTTGAAGACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTA
 CCACCTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGCCTCAGAAC
 ACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACCCGCCACGGTGGACCTCCGACAG
 CACTGTGGCCGAGGTGACCAAGCATTCAGCTGGAGTTCCGGGAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCA
 GGAGGCAGTGGAGAAGGTGACACAGCACATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCA
 CAATACCCACAGTGGCCTCTTCAACCCAGCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTA
 CCTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGTGGAAGACTACGTGGAAGCCATCGAGGG
 TGTCAGAACGCACCTGCTGCGGCACTCCGAGCCAGTAAGCTCACCTTTGTGGGGGAGCTTGCCACGGCCGCTT
 CAGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCAGGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGC
 CAGCCACATGGAGCTGGCCAGGAGCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAG
 TCCCGAGATCGTGCACTTCAACCTTTACCCCCAGCCGGGCGCTCGGACGTTGGAGGTCAAGCCAGCAGACAGGCA
 CAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTTACCTGTACCGCGTCACAGGGGACCGCAAATACCAGGA
 CTGGGGCTGGGAGATTCTGCAGAGCTTACGCCGATTACACGGGTCCCTCGGGTGGCTATTCTTCCATCAACAA
 TGTCAGGATCCTCAGAAGCCCCGAGCCTAGGGACAAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCT
 GTTCTTGCTCTTCTCCGATGACCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCACCTCT
 GCCTATCTGGACCCCTGCCTAGGGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTGCTGGG
 TCTGTGGCATTTCCTAAGGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCAGGCTCTGAAGTGGCTCTGGGCT
 CCTCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGAAGCCGTGAGTCTTGGTGTGATCGGGGGTGGG
 CTGGGCCGCTGGAGCCTCCGCTGCTTCTCCAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAG
 GTCTCTGTGGGCCGACCAGAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCAGGGT
 GCAGCTCTGCCCCGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGACTCCAGAG
 GCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTCTGGCCGCCCCGAGGGGGCT
 TGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCCCTCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAG
 TTGATTTGCTCTAACCGCAA

FIGURE 138

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDNSKSWRRRSCWRKW
KQLSRLQRNMILFLLAFLFLFCGLLFYINLADHWKALAFRLEEEQKMRPEIAGLKPANPPVLPAQKADTDPENLP
EISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEATKRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRR
AEVPTKPPLPPARTQGTPVHLNRYRQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSEWFGGLGLTLIDALDTMWI
LGLRKEFEEARKWVSKKLHFEKDVDVNLFEFSTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKIPYS
DVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAWEKVTQHIHGLSGKKDGLVPMFINTHSGLF
THLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRTHLLRHSEPSKLTFFVGELAHGRFSAKMDHL
VCFLPGTLALGVYHGLPASHMELAQELMETCYQMNRMETGLSPETVHFNLYPQPGRRDVEVKPADRHNLRLPET
VESLFYLYRVGTGRKYQDWGWEILQSFSRFRTRVPSGGYSSINNVQDPKPEPRDKMESFFLGETLKYLFLFSDD
PNLLSLDAYVFNTAEHPLPIWTPA
```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 139

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGACCTGAGTCATC
CCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACTTACAGCTGCACCGACAGTTG
CGATGAAAGTTCTAATCTCTTCCCTCCTCTGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGA
ATCCAGGGGTGCGCAGAGGCCACAGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAAT
GTGAGTGCAAAGATTGGTTCTCTGAGAGCCCCGAGAAGAAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGT
GCCCCGTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATT
CCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTGAGCGC
CCTCTTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACCTC
ACTCTCCCCTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGT
TGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTAC
CTGAAAGATTCCAGGAAACTGTAGCTTCTAGCTAGTGTCAATTTAACCTTAAATGCAATCAGGAAAGTAGCAAAC
AGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 140

MKVLISLLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFMTVSGLPKKQC
PCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

FIGURE 141

AATGGCTGCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCTGCTATGCAGACGA
CAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCAAAGCCAGACTTCCCCAAATTCCTAAG
CCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGAGTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTAT
GGAATTTGATGATAATGAAGGAAAACATTCATCAAAGTGAATCCTCAGGACACACCCATGTGGCTCCTGGACAA
TCCAAGAGCAGCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAACTCC
CAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACCCTGACTGCATTTTGC
TTTGTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTGATGGAGAGGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 142

MAVLVLRRLTVVLGLLVFLTCYADDKPKDPDDKPDDSGKDPKPDFPKFLSLLGTEIIEHAVEFILRSMRSTGFM
EFDDNEGKHSSK

FIGURE 143

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAGAGCTGGTCTG
CC**ATGG**ACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTACCCCTGCCCCTGACCTCATGGCTCTGC
TGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCCCCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCA
AGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTAC
TGGAGCTGGGCTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAA
ATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGG
CTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGCTGTGCTCTG
TGCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGC
ATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTTCGAGCCCACCTGGAAACACATTGGGG
ATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCCAGTTCTCCGAAATCCAAATGGAACGAC
AGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCT
CCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGA
GAGGGACCT**AG**CAGAATGAGAGAAGACATTATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGG
ACCTGTTGTATCCTCAACTGCAAGTTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTCCCTTTCCTT
CGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGTCTCTAGGAAGTGGTCACAAAAG
TCATGGTGCTGCATCCCTGCCAAGCCCCCTGACCCTCTCTCCCCACTACCACCTTCTTCCCTGAGCTGGGGGCA
CCAGGGAGAATCAGAGATGCTGGGGATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTT
TAATAAATAGACGAAACCACG

FIGURE 144

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMVLTTPKSNRKMESKKRELFSSQIKGLTGASGKVALL
ELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDMRQLADGSMDVVVCTLVLCVS
QSPRKVLQEVRRLRPGGVLFWEHVAEPYGSWAFMWQQVFPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQ
PPPLKWLPVGPHIMGKAVKQSFPSKALICSFPSLQLEQATHQPIYLPLRGT

FIGURE 145

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAGTTGCCTCATCGCAGGCAGATGTTGGGGC
 TTTGTCCGAACAGCTCCCCCTGCGCAGCTTCTGTAGATAAGGGTTAAAACTAATATTTATATGACAGAAGAAAA
 AGATGTCATTCCGTAAAGTAAACATCATCATCTGGTCCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATA
 ACTTCCTCAGCTTGAGCAGTTTGTAAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACT
 TTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATCTGAAG
 ACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTG
 TTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAA
 TTGTCAATTTTGACCTTAAACTTTTGGAAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTT
 TAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCGAGCGCAAAGAAGGCCATATACATGGATGATGATGTAA
 TTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATT
 GTGATTCAGCCTCTACTAAAGTTGTCTCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATA
 AAAAGGAAAGAATTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAACC
 TGACGGAATGGAACGACAGAATATACTAACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGT
 ATAGCAGAACCCTGGCTGGTAGCATCAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCG
 ATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCA
 AGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGT
 ATATTCCAGACCCAACAGGCAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAACAGAA
 TTTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGTAGGCTTC
 AATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTAGCTAGGTAAAGATGACAAACTGCCCTGTCTGGCAGT
 CAGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTG
 AATGACTGGAAAGAAGAACTGATATGGCTAGTTTCACTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTA
 ATTTTGTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTTT

FIGURE 146

MSFRKVNIIILVLAVALFLLVLHNFSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGRQEEIPVVIAASED
RLGGAIAAINSIQHNTSRNVIFYIVTLNNTADHLRSWLNDSLKSIRYKIVNFDPKLLEGKVKEDPDQGESMKPL
TFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNTALKPGHAAAFSEDCDSASTKVIRGAGNQYNYIGYLDYK
KERIRKLSMKASTCSFNPGVFVANLTEWKRQNTNQLEKWMKLNVEEGLYSRTLGSITTPPLLIVFYQQHSTID
PMWNVRLGSSAGKRYSPQFVKAALLHWNGHLKPWGRTASYTDVWEKWIIPDPTGKFNLIRRYTEISNIK

FIGURE 147

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTTCCTCCAAGCA
 AGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCTATTTGCATCTGTTTTGATAA
 ATGATGTTGACACCCTCCACCGAATTCCTAAGTGAATCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCC
 TCGCATTAGCCTTGTCTTTGGCCATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTT
 CATTGGTTATTTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCA
 GCATAGAATTGGACACAGAAAGGGAAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGG
 CAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAAGAGAAATAAAATTGACAGTTGAGCTTTTCCAAATCACAAATA
 AAGCCATCAGCAGTGCTCCCTTCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCC
 TCTGGGTGGCTGTGCTGCTGAGCCTGGGAACCTGCAGGAGCTGCCCAGGTTATGGAAGGCGGCCAAGTGAATATA
 AGCCCCTTTCGGGCATTCCGTACATGTGGTTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCATCCTTG
 CGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTATTTC AACAGAAGTAAAAATGATCCTCCTGATC
 ATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTAACTCT
 CTGTGGTGAGGATTCCGAGAATCATTGTCATGTACATGCAAAACGCACCTGAAAGAACAGCAGCATGGTGCATTGT
 CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATG
 CATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCTTGTCCAAGA
 ACTCAAGTCACCTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTCTAGGAAAGGTGTAGTGGTGTGTT
 TCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGG
 TAGCTTTTTTTGCCTACTTAGTAGCCCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCATTTTCTCTGT
 GTTTTGCTGTTGATCTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTT
 TCGTAAAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGAGGGAA
 CAGAACTCCAGGCCATTGTGAGATAGATAACCCATTTAGGTATCTGTACCTGGAAAACATTTCTTCTAAGAGCCA
 TTACAGAAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTTTTTAAAAGACCTAATAAACCTATTCT
 TCCTCAAAA

FIGURE 148

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIELDTERENMKC
VLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFAILIFFWVLWVAVLLSLGTAG
AAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFY
HQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFC
TSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLNAFNYNRAQVWAVPLLLVAFFAYLVAHSFL
SVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

FIGURE 149

[illegible]

FIGURE 150

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAGCQDPKYHVYG
TDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWRESFIVLESKPKKGVITYPSAL
TYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQE
MDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDG
STSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNVGRA
ISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAV
CRTNGFYSLHVQSWFGLHKTLLQPLVKRVCDTDRLLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKF
EISDTRIGAVQYTYEQRLFEFGFDKYSSKPDILNAIKRVGYWSSGTSTGAAINFALEQLFKKSKPNKRKLMILI
TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARHSSFVDEFDNLHQYVPRIIQNICTEFNSQPRN

FIGURE 151

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTATGCCTTTCCGGCT
GCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCCTCAGCACCATGGTGCGCCAGGTCCCGACGGCTCCGCGCC
AGATCCCGCCCACTACAGTTTTTCTCTGACTCTAATTGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTC
AGAATTCCAAAGAGTGGTTGAAGTGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGA
AACAAACATTTCGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGAGGC
TGGATGGCCCTGTTCGGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCCGAAAACCTCCTCCAGCCTTTCAGAC
CCCCACTGGCATGCCATATGGAACAGTGAACTTACTTCATGGCGTGAACCCAGGAGAGACCCCTGTCACCTGTAC
GGCAGGGATTGGGACCTTCATTGTTGAATTTGCCACCCTGAGCAGCCTCACTGGTGACCCGGTGTTTGAAGATGT
GGCCAGAGTGGCTTTGATGCGCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTTCGGAACCCACATTGATGTGCT
CACTGGCAAGTGGGTGGCCAGGACGCAGGCATCGGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGTGAAAGG
AGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTTCTAGAGTATAACAAAGCCATCCGGAACTACACCCG
CTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACTGTGTCCATGCCAGTCTTCCAGTCTTGGAGGC
CTACTGGCCTGGTCTTCAGAGCCTCATTGGAGACATTGACAATGCCATGAGGACCTTCTCACTACTACACTGT
ATGGAAGCAGTTTTGGGGGGCTCCCGGAATTCACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTA
CCCACTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCAACCTCCTAGAACT
CGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGCAGGATTTGCAACAATCAAAGATCTGCG
AGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTGCGCGAGACTGTGAAATACCTCTACCTCCTGTTTGA
CCCAACCAACTTCATCCACAACAATGGGTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGG
GGCTGGGGGGTACATCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAA
GGAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTGGAATTTTCAAG
AAACACTGTTAGTTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACACTCTTCTCACCAGAAAACCATGACCA
GGCAAGGGAGAGGAAGCCTGCCAAAACAGAAGGTCCCACCTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTT
GGCATTACTGGGACAGGTTTTCTAGACTCCTCATAAACCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCT
AAACTATAATAAATTGCTTTTGGCTATCATAAAA

FIGURE 152

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVEVLQDSVDFDIDVN
ASVFETNIRVVGGLLSAHLISKAGVEVEAGWPCSGPLLRMAEEAARKLLPAFQTPTGMPYGTVNLLHGVNPGET
PVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFE
YLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDWYLVWQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFL
NYYTVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMLYRATGDPDLLLGRDAVESIEKISKVECGFAT
IKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYIFNTEAHPIDLAALHC
CQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPSQP
FTSKLALLGQVFLDSS

FIGURE 153

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAAAGTGAAGAAAACA
GAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCCCTTCGT
CACTCACCTGTTCTTGCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACG
CCTATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGAT
GCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGGGGC
CCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTCATCCTGCTGTGAATAT
GCACCTGGGGATGTCTCTGT'TAGAGACAGATGGTGTATGGGGGATTCATGGTGAGCTAAAGGAGAGGGTGGTGGCAG
TGTCTCTGAAGGTCCATAAAAGAAAAAGAGAAGTGTGGTAAGGGAAAAATGGTCTGTGTGGAGGGGTCAAGGAGT
TAAAAACCTAGAAAGCAAAGGTAGGTAATGTGAGGGAGTAGTCTTCATGCCCTCCTTCAACTGGGAGCATGTTT
TGAGGGTGCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCCCTCTCTGGTCTCGTGCT
TGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGGAAGCCTGGCA
CCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGT'TCCAGAGGAGATACTGGGTGGGAAAAAGATG
GGGCAAAGCGGTATGATGCC'TGGCAAAGGGCCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCT
CCATGTTTCCCTAACAGATTCACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCCTAGCACTTTGGGAGGC
CAAGGTGGGCAGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACTCCATCTCTACTAA
AAAAAAAAAATACAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTCATCTACTCGGGAGGCTAAGACA
GGAGACTCTCACTTCAACCCAGGAGGTGGAGGTGCGGTGAGCCAAGATTGTGCCTCTGCACCTAGCGTGGGTG
ACAGAGTAAGCGAGACTCCATCTCAAAAATAATAATAATAATTCAGACTCCTTATCAGGAGTCCATGATCTG
GCCTGGCACAGTAACTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGA
GGTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

FIGURE 154

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPPEAEFGYSVLQHVGGGQRWMLVGAPWDGPGSGDRRGDVYR
CPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS
```

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

FIGURE 155

GCGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGAGGCTCCAGCTGC
 AGCGTCCCCGCGCCCTCTCGGGAGCTCTGATCTCAGCTGACAGTGCCCTCGGGGACCAAACAAGCCTGGCAGG
 GTCTCACTTTGTTGCCCAGGCTGGAGTTTCACTGCCATGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAA
 GCGATCCTGCTGAGTAGCTGGGACTACAGGACAAAAATTAGAAGATCAAAATGGAATAATATGCTGCTTTGGTTGAT
 ATTTTTACCCCTGGGTGGACCTCATTTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAAGGT
 ACCCGGATTGTCACTGAAAGGACTTTCATCTCACCAGCCCCGATTTGAGGCAGATGCTAAGATGATGGTAAA
 TACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCAGCCTTTCTGAATTGGAGGATTATCTTTCCCTA
 TGAGACTGTCTTTGAGAATGGCACCCGAACCTTAACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCA
 AAATATCACCACAAAGGGAGTATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCCGACAGCAGGTTTCAGCATCTT
 GGACAAAAGGTTCTTAACCAATTTCCCTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCATTTCTCAT
 TTCCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTATGATGGAAAGGACTATGTCAAAGGGAGTAAAAAGCT
 AAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAGAAACGTCGAGGTTCTAAGAGGAGCAGGAGAGA
 AGCTAGTGGTGGTGACCAAAGAGAGGGTACCAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAA
 AAAATCTGGCCGGGGTCAAGGATTGCCGAAGGGAGGCCTTCCCTTTCAGTGACCCGGGTCAAGAATACCCACAT
 TCCGAAGGGCTGGGCACGAGGAGGCATGGGGACGCTACCTTGACTATGACTATGCTCTTCTGGAGCTGAAGCG
 TGCTCACAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAATGCCCTGGTGGAATGATCCACTT
 CTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTATCGGTTTTGTCAGTGTGTCCGACGAATCCAATGATCT
 CCTTTACCAATACTGCGATGCTGAGTCGGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAA
 AAAGAATTGGAAGCGCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTTCAAGGA
 CTACAACGTTGCTGTTTCGCATCACTCCCTAAAATACGCCAGATTTGCCTCTGGATTACGCGGAACGATGCCAA
 TTGTGCTTACGGCTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAATCACAGAGAAAACCAGCTCTGCTTA
 CCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTTGAACTCTGTCAATAGCATTTCAACATTTTTCAAAATCA
 GGAGATTTTCGTCCATTTAAAAAATGTATAGGTGCAGATATTGAAACTAGGTGGGCACCTTCAATGCCAAGTATAT
 ACTCTCTTTACATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTTAA
 ACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCTTACTCTAAGAAGAAT
 CTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAAGGTAGATGGTAAAGCAATTAGTATCAGA
 ATAGAGACAGAAAGTTACAACACAGTTTGTACTACTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTAT
 ATTGTGTTATCTGTTGGGTCTGGGACATTTAGTTTAGTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGC
 ATTATAAACAAAACATAAAGTGTGTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAATGGGA
 GAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTTTAAGATCTCAAGTTTTTA
 TTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGGAAGACACTTCACAAATTATGAATGATCATGT
 GTTGAAAGCCACATTATTTTATGCTATACATTTCTATGTATGAGGTGCTACATTTTATAGGACAAAGAATTTCTGTAA
 TCTTTTTCAAGAAAGAGTCTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTTCTCTG
 ATTAGTAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

FIGURE 156

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFEADAKMMVNTVCGIECQKELPTPSL
SELEDYLSYETVVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQVYGTDSRFSILDKRFLTNFPFSTAVKL
STGCSGILISPQHVLTAACVHDGKDYVKGSKKLRVGLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQE
RAKGRRRRKKSGRGORIAEGRPSFQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIK
KMPGGMIHFSGFDNDRADQLVYRFCSVSDENLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKI IAVYSGHQW
VDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

FIGURE 157

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAGGAGCATGTCCGCG
 CCGGGGAAGGCCCGTCCCTCCGGCCGCCATAAGGCTCCGGTCGCCCGCTGGGCCCCGCGCCGCTCCTGCCCGCCCG
 GGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCGCTCGCCCCGAGGCCCGGCCCGCAGCATGAGGCCACCC
 GGACGCCGGCGGGGCGCGCGCAGCCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGA
 GCGGGCGGGCGGGCGGGCGCGCGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGCTGGCAGG
 GCGGGCGGGCGGCCCGAGGGCAAGGTGGTGTGAGCAGCCTGGAAGTCTCGCGCAGGTCCTGCCCCAGATACTCTG
 CCCAACCGCACGGTCACCCCTGATTCTGAGTAACAATAAGATATCCGAGCTGAAGAATGGCTCATTCTGGGGTTA
 AGTCTCCTTGAAAGATTGGACCTCCGAAACAATCTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCA
 TCTCTAAAAAGATTGGATCTGACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTGAGGACTCACCAAT
 CTGGTTCCGGCTAAACCTTTCCGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTGATTATCTTGCGTCATTA
 CGGTCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGATGCATCGCTGGGTAAAGGAG
 AAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGTCACTGCAGGCCCAACAGTCACAGGCGTGAAG
 CAGGAGCTGTTGACATGCGACCCCTCCGCTTGAATTGCCGCTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTG
 TTTGAAGGAGACAGCCTTCCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAG
 GATGGGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAACATGATTACAACTGCTCCTTG
 ATTGCAAGTGCCCTAACCATTTCTAATATTCCAGGCTGGATCTACTGGAAATTGGGGCTGTCTATGTCCAGACCAAA
 CGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAGAGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTG
 GTAAACAACAAAGGTGACTTCAGATGGCCGAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACCGGGAAC
 ACCCATGGCAGTGGGATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGC
 TTTTGGGCAGATGATGATTATTCTCGCTGTGAGTATGCAATGATGTCACTAGAGTTCTTTATATGTTTAATCAG
 ATGCCCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGCTTACACTGTGGAAGCAGCCAACCTTT
 TCTGACAAAATGGATGTTATATTTGTGGCAGAAATGATTGAAAATTTGGAAGATTTACCAAGGAGGAAAAATCA
 AAAGAGCTAGGTGACGTGATGGTTGACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCG
 CAGAGGGAAGCTAAAGCCTGCAGTAGGATTGTGCAAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTGA
 GCTCACGTTTATTCAACATATTACCCAATATTGCTCTGGAAGCTTATGTCAATCAAGTCTACTGGCTTCACGGGG
 ATGACCTGTACCGTGTTCAGAAAAGTGGCAGCCTCTGATCGTACAGGACTTTCGGATTATGGGAGGCGGGATCCA
 GAGGGAAACCTGGATAAGCAGCTGAGCTTTAAGTGCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTA
 TGTTACATTCTGCAATCATTTAAGACTATTTACAGTTAAATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAA
 CCTTATTAAAAGATTTTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGTACTGTTTTAAAGAAAACTAACCAG
 GAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCTTTTATTCCCTTTCTTCACATAAAAATATCA
 GAAATTACATTTTATAACTGCAGTGGTATAAATGCAAAATATACTATTGTTACATGTGAAAAAATTTTATTTGACT
 TAAAAGTTTATTTATTTGTTTTTTTGTCTCCTGATTTTAAAGACAATAAGATGTTTTTATGGGCCCCCTAAAAGTATC
 ATGAGCCTTTGGCACTGCGCCTGCCAAGCCTAGTGGAGAAGTCAACCCTGAGACCAGGTGTTTAAATCAAGCAAGC
 TGTATATCAAAATTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTAAAAAAGTATTTTCATTGAAGCA
 AGCAAAATGAAAGCATTTTTTACTGATTTTTTAAATTTGGTGTCTTTAGATATATTTGACTACACTGTATTGAAGCAA
 ATAGAGGAGGCACAACCTCCAGCACCCCTAATGGAACCACATTTTTTTTCACTTAGCTTTCTGTGGGCATGTGTAATT
 GTATTCTCTGCGTTTTTTAATCTCACAGTACTTTATTTCTGTCTTGTCCCTCAATAATATCACAACAATATTCC
 AGTCATTTTAAATGGCTGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTTAGTGTGAGCACTCAATAAA
 TATTGAATGAATGAACGAAAAAAAAAAAAAAAAA

FIGURE 158

MEPPGRRRRGRAQPPLLLPLSLLALLLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGKVVCSSLELAQVLP
PDTLPNRTVTLLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGAFWGLSSLKRLDLTNNRIGCLNADIFR
GLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLFQTEYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPV
TGVKQELLTCDPPELELPSFYMTPSHRQVVFEGDSLPPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIH
NCSLIASALTISNIQAGSTGNWGCCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLGITAYLQ
CTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLNTNAVATARQLLAYTVE
AANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLADERVLWLAQREAKACSRIVQCLQRIATYR
LAGGAHVYSTYSFNIALEAYVIKSTGFTGMTCTVFQKVAASDRGTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSL
ALKVCYILQSFKTIYS

Signal peptide:
amino acids 1-33

Transmembrane domain:
amino acids 13-40 (type II)

N-glycosylation site.
amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336, 433-437,
453-457, 592-596

N-myristoylation site.
amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57, 57-63, 99-105,
123-129, 142-148, 162-168, 317-323, 320-326, 384-390, 403-409, 554-560

FIGURE 159

GGGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGGCTGCTGTTGTTCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGAAAGTATTTATTGACCAAATTAACAGGTCCTTTGGAGAATTACGAACCATGTTCAAGTCAAACTGCAGCTGCTACCATGGTGTCTAGAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAGGAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCCTAAGAACAGACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATTTTGAAGTGTATCGGGCGTCTCCTGACATGGAGATGGTGTCAATGTACGAGATTATCCTCAGGTTCTTAAATGGATGGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACCATGATATCATGTATCCTGCTTGGACATTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTATCCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGAGCAGCACAGTGGCCATGGAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAGATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACCTTGTTGATGCAGAATACACCAAAAACAGGCCGTTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGTGGATCACTGCAAATACAAGTATCTGTTTAAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTAAACACCTCTTCTGTGTGGCTCACTTGTTTTTCATGTTGGTGTAGTGGCTAGAATTTCTTCTATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCAAGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAAGCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTGAGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTTATCCAAAAATGTTGAAAACTGAACTATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCAACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATATCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGAAAGATTTAAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGACCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTTCATTTTCTTAAGACCAATCACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCATGTGATGATGCCCTTTGTCCCATTAATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAACCTATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGCTCACTTTATTTTAAATGTAGGAAACCCTATGGGGTTTATGAAAAATACTTGGGGATCATCTCTGAATGGTCTAAGGAAGCGGTAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTTACTCAGGAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATTTTCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 160

MEWWASSPLRLWLLLFLLP
SAQGRQKESGSKWKVFI
DQINRSLNYPCCSSQNC
SCYHGVIEEDLTPFRGG
ISRK
MMAEVVRRKLGTHYQIT
KNRLYRENDCMFFSRCS
GVEHFILEVIGRLPDM
EMVINVRDYPQVPKWME
PAIPVFSF
SKTSEYHDIMYPAWTF
WEGGPAVWPITYPTGL
GRWDLFREDLVRSAQWP
WKKKNSTAYFRGSRTS
PERDPLILLS
RKNPKLVDAEYTKNQAW
KSMKDTLGKPAAKDVHL
VDHCKYKYLNFNFRGVA
ASFRFKHLFLCGSLVF
HVGDEWLEF
FYPQLKPWVHYIPVKTD
LSNVQELLQFVKANDD
VAQEIAERGSQFIRNHL
QMDDITCYWENLLSEYS
KFLSYNVT
RRKGYDQIIPKMLKTEL

FIGURE 161

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGCCAAA
 CCATGTCTTTTTTCTGTTTTTCAGAGTAGTTTCAACAACAGATCTGAGTGTTTTAATTAAGCATGGAATACAGAAAA
 CAACAAAAAACTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTT
 GGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCCGAGTGTAAGAACCCTTCGGCTCG
 CGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCCCTC
 AAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCTTCCCCACTACAATGTG
 ATAGAACCGTGAACCTGGATGTACTTCTATGAGTATGAGCCGATTTACAGACAAGACTTTCACTTCACACTTCGA
 GAGCATTCAAACTGCTCTCATCAAAATCCATTTCTGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCC
 AGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTA
 GGCCAAGAGGCTGAAAAGGAAGACAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGTGACATA
 ATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTTATGGCATTTCAGGTGGGTAACTGAG
 TTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAATAT
 CTTTTAAACCTAAACCACTCAGAGAAGTTTTTTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTT
 TACCAAAAAACCCATATTTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTAT
 ATAATGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTCACGTAAAACCCATCAAGTTTGAAGATGTT
 TATGTCGGGATCTGTTTGAATTTATTTAAAGTGAACATTTCATATTCAGAGAAGACACAAATCTTTCTTTCTATAT
 AGAATCCATTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTCTTCCAAGGAGATCATCACT
 TTTTGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAACTTCACATTCTACAAAAGCCTAGAAGGACAGG
 ATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTTACACT
 GAACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGGCCCTTCAAA
 GATGATATGTGGAGGAATTAATATATAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGGACCAACAATTTG
 GACATGTCTTCTGTAGACTAGAATTTCTTAAAGGGTGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAA
 AACAATGTAGAGTTTTATTTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAAT
 TTAAAAATATATGTAGTTCTGTGTCAAAAAAATTCTTCACTGAAAGTTATACTGAACAAAATTTTACCTGTTTTTG
 GTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTTACAGTTATTATTATTTAAATTTACTTCACTTTGTGTT
 TTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAATCATTCTTTACATGCAACATTTTCCAGT
 TACTTAACTGATCAGTTTATTATTGATACATCACTCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTA
 ATCTCTTGGACTTTGTAAATATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAA

FIGURE 162

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHFTLREHSNCSH
QNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEKEDKMLALSLEDEHLLYGDIIRQDFLD
TYNNLTCLKTIMAFRWVTEFCPNKYVMKTDTDVFINTGNLVKYLNLNLNHSEKFFTGYPLIDNYSYRGFYQKTHIS
YQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNHIHPEDTNLFFLYRIHLDVC
QLRRVIAAHGFSSKEIITFWQVMLRNTTCHY

FIGURE 163

CATTTCTGAACTAATCGTGTGAGAAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATATTAACCTTTTTAGG
 AGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCGCTCATATATAGGAAAATCGCATATGG
 TCCTAGTATTAAATCTTATTGCTTACTGATTTTTTTGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTG
 AATATAAATAAGAGAAGAAAAAGAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGTGGTT
 TGTTTACATGCAAGCTTATAGTTGAAATATTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTTG
 TTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGACAGCTAGAGCACTTCAGATTCCGTTGCCAA
 CTCGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCCAGGAAATCTGCATAGAAACACTTAGGC
 TTTATACCAGAAAAAGCCAACTATGAATTACTGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAG
 CCAAATTTAAAGCAAAGGGATTGAATCCGGATGGAATCCAGCCCTTCAACCTGGGTGGATTCTCCAGCCT
 CCAAGCCATCATCACCAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAGTCAAAA
 AAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAGAAAAGACAGCAAGAGAAGTAGAA
 ATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACGTTCTAGATCACATACTCCAAGAAGACACTATA
 ATAATAGGCGGAGTCGATCTGGAACATACAGCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTC
 GAAGACATCATAATCATGGTTCTCCTCACCTTAAGGCCAAGCATAACCAGAGATGATTTAAAAAGTTCAAACAGAC
 ATGGTCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAGCCAAGAAAC
 ACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTTGAGAGGTCCCATAAAAGCAAGC
 ACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCGCTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCT
 TGGTTTTGCCTATCTACAGTGTGATGTATGGACTCAATCAAAAACATTAAACGCAAACCTGATTAGGATTTGATTT
 CTTGAAACCTCTAGGTCTCTAGAACACTGAGGACAGTTTCTTTGAAAAAGAACTATGTTAATTTTTTTGCACAT
 TAAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGTTGTGTATTGTTT
 ATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTTTATACAGATAAAATTGCAGACACTGT
 TCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAATACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATT
 TTTACAAGGAAATAAAATACAAATCTTGTTTTTTCTAAAAAAGT

FIGURE 164

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFGTTEEEIQEICIETLRLYTRKKPNYELLEKE
VEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEKSPISINVKTVKKEPEDRQQASKSPYN
GVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYNNRRSRSGTYSSRSRSRSHSESPPRRHHNHGSPHLKAKH
TRDDLKSSNRHGHKRKKSRSRSQSKSRDHSDAAKKRHERGHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

FIGURE 165

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTTA
ATCTGAAGGTTCTCAGTCAAATTCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTT
GGCTGGTTTGGGCCCTTGAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGGCGC
TTCTGTTGCTGGTCTTGCCCTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACCTTCTGTATT
CAGAACTCTGTAAAGGTGCCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAG
ACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAG
ACGAGCCTGGCCTAGACAACCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACT
CTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAA
ATCGAGCTTTGAGTGTTCTTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGGAAA
ATTCTGAAAACACCACTGCCCTGAAGTCTTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACCAGCA
TCAAGATCAATCGAGTAGATCCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAACCCCACTGGTCC
ATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTC
TAAAGTCAACGGGATGGACATCAGCAATGTCCCTCACAACACTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGG
TGCTGTGGCTGACTGTGATGCGTGAAACAGAAGTTCGCGCAGCAGGAACAATGGACAGGCCCCGGATGCCTACAGAC
CCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAATAAACTGGTGCGCA
AGGTGGATGAGCCTGGGGTTTTATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGACATGGTCAGCTTGAGG
AGAAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAGTGGGCTCATCTGATT
AGGCCAGTGAAAGACGTGTTACCTCGTGTGTCGCGCAGGTTTCGCGCAGCGAGCCCTGACATCTTTCAGGAAG
CCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACTCCCAAGCCCCCTCCATCCTA
CAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCCGGTGAATCTCTCGGCATGACCGTCGCAGGGG
GAGCATCACATAGAGAATGGGATTTGCCATCTATGTCATCAGTGTTGAGCCCGGAGGAGTCATAAGCAGAGATG
GAAGAATAAAAAACAGGTGACATTTTGTGTAATGTGGATGGGGTCGAACTGACAGAGGTGAGCCGGAGTGAGGCAG
TGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGCCCCAGGAAG
ACTGCAGCAGCCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCTGGGTCA
TGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTCTGG
GCTTCTGCATTGTAGGAGGTTATGAAGAATAAATGGAAACAAACCTTTTTTTCATCAAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGCTGTCAATGGTAGAAGTACATCAGGAA
TGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACCTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTG
GCACTTTTTTATAGAATCAATGATGGGTGAGGAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACT
ATATTTATCTTGTCAGTTTTTATATTTAAAGAAAGAATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAA
TGAAAGCCAGTTACACCTCAGAAAATATGATTCCAAAAAATTAATACTACTAGTTTTTTTTTCAGTGTGGAGGAT
TTCTCATTACTCTACAACATTGTTTATATTTTTCTATTCAATAAAAAGCCCTAAAACAATAAATGATTGATT
TGTATACCCCACTGAATTCAGCTGATTTAAATTTAAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTAT
GGCCATTTTTAATTTACAGCTAAAATATTTTTTAAAATGCATTGCTGAGAAACGTTGCTTTCATCAAACAAGAA
AAATATTTTTTCAGAAGTTAAA

FIGURE 166

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPSPEVSAAATIS
LMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINRALSVLRRTKSGSAVANHADQ
GRESENTTAPEVFPRLYHLIPDGEITSIKINRVDPSELSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPG
DIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIK
LVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQRSPDI
FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVI
SRDGRIKTGDILLNVVGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPPSDWSP
SWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFPIKSIVEGTPAYNDGRIRCGDILLAVNGRS
TSGMIHACLARLLKELKGRITLTIVSWPGTFL

FIGURE 167

GGGAAAGCCATTTTCGAAAACCCATCTATACAAACTATATATTTTCATTTCTGCTGCTAGCTGCCTTGGGCCCTCAC
AATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAATGGAGTTGATCCCAACCATAACATCGTGGAG
GGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTGGTGTGGCTTTCCTTTCAGAGGATTCCACCTTCAAAATCA
TGAACTCTGGCTGTTGATCAAAAGAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCT
AGCAGAAGACTCAACCTGGCCTCCCATAAACAGGACAGATTATTCAAGTGATGGCAAAAATGGATTCTACATCAA
CGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAACCACAGAACAGCATT
CTGGGCCAGGCTGTAATCAGAATTGTCGTGCTACATGCTCAACAGCATTGCTTTTTTCCCCAAAATTAACACATT
GTGGAGAAGTGATGATACTCTCCCCTTACCTTTCCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATT
AAACCTTGCAGCAAGGGACCTTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATT
CCTGTATCATCCTTTTCAATAAACTGTATTCATTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLAEDSTWPPINRTDY
SGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

FIGURE 169

[illegible]

FIGURE 170

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYTIPCCRNEENE
CDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQVLRAPKGQILLESYPLNAHC
EWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQIIKRVCGNERPAPIQSIGSSLHVLHSDGSKN
FDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKCACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLI
NGRHAKIGTVVSFFCMNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLY
SAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIE
NITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLG
KFYRDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAG
WNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPG
RASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 171

CTGTCGTCCTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCCAAGTGTGGCTTA
ATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACCGCTGCCATGCCAGTGACGGTAACCCG
CACCACCATCACAACCACCACGACGTATCTTCGGGGCTGGGGTCCCCCATGATCGTGGGGTCCCCCTCGGGCCCT
GACACAGCCCCCTGGGTCTCCTTCGCCTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGT
GGGCGCCTGGACGGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGCTTCTGCTTCTCCGTGACCTGATCAT
CCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCCATCACCTTCGCCTG
CTATGCGGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCACCTATGTCCAGTTCCTGTCCACGGCCG
TTCGCGGGACCACGCCATCGCCGCCACCTTCTTCTCCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTG
GACCCGGGGCCCGGGCCGGCGAGATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTT
CGTTGCCTGCATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGTGCCT
GGCGGTGTACGCCATCTGCTTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGGGAGTGCACCAACGTGCT
ACCCATCCCCCTCCCCAGCTTCTGTGCGGGCTGGCCTTGCTGTCTGTCTCTCTCTATGCCACCGCCCTTGTTCT
CTGGCCCCCTCTACCAGTTCGATGAGAAGTATGGCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGAG
CCATGCCCTACTACGTGTGTGCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTA
TGTGGCTGACCTGGTGCCTCTGCCCCACCTGGTTTTTGTCAAGGTCTAAGACTCTCCCAAGAGGCTCCCGTTCCC
TCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCTCCGCCCTTCTCTGTTTTT
CTCTTCTGTCTCCCCCTCCCTCCACCTTTTTCTTTCTTCCCAATTCTTGCACTCTAACCACTTCTTGATGC
ATCTTCTTCTCTCCCTTTCTCTTGCTGTTTTCTTCTGTGTTTTGTTGCCCCACATCCTGTTTTCAACCTG
AGCTGTTTTCTCTTTTTCTTTCTTTCTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCAGGCTG
GAGTGCAGTGGTGCATCTCAGCTCACTGCAACCCCGCCTCCTGGGTTCAAGCGATTCTCCTCCCCAGCCTCC
CAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTCTCTTTTTTCACTCTTCTTTTTTCTCATC
TCTTTTCTGGGTGCTGCTCGGCTTCTTATCTGCCTGTTTTGCAAGCACCTTCTCCTGTGCTCTGGGAGCCCT
GAGACTTCTTTCTCTCCTTGCTCCACCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGACGCCGTCC
ATGCCACAGCCCCCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCTTGTAGTCACTGTGTAC
GTGTGTGTGTGTGTGTGTTGGGGGGTGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTCTCCCAGTGGAGGAA
GGTGTGCAGTGTACTTCCCCCTTTAAATTAAAAAACATATATATATATATATTTGGAGGTCAATTTCCAATGG
GCGGGAGGCATTAAGCACCGACCTGGGTCCCTAGGCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAG
AATTTTTGCCAGGCTTACAGAACACCCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTTCT
CCCAACTATTCTCTGTGGTATGAAAAAG

FIGURE 172

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTGSMGNWSMFTWCFC
FSVTLIILIVELCGLQARFPLSWRNFPI TFACYAALFCLSASIIYPTTYVQFLSHGRSRDHAI AATFFSCIACVA
YATEVAVTRARPGEITGYMATVPGLLKVLETFVACII FAFISDPNLYQHQP ALEWCVAVYAICFILAATAILLNL
GECTNVLPIPFPSFLSGLALLSVLLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILT
AINLLAYVADLVHSAHLVFVKV

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 173

GAACGTGCCACCATGCCAGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTC
TTGAACTCGTGACCTCATGATCCGCTCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGACGC
CTGGCCAGCCTATGCATTTTTAAGAAATTATTCTGTATTAGGTGCTGTGCTAAACATTGGGCACTACAGTGACCA
AAACAGACTGAAT'TCCCCAAGAGCCAAAGACCAGTGAGGGAGACCAACAAGAAACAGGAAATGCAAAAGAGACCA
TTATTACTCACTATGACTAAGGGTCACAAATGGGGTACGTTGATGGAGAGTGATTTGTTAAGAGACTACAGAGGG
AGGACAGACTACCAAGAGGGGGGCCAGGAAAGCTCCTCTGACGAGGTGGTATTTTCAGCCCAAAGTGAAGAATGA
GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGGAGCACTACACTCACTACACTTTGGCCTGAGAA
AATAGCATGGGATTGGAGGAGGCTGGGGGAACACCACCTTCTGCCGACCTGGGCAGGAGGCATTGAGGGCTTGAGA
AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTTCAGGTGGAATCATTAGGTCTTATC
AACAGATATGGGCAAGCAAAGCCAGGGGAGAATTGATGGTAATGCTGAGGTTTGGAGCCAGGCTAGATGGGACAG
TGGTGGGTGATGCAAAGGAAAGAGGTGAGGAAGCAGGGCCAGACGTGGGGAGAAGGTGTGGGGGTTTGGTTTCCA
CTTGCCGAGCTGCGCGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGGCAGAGGGGAAGGGAATCTTAA
AGAAGTCCCTGGATGCCACACTCTTCTTCCCTTCCCTCCTTCCCTCCTCAGAGGTCTCACTCGTGGTCTTTCAT
TTCCCTGCCCTGCCCTCCATCTCCTCTGGGTGCTGGGAAAGTGGAGGATTAGCTGAAGTTTTCCTTCTCGGGGCTG
TCTGAATCTCCATTGCTTTCTGGGAGGACATAATTACCTGTCTCTAGCTTCTTATCATCTTACATTTCCCTGTAG
CCACTGGGACATATGTGGTGTCTCTTCCCTAGCTCCTGTCTCCTCCTCATGCCTTTGCTGGGTATGGGCATGTTAG
GGGGAAGGTCAATTGCTGTCAGAGGGGCACTGACTTTTCTAATGGTGTACCCAAGGTGAATGTTGGAGACACAGTC
GCGATGCTGCCAAGTCCCGGCGAGCCCTAACTATCCAGGAGATCGCTGCGCTGGCCAGGTCTCTCCCTGCATGGT
ATGCAGCCCCCTCCCAATGTTTCTGGCCACTTTGTCTTTCTCCTCCCGTTTGACATCCCTTTTGAAGCTGTTTCCT
GTAGTACATGTGGGTCTCCCCCTTTCTCCCTTGTCTCAGGTGAATCTCAGCCCCCTTCTCCACCCAAAGGTTT
ACATGGATCCTAAGTATGCGACCCCTTCCACCTCCCTGCACCTGTGCTCCCTGGCCTGGTCCCTTACCAGGCTTC
TCCACCCCTCCCTATCTCCAGGTATTTCCAGGTGGTGAAGGACCACGTGACCAAGCCTACCGCCATGGCCCAAG
GCCGAGTGGCTCACCTCATTGAGTGAAGGGCTGGAGCAAGCCGAGTGAATCACCTGCTGCCCTGGAATCAGCCT
TTTCTCCTATTCAGACCTCAGCGAGGGCGAACAAGAGGCTCGCTTTGACAGCAGGAGTGGCTGAGCAGTTTGCCA
TCGCGGAAGCCAAGCTCCGAGCATGGTCTTCGGTGGATGGCGAGGACTCCACTGATGACTCCTATGATGAGGACT
TTGCTGGGGGAATGGACACAGACATGGCTGGGCAGCTGCCCTGGGGCCGACCTCCAGGACCTGTTACCCGGCC
ACCGGTTCTCCCGGCTGTGCGCCAGGGCTCCGTGGAGCCTGAGAGCGACTGCTCACAGACCGTGTCCCCAGACA
CCCTGTGCTCTAGTCTGTGACGCTGGAGGATGGGTTGTTGGGCTCCCCGGCCCGGCTGGCCTCCAGCTGCTGG
GCGATGAGCTGCTTCTCGCCAAACTGCCCCCAGCCGGGAGGCTCCCTCCGACGCTGGGCCCACTGGAGGCC
AGGACTCACTCTACAACTCGCCCCCTCACAGAGTCTCTGCTTTCCCCCGCGGAGGAGGAGCCAGCCCCCTGCAAGG
ACTGCCAGCCACTCTGCCACCCTAACGGGCAGCTGGGAACGGCAGCGGCAAGCCTCTGACCTGGCCTCTTCTG
GGGTGGTGTCTTAGATGAGGATGAGGCAGAGCCAGAGGAACAGTGAACCCACATCATGCCTGGCAGTGGCATGCA
TCCCCCGGCTGCTGCCAGGGGAGAGCCTCTGTGCCCAAGTGTGGGCTCAAGGCTCCAGCAGAGCTCCACAGCC
TAGAGGGCTCCTGGGAGCGCTCGCTTCTCCGTTGTGTGTTTTGCATGAAAGTGTGTTGGAGAGGAGGCAGGGGCTG
GGCTGGGGGCGCATGTCTGCCCCCACTCCCGGGGCTTGCCGGGGGTTGCCCGGGGCTCTGGGGCATGGCTACA
GCTGTGGCAGACAGTGTATGTTTCAATGTTTAAATGCCACACACATTTCTCTCGGATAATGTGAACCACTA
AGGGGGTTGTGACTGGGCTGTGTGAGGGTGGGGTGGGAGGGGGGCCAGCAACCCCCCACCCTCCCCATGCCTCTC
TCTTCTCTGCTTTTCTTCTCACTTCCGAGTCCATGTGAGTGTCTTGATAGAATCACCCCCACCTGGAGGGGCTGG
CTCCTGCCCTCCCGAGCCTATGGGTTGAGCCGTCCCTCAAGGGCCCCCTGCCAGCTGGGCTCGTGTGTGCTTC
ATTCACCTCTCCATCGTCTCTAAATCTTCTCTTTTCTTAAAGACAGAAGGTTTTTGGTCTGTTTTTTCAGTC
GGATCTTCTCTTCTCTGGGAGGCTTTGGAATGATGAAAGCATGTACCCTCCACCCTTTTCTGGCCCCCTAATGG
GGCCTGGGCCCTTTCCCAACCCCTCCTAGGATGTGCGGGCAGTGTGCTGGCGCCTCACAGCCAGCCGGGCTGCCC
ATTCAGCAGAGCTCTCTGAGCGGGAGGTGGAAGAAAGGATGGCTCTGGTTGCCACAGAGCTGGGACTTCATGTT
CTTCTAGAGAGGGCCACAAGAGGGCCACAGGGGTGGCCGGGAGTTGTGAGTGTGCTGATGCTGCTGAGAGGCAGGAAT
TGTGCCAGTGAAGTACAGTACAGGGGCCCCGCCCCAGCCAGGGTGTAAATGCCACGTAAGTGGAGGCTCTGGCAG
ATCCTGCATTCCAAGGTCACTGGACTGTACGTTTTTATGGTTGTGGGAAGGTTGGTGGCTTTAGAATTAAGGGC
CTTGTAGGCTTTGGCAGGTAAGAGGGCCCAAGGTAAGAACGAGAGCCAACGGGCACAAGCATTTCTATATATAAGT
GGCTCATTAGGTGTTTATTTTGTCTATTTAAGAATTTGTTTTATTAAATTAATATAAAAAATCTTTGTAAATCTC
TAAAA

FIGURE 174

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKVMHDPNYCHPSTSLHLCSLAWSFTRLLHPPL
SPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALSAFSSYSDLSEGEQEARFAAGVAEQFAIAEAK
LRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLGPHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSS
LCSLEDGLLGSPARLASQLLGDELLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEEPAPCKDCQPL
CPPLTGSWERQRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:
amino acids 1-15

Casein kinase II phosphorylation site.
amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232, 285-289,
324-328

Tyrosine kinase phosphorylation site.
amino acids 44-52

N-myristoylation site.
amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 11-22

FIGURE 175

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTGGCACCCCTCCTGC
TCAGTGCACATTTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGACAGATTCCCTTTCAGACAGGACAACCTG
TGATATTTTCTGTTCCCTGATTGTAAATACCTCCCTAAGCCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTT
CTTCATCTGCAAAATGGGCATAATACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACC
AATACCAAAGAAGCCTACAATGTTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCTATC
GGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTTTTAAAAACAATGGAAAA
TAAACCTATTTCTTTGGAAAGTGAAGCAAACTTAAACTCAGATAAAGAAAAATATAACCACCTCAAATCTCAAGGC
GAGTCATTCCCCTCCTTTGAATCTACCCAACAACAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGA
GCATTCTTTGGGCAGTCTAAAACCCACATCTACCATTTCACACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAA
AGTGCCCTTGGAAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACCTGCTCT
GTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATAACAGTTCCATTACAGTTAG
CATCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTGATAGTGGAACCAAGTGGATGGCTTACCACAAA
CAGTGATAGCTTCACTGGGTTTACCCCTTATCAAGAAAAACAACCTCTACAGCCTACCTTAAATTCACCAATAA
TTCAAAACCTCTTTCCAAATACGTCAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTT
AGGTGCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAAAAGGAAAACGGATTCATT
TTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACAATGCACCGGAACCTTATGATGT
GAGTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAATGATTGAGCCATGCCAGAAAGTGAAGAAAATGCACG
TGATGGCATTCCATATGGATGACATACCTCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACA
GCAAGTGTCATCTACATCCTAGCCTTTTGACAAATTCATCTTTCAAAAAGGTTACACAAAATTACTGTCACGTGGA
TTTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCATCCAAAGGTTTTTC
TTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATTTGTATTTTAGTAGTATTTCTTAGT
AGAAAATATTTGTGGAATCAGATAAACTAAAAGATTTCAACATTACAGCCCTGCCTCATAACTAAATAATAAAA
ATTATTCCACCAAAAAATTCTAAAACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATT
CAAGATTGCATTTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAGGA
CATAGCCCAGAGTTTCTGTTATTTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTCTAGTACGTTATAATT
TTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGACAATGACTGCATTCAACGGGGCCATGGC
AGGAAAGCTGACCCTACCCAGGAAAGTAATAGCTTCTTTAAAAGTCTTCAAAGGTTTTGGGAATTTAACTTGTC
TTAATATATCTTAGGCTTCAATTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTONIAEVFKTMENKPISLESEANLNSDKENITTSNLKASHSPPL
NLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNAPIADEDLLPISAHPNATPALSSSENFT
WSLVNDTVKTPDNSSITVSISSSEPTSPSVTPLIVEPSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNP
TSDPQKENRNTGIVFGAILGAILGVSLTLVGYLCCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSGNNS
YYNPTLNDAMPSEENARDGIPMDIPPLRTSV
```

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159, 163-167, 218-222,
225-229, 298-302, 307-311

FIGURE 177

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTTCTTGCCCT
 GCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACTTTCCACCTTTCCCTA
 CAAATTCGATTACTGTTGCTGTTGACTTTGTGCTGACAGTGGTTGGGTGGGCCACCAGTAACTACTTCGTGGG
 TGCCATTCAAGAGATTCTAAAGCAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAA
 AACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGTCTTCTGTGTCTCCTTACCTCAGAGG
 CCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGG
 CCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAAACA
 CCTGATGTACCTGCTGGAACATCTGCATCCCTTCTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCA
 CCAGGCTGAAGGTAAAAAGTTTAAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAA
 TTGGGACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAGCA
 TCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGGGGGTGTAC
 TGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACCTACTGGGGATGGGGAGGCGAAGACGA
 TGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAAT
 GGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACCGAGT
 CTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATATATCAACAT
 CACAGTGGATTTCTGGTTTGGTGCATGAACCTGGATCTTTTGGTGATGTTTGAAGAAGTATTCTTTGTTTGCA
 ATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTAAAGAACCTGTACAGCTCATTTGTTGAGCTGAATTTT
 TCCTTTTGTATTTTCTTAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAG
 TCATTTTGATCATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAAGGATGACTCAAAGGA
 TAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGATAAAA
 GGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACAGAGTTGTTCTCGTCCAAGGTAGAAAGGTACGAAGA
 TACAATACTGTTATTCAATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAA
 GAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGGC
 TGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCTTC
 CAGTGATGCCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGG
 ATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAAT
 GTGAAAAGCAAAA

FIGURE 178

MGFNLT FHLSYKFRL L L L L L L T L C L T V V G W A T S N Y F V G A I Q E I P K A K E F M A N F H K T L I L G K G K T L T N E A S T K K V E L D
N C P S V S P Y L R G Q S K L I F K P D L T L E E V Q A E N P K V S R G R Y R P Q E C K A L Q R V A I L V P H R N R E K H L M Y L L E H L H P F L Q R
Q Q L D Y G I Y V I H Q A E G K K F N R A K L L N V G Y L E A L K E E N W D C F I F H D V D L V P E N D F N L Y K C E E H P K H L V V G R N S T G Y R
L R Y S G Y F G G V T A L S R E Q F F K V N G F S N N Y W G W G G E D D D L R L R V E L Q R M K I S R P L P E V G K Y T M V F H T R D K G N E V N A E
R M K L L H Q V S R V W R T D G L S S C S Y K L V S V E H N P L Y I N I T V D F W F G A

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

FIGURE 179

CGTGGGCGGGGCTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGAGTTCTCGAGCTCCAGCTGC
ATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCCGCAATGGCCCCAGGCAGTGTGGTTCGCGCCTCGG
CCGCATCCTCTGGCTTGCTGCCTCCTGCCCTGGGCCCCGGCAGGGGTGGCCGCAGGCCTGTATGAACTCAATCT
CACCACCGATAGCCCTGCCACCACGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAG
CCTGGCCCTGCCCGCTGACGCCCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAAGAT
GGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTTCGGCCACGTGCCCGGGGAATTCCCGGTCTCTGTCTGGGTAC
TGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTGGTCTCTCCCATCACAGAGTTCTCTCGTGGG
GGACCTTGTTGTACCCAGAACACTTCCCTACCCTGGCCAGCTCCTATCTCACTAAGACCGTCTCTGAAAGTCTC
CTTCTCTCTCCACGACCCGAGCAACTTCTCAAGACCGCCTTGTTTCTCTACAGCTGGGACTTCGGGGACGGGAC
CCAGATGGTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCTCAAAGT
GGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGACCGGGGACTTCTCCGCCCTC
GCTGAAGCTGCAGGAACCCCTTCGAGGCATCCAAGTGTTGGGGCCCCACCCTAATTGAGACCTTCCAAAAGATGAC
CGTGACCTTGAAGTCTCTGGGGAGCCCTCCTCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCCTCCCGCTGGA
GGAAGGGGAGTGCCACCCCTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCCCTGGGGGA
CTACTGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGTGTGGCCCTC
CAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGATGTTGGCCTTCATCATGTACAT
GACCTTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAGAACCCGGAGCCACCCTCTGGGGTCAGGTGCTGCTG
CCAGATGTGCTGTGGGCCTTTCTTGCTGGAGACTCCATCTGAGTACCTGGAAATTGTTCTGTGAGAACCACGGGCT
GCTCCCGCCCCCTCTATAAGTCTGTCAAACTTACACCGTGTGAGCACTCCCCCTCCCCACCCCATCTCAGTGTTA
ACTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCAATTTGCGTGGGGCTG
TTGGCCTGGATCATCCATCCATCTGTACAGTTGAGCCACTGCCACAAGCCCCCTCCCTCTCTGTACCCCTGACCC
CAGCCATTACCCATCTGTACAGTCCAGCCACTGACATAAGCCCCACTCGGTTACCACCCCTTGACCCCTACC
TTTGAAGAGGCTTCGTGCAGGACTTTGATGCTTGGGGTGTTCGGTGTGACTCCTAGGTGGGCCTGGCTGCCAC
TGCCCATTCCTCTCATATTGGCACATCTGCTGTCCATTGGGGGTTCTCAGTTTCTCTCCCCAGACAGCCCTACCT
GTGCCAGAGAGCTAGAAAGAAGGTCAAAAGGGTAAAAATCCATAACTAAAGGTTGTACACATAGATGGGCACA
CTCACAGAGAGAAGTGTGCATGTACACACACACACACACACACACACACAGAAATATAAACACATG
CGTCACATGGGCATTTGAGATGATCAGCTCTGTATCTGGTTAAGTCGGTTGCTGGGATGCACCCCTGCACTAGAGC
TGAAAGGAAATTTGACCTCCAAGCAGCCCTGACAGGTTCTGGGCCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCA
GTTCTTGCGCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACTAATAC
TGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTGAACTTTCACTGAGGAAA
AGGCCTTGACGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGG
AGGCCGAGGCGGGTGGATCACGAGATCAGGAGATCGAGACCACCCTGGCTAACACGGTGAACCCCGTCTCTACT
AAAAAATACAAAAGTTAGCCGGGCGTGGTGGTGGTGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGA
GAATGGTGCAGAACCCGGGAGGCGGAGCTTGCAGTGAGCCAGATGGCGCCACTGCACTCCAGCCTGAGTGACAGA
GCGAGACTCTGTCTCCA

FIGURE 180

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLALPADAHLRFRHWI
HTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVWTAADCWMCQPVARGFVVLPITEFLVGDLVVTQNTSLPWPS
YLTKTVLKVSFLLHDPNFKTALFLYSWDFGDTQMVTEDSVVYYNYSIIIGTFTVKLKVVAEWEEVEPDATRAV
KQKTGDFSASLKLQETLRGIQVLGPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYN
LTHTFRDPGDYCFSSIRAENIISKTHQYHKIQVWPSRIQPAVFAPPCATLITVMLAFIMYMTLRNATQQKDMVENP
EPPSGVRCCCMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 181

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGGTGGGCCCTCGGGCCTGACAGATGGCAGTGGC
 CACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCGGCCCGCCGGTTCTGTGGGCGCCAGGGT
 CCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCATGCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGG
 CCTGGGCGCGCCACGGCCGCGGAGCTACTGCGCCTGGGAGCGCGGTGATCATGGGCTGCCGGGACCGCGCGCG
 CGCCGAGGAGGCGCGGGTCACTCCGCGCGGAGCTCCGCCAGGCGCGGAGTGCGGCCAGAGCCTGGCGTCAG
 CGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCGCCTTCTGCCAGGAAAT
 GCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGGATCTTCCAGTGCCCTTACATGAAGACTGA
 AGATGGGTTTGAGATGCAGTTCGGAGTGAACCATCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCT
 CAAAAGTTCAGCTCCAGCAGGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGA
 CTTGAACAGTGAACAAAGCTATAATAAAAGCTTTTGTTATAGCCGAGCAAACCTGGCTAACATTCTTTTTACCAG
 GGAAGTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTGTCATCCTGGTATTGTACGGACAAATCT
 GGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTCAATTTGGTGTGTCATGGGCTTTTTTCAAACCTCC
 AGTAGAAGGTGCCCAGACTTCCATTTATTTGGCCTCTTCACTGAGGTAGAAGGAGTGTGAGGAAGATACCTTTGG
 GGATTGTAAAGAGGAAGAAGTGTGCCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGA
 AGTGATGGTTGGCTGCTAAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAGTTATATCTG
 TGATCAGGAATGGTGTGGATTGAGAACTTGTACTTGAAGAAAAAGAAATTTTGATATTGGAATAGCCTGCTAAGA
 GGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTTGGGATAAGAGAATTCAGCAAAGATGTTTAAAT
 ATATATAGTAAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATACTGGGCAAGCA
 TGGATGACATATTAATATTTGTCAGAATTAAGTGAAGTCAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGT
 TTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAATATCTGCCTGGTGTGTGCA
 CACAAGTCTTACTTGAATAAAATTTACTGGTAC

FIGURE 182

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAELLRLGARVIMGCR
DRARAEAAAGQLRRELRLQAAECGPEPGVSGVGELIVRELDLASLRSVRAFCQEMLQEEPRLDVLINNAGIFQCPY
MKTEDGFEMQFGVNHFGHLLTNLLLGLLKSSAPSRIVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANI
LFTRELARRLEGTVNVTNVNLHPGIVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSG
RYFGDCKEEELLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

FIGURE 183

AACAGGATCTCCTCTTGCACTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGCAGCCCGAAGATTCT
ACTATGGTGAAAATCGCCTTCAATACCCCTACCGCGTGCAAAAGGAGGAGCGCGGCAAGACGTGGAGGCCCTC
CTGAGCCGCACGGTCAGAACTCAGATACTGACCGGCAAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCC
TCTGGGAGATGTATGCTTACTCTCTTAGGCCTTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATT
TACAAGTACTTCATGCCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCAAAAT
TCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCTGTGAGGATGACAACATTGCA
ATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCTGCAGCAATTATTCATGACTTTGAAAAGGGAATG
ACTGCTTACCTGGACTTGTGCTGGGGAACCTGCTATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAA
AATCTGGTAGAGCTCTTTGGCAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTA
GTTGCTGTGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGAAAGTCC
TTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTCACCAAACGTGCCATTGATAAATGCTGGAAGATTAGACAC
TTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGTAAGAGGCAACAGATAGAGTGTCTTGGTAATA
AGAAGTCAGAGATTTACAATATGACTTTAACATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTAC
TCTATTGCTTATGCTTTAAAAAAGGAAAAAAAAAAAAAATACTAACCAGTCAAGCTCTTGTCAAATTTTAGTT
TAATTGGCATGCTTGTTTTTTGAACCTGAAATTACATGAGTTTCATTTTTCTTTCATTTATAGGGTTTAGAT
TTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCCGTTGTTTTTTTGTGTTTGT
TTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATGGTGGAGCAATTTTAAATTTGAAATATTTAAAT
GTTTTTGAACTTTTTGTGTAAAATATATCAGATCTCAACATTGTTGGTTTCTTTGTTTTTCATTTGTACAACT
TTCTTGAATTTAGAAATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAAT
TTTCATGAGACAGTCATTTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGGAATGCACAAAAT
TGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATCTACAACCTATAATAAATTTTACTCTATAC
AAAAAAAAAAAAAAAAAAAA

FIGURE 184

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSFILAGLIVGGACIY
KYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIAI IDVPVPSFSDSDPAAI IHDFEKGMT
AYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASGRYLPQTYVVREDLVAVEEIRDVSNLGIFTYQLCNNRKSF
RLRRRDLLLGFNKRAIDKCWKIRHFPNEFIVETKICQE

Type II transmembrane domain:
amino acids 53-75

N-glycosylation site.
amino acids 166-170

Casein kinase II phosphorylation site.
amino acids 35-39, 132-136, 134-138

N-myristoylation site.
amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 63-74

FIGURE 185

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGGCCGCTTGCCCT
CCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCACAACAGACGGGACAACCTGCAGAGCT
GCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCA
CTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCT
ACCTGCCCTGCCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGG
CTGGTTCTTTGTTTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 186

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPICIFCCGCCHR
SKCGMCCKT

FIGURE 187

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGCCTGGATCTTCCAC
CATGTTCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGCATCTCCCTGACTGTCTCTTACCCT
CCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGGAGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCT
GTTAAAAATCTTTGCGTGGGCTACCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCC
CTACACCAACGGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTTCGTCGAAGTGGTAG
TAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGGCCGAAAGGAATGGAGAC
CATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTGGAGTCTTGGAACCTGCTGAGCAGAACCAA
TTATAACTTCCAGTACATCAGCCTTCGGCTCACGGTCTGTGGGGGTTAGGAGTGCTGATTCCGTACTGCTTTCT
GCTGCCGCTCAGGATAGCACTGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTT
GCCAAATGGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCGAGCGCT
GACAGCCATCATCACTACCATGACAGGGAACAGACCAAGAAATGGTGGCATCTGTGTGGCCAATCATACCTC
ACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCCATGGTGGGTCAAGTGCACGGGGGACTCATGGG
TGTGATTTCAGAGAGCCATGGTGAAGGCTGCCCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCT
GGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAAGGAACCTG
CATCAATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCCTGTTGCTAT
CAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGATGGTGACGTACCTGCTGCGAAT
GATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTGCCTCCCATGACTAGAGAGGCAGATGAAGATGCTGT
CCAGTTTGCGAATAGGGTGAAATCTGCCATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCT
GAAGAGGGAGAAGGTGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
CAAGGACAGGAGCCGCTCT**TGAG**GCCTGCCTCCAGCTGGCTGGGGGCCACCGTGCGGGGTGCCAACGGGCTCAGAGC
TGGAGTTGCCGCCGCCGCCCTGCTGTGTCTTTCCAGACTCCAGGGCTCCCCGGGCTGCTCTGGATCCCAG
GACTCCGGCTTTTCGCCGAGCCGCAGCGGGATCCCTGTGCACCCGGCGCAGCCTACCCTTGGTGGTCTAAACGGAT
GCTGCTGGGTGTTTGCACCCAGGACGAGATGCCTTGTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAG
TGAAGTCCCCACCTTTGCACGCTGTGCGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGATGG
CGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCGCTCTCCAGGAAAGGC
ACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCAGCCTTGGAGCTCTGCAGACATGATAGGAAG
GAAACTGTCTATCTGCAGGGGCTTTTCAGCAAATGAAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAA
GGGAGGGGAAGAGGCCAGGTGGGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTGCTACTCCAGGCTAACCTG
AACTCCCCATGTGATGCGCGCTTTGTTGAATGTGTGTCTCGGTTTCCCCTCTGTAATATGAGTCGGGGGGAATG
GTGGTGATTCTTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGAAGGACACATCACGTTTCA
GTTTTCAAGTACAGGCCCAAAAACGGGGCACGGCAGGCCTGAGCTCAGAGCTGCTGCACTGGGCTTTGGATTG
TTCTTGTGAGTAAATAAACTGGCTGGTGAATGA

FIGURE 188

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIIVPAIFGVSGIRKLYMKSLLKIFAWATLRMERGAKEKNHQLYKP
YTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKG METIMDDEVTKRFS AEELESWNLLSRTN
YNFYISLRLTVLWGLGVLIRYCFLLPLRIALAF TGISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRL
TAIITYHDRENRPNGGICVANHTSPIDV IILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHL
VAKRLTEHVQDKSKLPILIFPEGTCINNTSVM MFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYLLRM
MTSWAIVCSVWYLPPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTFKEEQQKLYSKMIVGNH
KDRSRS

FIGURE 189

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCACGTCTCCTCCAGG
GATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCACACCTGGCAGGCCCAGGCTGTTCCAC
CATCCTGCCCCCTGGGCCTGGCTCCAGACACCTTTGACGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAA
GGCAGCCCCCTGCTAAAGGAGGAAATGGCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGAC
CTGGGAGGACAAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGTCTA
CACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAGGCTCCCGGAGCTCTA
CATGAGGCACTTTCCCTTCAAGGCCCTGCATTCTACCTGATCCGGGCCCTGCAGCTGCTGCGAGGCAGTGGGGG
CTGCAGCAGGGGACCTGGGGAGGTGGTGTTCGAGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGA
CTCTGTCCGCTTGGGCCAGTTTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCG
GGGCTGTGTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTGGAAGAC
TCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCCCCTGAAGTCCAACATCTGCCACTTAGGAGC
CCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAGCAGCCTTGAGAAGCAAGAACATGGTTCCGGAC
CCAGCCCTAGCAGCCTTCTCCCCAACCAGGATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACTCTGCTA
TGTGATGGGGACTTCCTGGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGA
GACATGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 190

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHHALLRESWEAAQET
WEDKRRGLTLPPGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSRELYMRHFFFKALHFYLIRALQLLRGSGG
CSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSSLDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKT
LLLAPGEFQLSGVGP

FIGURE 191

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCCCTCATCTATAT
CCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGAC
TTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCAT
ACAGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTA
CTCCCTGAAGCTCAGCAAACTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCA
GCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCA
GAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATAC
CTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGA
AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAA
GCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCT
CAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAA
GAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCC
TCACACTAATAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGC
AGTGCACTCCCTAAGTCTCTGCTCA

FIGURE 192

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGTIIIVTON
RNRERVDFPDGGYSLKLSKLLKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLT
CCMEHGEEVDIYTWKALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSS
MVLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA
NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI

FIGURE 193

[illegible]

FIGURE 194

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLILLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPALSPTSMGPQPTTLG
GPSPTNFDLGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKASAYYPSSFPKKKYVDQSDRAGGPRAF
SEVPDRAPDSRPPEALDSSRQLQADILAAATQNLKSPTRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVP
VETPEAQEEPCSGVLEGAVVAGEGQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV
```

Signal peptide:
amino acids 1-25

Transmembrane domain:
amino acids 94-118

N-myristoylation site.
amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199, 211-217, 238-244,
242-248

FIGURE 195

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCTGCTGTGTTTGGGA
CTGACCCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGAACTTTAATGTAGAAAAGATTAATGGG
GAATGGCATACTATTATCCTGGCCCTCTGACAAAAGAGAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTG
GAGCAAATCCATGTCTTGGAGAATTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTA
TCTATGGTTGCTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACTATA
CCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGAAACCTTCCAGCTGATG
GGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAAGGTTTGCACAACCTATGTGAGGAGCATGGA
ATCCTTAGAGAAAATATCATTGACCTATCCAATGCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGA
GCCTCCAGTGTTGAGTGGAACACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTA
TAAATTCTGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACCTAGGAT
ACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAATTTTTTCATGAAATTATTCTT
CTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

FIGURE 196

MKMLLLLCGLTLVCHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQIHVLENSLVLKVH
TVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLINEKDGETFQLMGLYGREPDLSSDIKE
RFAQLCEEHGILRENIIDLSNANRCLQARE

FIGURE 197

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGATTTCAGCCTG
CTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCTTAGTTGAGGAAGACCAATTT
TCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCTCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCA
ACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTC
AGTGTGATCACAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATG
TGTAATTCCTCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCC
TTCAACTTGCAGTGGTTTTTCAATGACTCTTGTCACCTCCTACTGGTTTCAATAAAACCCACCAGTAACGACACC
ATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCA
GTATTTTTAGGTCTATTGCTTGTTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTT
GGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTATCAGTA
GTTTGAAAAAAAAAAAA

FIGURE 198

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPATTMSLTARKR
ACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDS
CAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRR
SQIV

FIGURE 199

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGAAGGAGCAGTG
AGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAGATCCGTGGGCTGCAGACCCC
CGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGACATGGGAGAGAGTGACCCTGGCCCTTCTCCT
ACTGGCAGGCCTGACTGCCTTGAAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAA
AAACCTGCAGCTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAA
ATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTC
TGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACCTCCTC
CCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGC
TTCTTTTATGAATTAACTCGCCCCACCACCCCTCA

FIGURE 200

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLA¹AGIAAVLSGKCKYKSSQKQHSFVPE
KAIP²LITPGSATTC

FIGURE 201

[illegible]

FIGURE 202

[illegible]

Signal peptide:
amino acids 1-21

N-glycosylation site.
amino acids 265-269

Glycosaminoglycan attachment site.
amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.
amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.
amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.
amino acids 301-304

FIGURE 203

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGGCTGGGCCTCA
GACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCTACTCGCCCGCATCCTGGCTT
GGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCCAGTGTTCACACAGCCCCAAAACGGAACCTGGTTTTGGG
GTCACCTGGGCCTGATCACTCCTACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGGCCACCTATTCCACAGG
GCTTTACGGTATGGCTGGGTCCCATCATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCA
ATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATAC
TGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCTTCCATTTCAACATCCTGAAGT
CCTATAAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCA
GTCGCTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACA
GCCATTGTGAGGAGAGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCC
AGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCC
TGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCGCACCCTCCCCACTCAGGGTATTGATGATTTTT
TCAAAGACAAAGCCAAGTCCAAGACTTTGGATTTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCC
TCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGCAAGAGCTTC
TGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCCGAGCTGCCCTTCTGACCATGTGCGTGAAGG
AGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCC
GAGTCATCCCCAAAGGCATTACCTGCCTCATCGATATTATAGGGTCCATCACAACCCAACTGTGTGGCCGGATC
CTGAGGTCTACGACCCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCT
CCGCAGGGCCCAGGAAGTGCATCGGGCAGGCGTTCCGATGGCGGAGATGAAAGTGGTCTGGCGTTGATGCTGC
TGCACTTCCGGTTCTGCGAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGCGCGCCGAGGGCGGGC
TTTGGCTGCGGGTGGAGCCCCCTGAATGTAGGCTTGAGTGAATTTCTGACCCATCCACCTGTTTTTTTGCAGATT
GTCATGAATAAAACGGTGTCTGTCAAA

FIGURE 204

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWGHLGLITPTEEGLK
DSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKPWLGEKILLSGGDKWSRHRM
LTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATI
LELSALVEKRSQHILQHMDFLYYLSHDGRRFHRACRLVHDFDVAIRERRRTLPTQGIDDFKDKAKSKTLDLDFID
VLLLSKDEDGKALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDL
AQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENS
KGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 205

TCCCTTGACACAGGCTCTGGTGGCTGGTTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAAACTGAAGACTCTCTGCT
TTTGCCACAGCAGTTTCTGTCAGCTTCTTGGAGTGTGAACCCACATCCCTGCCCCAGGGCCACCTGCAGGACGC
CGACACCTACCCCTCAGCAGACGCCGGAGAGAAATAGTAGTACCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATC
CTCTTTGCCCTCATACCATCTCTCATCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTG
CGGGCCGTAGCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCATCTGACGGCTATGTCCCCATTCTCGGCAAC
AAGACACTGCCCTCTCGGTGCCACAGTGTGTGATTGTGACAGCTCCAGCCACCTGCTGGGCACCAAGCTGGG
CCTGAGATCGACGCGGGCTGAGTGTACAATCCGATGAATGATGCACCCACCTAGCTACTCAGCTGATGTGGGC
AACAAGACCACCTACCGCGTCTGTGGCCATTCCAGTGTGTTCCGCGTGTGAGGAGGCCCCAGGAGTTTGTCAAC
CGGACCCCTGAAACCGTGTTCATCTTCTGGGGGCCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCCT
GTGATCCAGCGAGCGGGCTTGGTGTTCGCCAACATGGAAGCATATGCCGTCTCTCCCGCCGCATGCGGCAATTT
GACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCTGTGGTTGAGCACAGGCTGGTTTACC
ATGGTGATCGCGGTGGAGTTGTGTGACCACTGTCATGTCTATGGCATGGTCCACCCCACTACTGTCAGCCACGGC
CCCCGCTCCAGCGCATGCCCTACCCTACTACTACGAGCCAGGGGCCGAGCAATGTGTCACTACATCCAGAAT
GAGCACAGTCCGCAAGGGCAACCACCACCGCTTCATCACCAGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTAT
GGCATCACCTTCTCCACCCCTCTGGAACCTAGGCCACCAGCCTGTGGGACCTCAGGAGGGTCAGAGGAGAAGC
AGCCTCCGCCAGCCGCTAGGCCAGGGACCCTCTTCTGGCCAATCAAGGCTTGTCTGGAGTGTCTCCAGCCAATC
AGGGCCTTGAGGAGGATGTATCTCTCAGCCAATCAGGCCTGGGGAATCTGTTGGCGAATCAGGGATTGGGGAGT
CTATGTGGTTAATCAGGGGTGTCTTTCTGTGTCAGTTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATT
TCTGAGTCAATCTGAGGATAAGGACATGTCTTTCCCATGAGGCCCTTGGTTCAGAGCCCCAGGAATGGACCCCC
AATCACTCCCCACTCTGCTGGGATAATGGGTCTGTGCCAAGGAGTGGGAACCTGGTGTGGTGGCCCCCTCAATTT
CCAGCACCCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCCCGGCCAGAGAATTTGTGGGGTTGTGG
AGTTTGTGGGGGCGGTGGGGAGGTCCAGAGGTGGGAGGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTG
GACAAACCTTCCCCCTCTCTGGGCACCTTCTGCCACACCAAGTTTCCAGTGCGGAGTCTGAGACCTTTCCAC
CTCCCCCTACAAGTGCCCTCGGGTCTGTCTCCCTCCCGCTCGGACCTCCCAAGCCATATCTCTGTGGAAGGCTCA
GCTCTTTTGGGGGTCTGGGTGACCTCCCCACCTCTGGAACACTTTAGGGCTATTTTGGCAAACTCCTTCAGG
GTTGGGGGACTGTGAAGGAAACGGGACAAAACCTTAAGTGTGTTTTCTTAGCCCTCAGCCAGCTGCCATTAGCTT
GGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCTCTAGCAGGGAGGTTTTCCAACCTGTTGGAGGCGCCTTTGGGG
CTGCCCCCTTGTCTGGAGTCACTGGGGGCTTCGAGGGTCTCCCTCGACCTCTGTCTGCTCTGGGATGGCTGTCTG
GGAGCTGTATCACTGGGTCTGTCTCCCTGGCTCTGTATCAGGCATTTATTAAAGCTGGGCCTCAGTGGGGTGT
GTTTGTCTCTCTCTCTCTGAGGACCTGGAAGGAAGGGCTTCAGGAGGAGGCTGTGAGGCTGGAGGACCATGT
GAGGAGGCCAGCAGCTAGCCATTGCACTCTGGGTGATGGGTGGGGGGGTGACTGCCCCAGACTTGGTTTTGTA
ATGATTTGTACAGGAATAAACACACCTTACGCTTCGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 206

MSSNKEQRSVAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPILGNKTLPSRCHQCV
IVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRVLRRPQEFVNRTPETVFIFWG
PPSKMQKPQGS�VRVVIQRAGLVFPNMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHV
HVGVMVPPNYCSQRPRLQRMPIHYEYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:
amino acids 1-29

Transmembrane domain:
amino acids 9-31 (type II)

N-glycosylation site.
amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 50-54

Casein kinase II phosphorylation site.
amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.
amino acids 253-262

N-myristoylation site.
amino acids 37-43, 114-120, 290-294

FIGURE 207

GTAGCGCTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCGTGGAGCCAGGAGCGACGTCAC
CGCCATGGCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTTGG
ATGTGCCCTTCCAATATACAACAAATACTGGCCCCCTCTTTGTCTATTTTTTTACATCCTTTCACCTATTCCATA
CTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAGGAACCTGCCATCTTCTTAC
AACGGGCATTGTGCTGTGAGCTTTTGGACTCCCTATTGTATTGGCCAGAGCACATCTGATTGAGTGGGGAGCTTG
TGCACTTGTCTCACAGGAAACACAGTCATCTTTGCAACTATACTAGGCTTTTCTTGGTCTTTGGAAGCAATGA
CGACTTCAGCTGGCAGCAGTGGTGAAGAAATTACTGAACTATTGTCAAATGGACTTCCTGTCAATTGTTGGCC
ATTACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTAGGTGCTCC
CTTCTCACTTTTATTGTAAGCATACTATTTTCACAGAGACTTGCTGAAGGATTAAAAGGATTTTCTCTTTGGAA
AAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTTGTGGTGTCTGCTGAATTTAAATATTTATGTGTTT
TTCTGTTAGGTTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCATTTGCATTGGT
TAGGAATTCAGAATTCGCCCGGCTCTATTACTGGTCAAGTACATCTTTCTCTTAAAATTATTTAGCCTCCATTA
TTACAAAAAATTATAAAAAATAAGTTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATGCAGACATACAGAC
GGTTGGCATACTGTTATAGACTGTATACTCAGTGCAATATAGCTGCATTTATACCTCAGAGGGGCCAAGTGTTAA
TGCCCATGCCCTCCGTTAAGGGTGTGGTGTACTGGTAGACAGATGTTTGTGGATTGAAAATTATTTATGG
AATTGCTACAGAGGAGTGCTTTCTCTCAATTGTTAGAAGAATTTATGTTAACTTTAAGGTAAGGGTGTA
ACATTTTGTAGATAAGGTTTTTATTATGTTTATTATTGTTAGAGTGAGTTGCAATGTGGGAAGAAATGACATTG
AAATTCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAAATTTGTGATCTCCTATCAACCTTTCATGTTTTACC
CTGTTAAAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTGCATCATATATGCCAGAAAAC
CTTCTCTGCTTCTCCTTTTGACTTATTGGTATGTTGTATATATTACATAAAATAACTTTTCAAATATAGTTT
AATAACACTTAGAAGTGTTTACTTACCTGGAAAATAATTGCTATGCCGTACATTCAGAGTGCCCCCTCCCTGCA
AGGCCTTGCCATGATTAACAAGTAACCTGTTAGTCTTACAGATAATTATGCATTAAACAGTTTAAGATTAGACC
ATGGTAATAGTAGTTCTTATTCTTAAGGTTATATCATATGTAATTTAAAAGTATTTTAAAGACAAGTTTCTGT
ATACCTCTGAAGTGTGTTGATTTTGTGTTTATCATGATAGATCTGCTGTTTCTTATAAAAGGCATTTGTTGTGT
GAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACATACCTGACCAAAAAATTTCCAGTAAC
CAGGCATGATCAATTTATAGTGCTCGTTTACATCTAATAATTATCAGGACTTTTTCAGGAGTGGGTTATAAAAA
CATTCAAGTTGGTCTGACAGTATTTTGTGTTAAGGATATTTGTTTGTATGTTTATTTCAGTATACTTACATAAAAT
ATTTGCCCATCAGCCAAAACTCAGTAATCATGACAGCTGTCTGTTGTTTATGAAGTTTATTTCTCAAGAAAATG
GGAATAAATTTGGGATTTGTTTCACTTTTTTACTAAAGATGCCTAAAGCCACAGGTTTTTATGCTTAAGC
CATGACTTTTATGATATGAGATGACGGGAAGCAGGACGAAATATCGGCGTGTGGCTGGAGCCTTCCCACTGGAGGC
TGAAAGTGGCTTGTGGTATTATAATGTTTCAAGAGGAAGGTGCAGGTACACATGAGTTAGAGAGCTGGT
GAGACAGTTGGGAACCTTTTGTGCTGTGATCTACTGGACTTTTTTTTTGCAGGAAGTGCATTCTCTGGTCTTC
CCTATTTTCTGTTCTGGATGTCAGTGCAGTGCAGTGTCTGTTTATCCACTTGGCCACAGACTTTTTCTAACA
GCTGCGTATTATTTCTATATACTAATTGCATTGGCAGCATTTGTGCTTTGACCTTGTATACTAGCTTGACATAGT
GCTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAATTTTCCATAGAATATGCACTGATACAACATTACCAT
TCTTCTATGGAAAGAAACTTTTGTATGATGAAACAATAAAGATTTTAAATATCTATTTTAAAAA

FIGURE 208

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAMSNACKELAI FLTT
GIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSNDDFSWQQW

FIGURE 209

CTTGACAGAGAAAGAGTCTTTTGTGCAGCACCCCTTTAAAGGGTGACTCGTCCCACCTTGTGTTCTCTCTCCTGGTG
AGAGTTGCAAGCAAGTTTATCAGAGTATCGCCATGAAGTTTCGTCCCCCTGCCTCCTGCTGGTGACCTTGTCTGCTG
TGGGGACTTTGGGTGAGGCCCCGAGGCAAAAGCAAGGAAGCACTGGGGAGGAATTCATTTCCAGACTGGAGGGA
GAGATTCCTGCACTATGCGTCCCAGCAGCTTGGGGCAAGGTGCTGGAGAAGTCTGGCTTCGCGTCGACTGCCGCA
ACACAGACCAGACCTACTGGTGTGAGTACAGGGGGCAGCCCAGCATGTGCCAGGCTTTTGCTGCTGACCCCAAAC
CTTACTGGAATCAAGCCCTGCAGGAGCTGAGGCGCCTTCACCATGCGTGCCAGGGGGCCCCGGTGCTTAGGCCAT
CCGTGTGCAGGGAGGCTGGACCCAGGCCCATATGCAGCAGGTGACTTCAGCCTCAAGGGCAGCCCAGAGCCCA
ACCAGCAGCCTGAGGCTGGGACGCCATCTCTGAGGCCCAAGGCCACAGTGAAACTCACAGAAGCAACACAGCTGG
GAAAGGACTCGATGGAAGAGCTGGGAAAAGCCAAACCCACCACCCGACCCACAGCCAAACCTACCCAGCCTGGAC
CCAGGCCCGAGGGAATGAGGAAGCAAAGAAGAAGGCCTGGGAACATTGTTGGAAACCCCTCCAGGCCCTGTGCG
CCTTTCTCATCAGCTTCTTCCGAGGGTGACAGGTGAAAGACCCCTACAGATCTGACCTCTCCCTGACAGACAACC
ATCTCTTTTATATTATGCCGCTTTCAATCCAACGTTCTCACACTGGAAGAAGAGAGTTTCTAATCAGATGCAAC
GGCCCAAATTCTTGATCTGCAGCTTCTCTGAAGTTTGGAAAAGAAACCTTCCTTTCTGGAGTTTGCAGAGTTTCA
CAATATGATAGGGAACAGGTGCTGATGGGCCCCAAGAGTGACAAGCATAACAATACTTATTATCTGTAGAAGTT
TTGCTTTGTTGATCTGAGCCTTCTATGAAAGTTTAAATATGTAACGCATTTCATGAATTTCCAGTGTTTCACTAAAT
AGCAGCTATGTGTGTGCAAAATAAAAGAATGATTTTCAAAAAA

FIGURE 210

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59602
<subunit 1 of 1, 223 aa, 1 stop
<MW: 24581, pI: 9.28, NX(S/T): 0
MKFVPCLLLVTLSCLGTLGQAPRQKQGSGTEEFHFQTGGRDSCTMRPSSLGQGAGEVWLR
VDCRNTDQTYWCEYRGQPSMCQAFADPKPYWNQALQELRRLHHACQGAPVLRPSVCREA
GPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKATVKLTEATQLGKDSMEELGKAKPTTR
PTAKPTQPGPRPGGNEEAKKKAWEHCWKPFQALCAFLISFFRG
```

Important features:

Signal peptide:

Amino acids: 1-19

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

DNA photolyases class 1 proteins:

Amino acids: 58-69

Tyrosine kinase phosphorylation site:

Amino acids: 64-71

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids: 4-15

FIGURE 211

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCGGGTCCTGCTGTGGCTGCAGCTCTGCGCACTGACCCAGGCG
GTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTTCGAGCCAACTGGAGCCAGAACCGGACCCCGTTCGCC
GGCGGCGCCGTTGAGTTCCCGGCGGACAAGATGGTGTTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATG
CTCCTGCCGCTGGATGGGGAACCTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTG
GACTGTGGCGCGGGCGAACCTGCCGTCTTCGCGGACTCTGACCGCTTCTCCTGGCATGACCGCACCTGTGGCGCT
CTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGCCACGACGACGTCTTCTTTC
CGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAGCCCCGTGCGTGTCCGCAGCATCTCGGCTCTGG
GCCGACGTTTCACGCGCGACGAGGACCTGGCTGTTTTCTGGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGC
CGGGCGCGCTGAGCGTGGGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGC
CGTGGATCTGCGCGGCCCTGCTCCAGCCCCT

FIGURE 212

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59603

<subunit 1 of 1, 197 aa, 1 stop

<MW: 20832, pI: 8.74, NX(S/T): 2

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLV
QEGHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDRTCGAL
GTRHLASSSWTPSACPAATTTSSFRLVPPSAWGSALALAPCVSAASRLWAGRSRATRTWL
FSWRPARAAYASTGRAR

Important features:

Signal peptide:

Amino acids 1-19

N-glycosylation site:

Amino acids 35-39

Glycosaminoglycan attachment site:

Amino acids 81-85

N-myristoylation sites:

Amino acids 82-88;118-124;153-159

C-type lectin domain proteins:

Amino acids 108-118

FIGURE 213

[illegible]

FIGURE 214

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFARDAVKKCFVCLA

FIGURE 215

GGATTTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAGTGCGGGAGGCCAGGACAGGCCACCC
TGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGCAGAGAGGCCAAGCCCCTTGCCCTGGG
TCACACAGCCAAAGGAGGCAGAGCCAGAACTCACAACCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACG
AAAAGGCAGTCACCCGCAGGGCCAAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTTCACGGTCG
TGGGAGACGACTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGC
AGCCACCACCCACACCACTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCCCTGCCCTGGCCCCG
CACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTTTCAGCTCCACAGGTTTCAGGTCATCATCA
TCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGCTTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACA
AGAATAACTATGCTGCCATGGTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCT
TTAAATTATTTGTCTTCCGCCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGGTGGTCT
CATTTCATCCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGCCTGCTGATTCTGCTCCGGC
TGTGGCGGGTGGCCCGATCATCAATGGGATTATCATCTCAGTTAAGACACGTTTCAGAACGGCAACTCTTAAGGT
TAAACAGATGAATGTACAATTGGCCGCCAAGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCTGGACT
GATGAGTTTGCTGTATCAACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTA
CTCTCACACAGCCACCGTGAAAGTCCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAGCAGGCTGGC
ATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTATCACTTCAGATTACAAATCACA
CAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACCAAATCTATAAAGATATTCTGAAAATATGACAGAA
TTTGACAAATAAAAGCATAAACGTGTAAAAA

FIGURE 216

MATWDEKAVTRRAKVAPAERM SKFLRHFTVVGGDYHAWNINYKKWENEEEEEEEEEQPPPTPVSGEEGRAAAPDVA
PAPGPAPRAPLDFRGMLRKLFSSHRFQV I I ICLVVL DALLVLAELILD LK I I QPDKN NYAAMVFHYMSITILVFF
MMEI I FKL FV FRLSSFTTSLRSWMPVVVVVSFILDIVLLFQEHQFEALGLLILLRLWRVARIING I I ISVKTRSE
RQLRLKQMNVLAAKIQHLEFSCSEKPLD

FIGURE 217

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGCTTCCCTGGGG
CAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTGGCTTTGGT
ATTTCAAGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGC
TGCACTTTGAACCTGACATCAAACCTTCTGATATCGTGATACAAATGGCTGAAGGAAGGTGTTTTAGGCTTGCTC
CATGAGTTCAAAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTGCT
GATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGT
TATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGGAAGTG
AATGTGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCACAGTGGTC
TGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAAT
GTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAAAATGAC
ATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAAC
TCAAAGGCTTCTCTGTGTGTCTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATG
CTAAAATAATGTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAG
AGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAAGACATATTA
GAAGTTGGGAAAATAATTATGTGAACTAGACAAGTGTGTTAAGAGTGATAAGTAAATGCACGTGGAGACAAGT
GCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTG
TCTCTGAATTTTATGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCA
CATCTTATATTTCCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAG
GGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTC
CCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGTCGGGGACACCGATTT
TATAAATAAAGTGAACACCTTCTTTTTTAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAA

FIGURE 218

MASLGQILFWSIISIILLAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLR.LKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF
SMPEVNVNDYNASSETLRCEAPRWFPQPTVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSC
MIENDIAKATGDIKVTESI.KRRSHLQLLSKASLCVSSFFAISWALLPLSPYLMLK

FIGURE 219

GAATTTGTAGAAGACACGCGCGCTTGCCATGGCGCGCTCTCTGGGGCAGGTGTTGGCTCTGGTGCTGGTGGCCGCT
CTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCCTCCGCCGGCTGCAGCGGGTTCATGAGCCGACCTGGGCC
CAGCAGTTGCTACAGGAGATGAAGACCCCTCTTCTTGAATACTGAGTACCTGATGCCCTTTCTCCTCAACCAGTGT
GGATCCCTTCTCTATTACCTCACCTTGGCATCGACAGATCTGACCTGGCTGTGCCCATCTGTAACCTCTCTGGCT
ATCATCTTCACACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGCGAG
TGCGGGACGCAGCTCTGTGGATCTCGACATACCTGTGTTAGTTCCTTCCCAGAACCCATCTCCCAGAGTGGGTG
AGGACACGGCCCTTTTCCCATCCTGCCCTTCTCTGCAGCTGTTTTGCTTCCCTGTGGCCATCAGAGTCTCCCTTC
CCCTGGACAGTCTGGAGAAAAGACAGAGGCTGGGGTTGGGATTGAAGACCAGACCCCATCTGAGCCCTTCCCTCA
GCCCTGTACCAGCTCCCTACTTGGCATGGCTGAGCTCAGACCCCTCTGATTTCTGCCTATTATCCCAGGAGCAGTTG
CTGGCATGGTGTGCTCACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGGCAACAGT
CTACCTTTTGAGTGGGCGGAACCCACTTCCAGCTCTGCTGCCCTCAGGAAGCCCTGGGGCCATGAAGTGCTGGCA
GTGAGCGGATGGACCTAGCACTTCCCCTCTCTGGCCTTAGCTTCCCTCCTCTCTTATGGGGATAACAGCTACCTCA
TGGATCACAATAAGAGAACAAGAGTGAAAGAGTTTTGTAACTTCAAGTGCTGTTCAGCTGCGGGGATTTAGCAC
AGGAGACTCTACGCTCACCCCTCAGCAACCTTTCTGCCCAGCAGCTCTCTTCTGCTAACATCTCAGGCTCCCAG
CCCAGCCACCAATTACTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAACTCCAGCTGCA
TGGAAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAAACGGGAGGCCTCTGGGACTCAGTCAGAGCGCTTTGG
CTGAATGAGGGGTGGAAACCGAGGGAAGAAGGTGCGTCGGAGTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCT
TGCTTGCCCCACCCATGAGGTAGGCAGAAATCCTCACTGCCAGCCCTCTTAAACAGGTAGAGAGCTGTGAGCCC
CAGCCCCCACTGACTCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAAACAGACAAAAA
AAAAA

FIGURE 220

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMFPFLNQCGSLLYYLTL
ASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISP EWVRTRPFPILP
FPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

FIGURE 221

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCCTCCAGCTTTCTCTGTGGAAGATGACAGCA
ATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACTTTGCCAGTGGGAAAGTACCTAGTGAAA
CGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCTTGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTC
CAGCACCAATGAAGGGCATCCTCGTTGCTGGTATCACTGCAGTGCTTGTTGCAGCTGTAGAATCTCTGAGCTGCGT
GCAGTGTAATTCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAGCTG
TATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGTTCTGCTCAGCGGAGAA
CTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCTGCTGAAGAACAACCTTTCATTTTGTAAGCCA
GTGCTGCCAAGGAAAGGAATGCAGCAACACCAGCGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGC
AGAGTGCCCTGCTTGTTATGAATCTAATGGAACCTTCCTGTCTGCGGGAAGCCCTGGAAATGCTATGAAGAAGACA
GTGTGTCTTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTCCAACGT
CAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAACAAGACTCTTGAGGAGTCATCTTTCGAAAGTTTGAGTG
TGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACTTCCCAACAGTGGGCTCCAAAGCTTCCCTCTA
CCTCTTGCCCTTGCCAGCCTCCTTCTTCGGGGACTGCTGCCCTGAGGTCCTGGGGCTGCACTTTGCCAGCACC
CCATTTCTGCTTCTCTGAGGTCCAGAGCACCCCCCTGCGGTGCTGACACCCTCTTTCCCTGCTCTGCCCCGTTTAA
CTGCCCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTAAAGCACTGG
TTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 222

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLETPVRLYQNMFCSAENC
EETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAECPACYESNGTSCRGKPWKCYEEEQCV
FLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENKTLGGVIFRKFEKANVNSLTPTSAPTTSNHNVGSKASLYLL
ALASLLLRGLLP

FIGURE 223

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCAGGGCTTGCCTCAC
TGGCCACCCTCCCAACCCCAAGAGCCCAGCCCCATGGTCCCCGCCGCCGGCGCGCTGCTGTGGGTCTGCTGCTG
AATCTGGGTCCCCGGGCGGCGGGGGCCCAAGGCCTGACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGC
TTTGGGGGCCCCATGACCCGCAGCTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTA
GAGGACGAGAATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCCACG
GTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGAGGGGGTTGTGATTAAT
GCCGAAAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCGACTCCCAATACAGCGGGGAGTTCCAGCACGAGGTTT
ATAGCCAATAGTCAGGAGCCTGAAATCAGGCTGACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGAC
CTGCCAGGCTCGCAGGCCACCCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCTCA
CCCACAGCCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCACTGCAAG
TCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCTTCGAGTTGGGGCGCTGAGC
CAGCTCCGCACGGAGCACAAGCCTTGACCTATCAACAATGTCCCTGCAACCGACTTCGGGAAGAGTGCCCCCTG
GACACAAGTCTCTGTACTGACACCAACTGTGCCTCTCAGAGCACCAACAGTACCAGGACCACCACTACCCCTTC
CCCACCATCCACCTCAGAAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGG
GTCAGGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTTCACAGAGATGCAACCAATAGACAGAAAC
CAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCTCTTGCCCTTTCAATCCTAGCAC
CCACTAGATATTTTGTAGTACAGAAAAACAAAACCTGGAAAAACACAA

FIGURE 224

MVPAAGALLWVLLLNLFRAAGAQGLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRIILEDENDAMADAD
RLAGPAAAEELLAATVSTGFSRSSAINEEDGSSEEGVINAGKDSTSRELPSATPNTAGSSSTRFIANSQEPEIRL
TSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWPSPTSPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGK
LHGLSGRLRVGALSQRLTEHKPCTYQQPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSPSL
PPASPCPALAFWKVRIGLEDIWNSLSSVFTEMQPIDRNQR

FIGURE 225

CCCGGGTCGACCCACGCGTCCGGGGAGAAAGGATGCGCCGGCCTGGCGGCGCGGTTGGTCTGCTAGCTGGGGCAG
 CGGCGCTGGCGAGCGGCTCCAGGGCGACCGTGAGCCGGTGTACCGCGACTGCGTACTGCAGTGCGAAGAGCAGA
 ACTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCTGTC
 GGGACGACTGTAAGTATGAGTGTATGTGGGTACCGTGGGCTCTACCTCCAGGAAGGTCACAAAGTGCCTCAGT
 TCCATGGCAAGTGGCCCTTCTCCCGGTTCCCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCTCGTTTCTCAATG
 GCCTGGCCAGCCTGGTGTATGCTCTGCGGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACCACACCTGTG
 TGGCCTTCGCTGGGTGTCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACCAGGGACACTGACCTCACAG
 AGAAAATGGACTACTTCTGTGCCTCCACTGTATCTTACCTCAATCTACCTGTGCTGCGTCAGGACCGTGGGGC
 TGCAGCACCCAGCTGTGGTCACTGCTTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCTCCTACCTGA
 GCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTGGTGTGGTGGC
 TGGCCTGGTGCCTGTGGAACAGCGGCGGCTGCCTCAGTGCAGCAAGTGGTGGTGGTGGTCTTGTCTGCTGCAGG
 GGCTGTCCCTGCTCGAGCTGCTTGACTTCCCACCGCTCTTCTGGGTCTGGATGCCATCTGGCACATCA
 GCACCATCCCTGTCCACGTCCTCTTTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTGAAGGAATCAGAGG
 ACAAGTTCAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCCGCCCTGCTGGCCTC
 CCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAAGTGGACATGAAGGATGTGGGGCCAG
 AATCATGTGGCCAGCCACCCCTGTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGGAAGGCCTCCAGCATC
 TGGGACTCGAGAGTGGGCAGCCCTCTACCTCCTGGAGCTGAACTGGGGTGGAACTGAGTGTGTTCTTAGCTCTA
 CCGGAGGACAGCTGCCTGTTTCTCCTCCACAGCCTCCTCCACATCCCGAGCTGCCTGGCTGGGTCTTGAAG
 CCCTCTGCTTACCTGGGAGACCAGGGACACAGGCCTTAGGGATACAGGGGGTCCCCTTCTGTTACACCCCCCA
 CCCTCCTCCAGGACACCACTAGGTGGTGTGCTGGATGCTTGTCTTTGGCCAGCCAAGGTTACGGCGATTCTCCCC
 ATGGGATCTTGAGGGACCAAGCTGCTGGGATTTGGGAAGGAGTTTACCCTGACCGTTGCCCTAGCCAGGTTCCTCA
 GGAGGCCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCAGGGCAAGGATCCTGTGCTGCTGTCTGG
 TTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGGTGACAGGGCCGTGAGCATGGGCC
 TGGGTGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTTGTGCGGGGAAGAGGTGTGGCTTCAAAG
 TGTGTGTGTGCAGGGGGTGGGTGTGTTAGCGTGGGTAGGGGAACGTGTGTGCGCGTGTGCTGGTGGGCATGTGAGA
 TGAGTGACTGCCGGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGATGAGGGAATCCTGTACCATCAATAAT
 CACTTGTGGAGCGCCAGCTCTGCCCAAGACGCCACCTGGGCGGACAGCCAGGAGCTCTCCATGGCCAGGCTGCCT
 GTGTGCATGTTCCCTGTCTGGTGGCCCTTTGCCCGCCTCCTGCAAACCTCACAGGGTCCCCACACAACAGTGGCC
 TCCAGAAGCAGCCCCCTCGGAGGCAGAGGAAGGAAAATGGGGATGGCTGGGGCTCTCTCCATCCTCTTTCTCCT
 TGCCCTTCGCTAGCTGGCCTTCCCCCTCCAAACCTCCATCCCCCTGCTGCCAGCCCCCTTGCCATAGCCTGATTT
 TGGGGAGGAGGAAGGGGCGATTTGAGGGAGAAGGGGAGAAAGCTTATGGCTGGGTCTGGTTTCTTCCCTTCCCAG
 AGGTCTTACTGTTCCAGGGTGGCCCCAGGGCAGGCAGGGGCCACACTATGCCTGTGCCCTGGTAAAGTGACCC
 CTGCCATTTACCAGCAGCCCTGGCATGTTCTGCCCCACAGGAATAGAATGGAGGGAGCTCCAGAACTTTCCAT
 CCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGTCTCTGCCCCTGACCCCTTGTCCCTCTTTGAGGGGA
 GGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTGGCCTGCGCTAGCTTCTTTTGATACTGAAAACCTTTT
 AAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAATTCAGCCTCAAAAAAAAAAAAAAAAAA

FIGURE 226

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGWTCRDDCKYECMWV
TVGLYLQEGHKVPQFHGKWPF SRFLFFQEPASAVASFLNGLASLVMLCRYRTFVPASSPMYHTCVAFAWVSLNAW
FWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVRTVGLQHPAVVSAFRALLLMLTVHVSYLSLIRFDYGYNL
VANVAIGLVNVVWWLAWCLWNQRRRLPHVRKCVVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFS
FLEDDSLYLLKESEDKFKLD

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 227

TTCGGCTTCCGTTAGAGGAAGTGGCGCGGACCTTCATTGGGGTTTCGGTTCCCCCCCCCTTCCCTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTGCCTGTGCCACCCACGCGGACTCCCCAGCTGGCGCGCCCCTCCCATTTGCCTGTCTGGTACAGCCCCCACCCCCCTTCCACCTGACCAGCCAATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTTCGTGCGGTTTCGGCCCCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCTCGTTCGACAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCACTTGGTCCATGTGACCGCATGATTTTTCTGGCTCCAGTACCGCTCCAGTACCGCTCTGCTGTCTCTCTCTACAGGAGTGTTCGCTTTGGCTACTACAGCTGCTTAAGAAGGCAGATGAAGGGTAGCATCGTGAAGTGAAGGAGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCCTGACTTCAGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATGCCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCTGGTGGTTGGGAGTCACTACTGACATCGGGACTGACATTCTGAACCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGTTTCCATGGGGCTCTGGGCCTTCATCACAGCTGAGGGTCCCTCCGAAGTATTTCCAGCTAGCAGCCTCTGTGTAAAGCATGATACTCTGGACTGATCGCTGACAGATCCCACTGCCCTGTCCACTGCCATGACCTGAGCTGAGCCAGCCCGGCTCCATTGCCACATTCTGTCTCTCTTCTCGTCCGTTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTTTACAGGAGCAGCCTGGGTTTCAGCCAGTCACTGACTGGTGGGTTTGAATCTGCACTTATCCCCACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTCACTGCTCTGCTCTCACCTGCCCAAGACTCACCTCCCTTCCCTCTGCAGCCGACGGCAGGAGACAGTCCGGTGATGGTGTATTCTGCCCTGCGCATCCCACCCGAGGACTGAGGGAACCTAGGGGGACCCCTGGGCCTGGGGTGCCCTCCCGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAGGTTGCCAAGAAAAGGGACCTAGTTTTAGCCATTGCCCTGGAGATGAATTAATGGAGGCTCAAGGATAGATGAGCTGTGATGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTCAGGCCTGAGGGGGAACCTTTTTGGTGTGATAAAATACCTTAAACTGCCCTTTTTTCTTTTTTGAGGTGGGGGAGGGAGGAGGTATATTGGAACCTTCTAACCTCCTTGGGCTATATTTTCTCTCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTTCGGTCCCTTTCTCCTTGGTCCCAGACCTTGGGGGAAAGGAAGGAAGTGCATGTTTGGGAACTGGCATTACTGGAACATAATGGTTTTAACCTCCTTAACCACCAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGGCCACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAAGACTACCATGACATCGTAGGGAAGGAGGGGAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAAC'TGTATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAATCAAGGTGATTGTGATTTTGAATAAAAAAGAAATTTGTAAAAA

FIGURE 228

MGAAVFFGCTFVAFGPALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYGLLIFG
AAVSVLLQEVFRFAYYKLLKKADEGLASLSEGRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVGIIH
GDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMG
LWAFITAGGSLRSIQRSLLCKD

FIGURE 229

CGGGAGGCTGGGTGCTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTCCCAGGCTCCCGCG
 GCCGACCCCGCGCAACATGTCAGCCACGGGCCGCGAGGGTTCCCGCGCGCTCAGCCGGCGGTATCTGCGGCGTC
 TGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGCCCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAG
 CCTCTCCACGCTGGGCTCCCCCAGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCA
 CTACGCCAGGCACCCCCAAAACCTGGACCTTCGGGGTTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCGTGG
 ACGGCCACAATGACCTGCCCCAGGTCTTGAGACAGCGTTACAAGAATGTGCTTCAGGATGTTAACCTGCGAAATT
 TCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGTGGGTGCCAGTTCTGGTCAGCCTCCGTCT
 CATGCCAGTCCCAGGACCAGACTGCCGTGCGCCTCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCT
 CCTACTCTGAACCTCGAGCTTGTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTTGGCG
 TGNAGGGTGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCTACCTGA
 CACTTACCTTCACTGCACTACACCATGGGCAGAGAGTTCCACCAAGTTTCAAGACACCATGTACACCAACGTCA
 GCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAACCGCCTGGGCATGATGATAGATTTGTCTTATG
 CATCGGACACCTTGATAAGAAGGTCTTGGAAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAG
 CTGTGTGTGACAATTTGTTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGA
 CACTGTCCATGGGGGTGCTGCACTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTGACCACATCA
 GGGCAGTCATTGGATCTGAGTTTATCGGGATTGGTGGAAATTATGACGGGACTGGCCGGTTCCCTCAGGGGCTGG
 AGGATGTGTCCACATACCCAGTCTGATAGAGGAGTTGCTGAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTG
 TCCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAAGTGAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCG
 TGGAGGCTGAGTTTCCATATGGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCTCAGAATGGACACCAGG
 CTACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCTGGAGGTCCTCAAATGCCTCCCCATACCTTG
 TTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTCTGCTGACACAGTCGGTCCCCGCAGA
 GGTCACGTGTGGCAAAGCCTCACAAGCCCCCTCTCCTAGTTTATTACAAAGCATATGCTGAGAATAAACATGTTA
 CACATGGAAAA

FIGURE 230

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLLRQPVTTRAETTPGAPRALSTLGSPSLFTTPGVPSALTTPGLTTPGTP
KTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQTSLDRLRDGLVGAQFWSASVSCQSQD
QTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSSQKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTC
STPWAESSTKFRHHMYTNVSGLTSGEKKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNL
LNPDDILQLLKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGNYDGTGRFPQGLEDVSTY
PVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVRRESRAQSPVEAEFFPYGQLSTSCHSHLVPQNGHQATHLEV
TKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:

Signal peptide:

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 231

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGATTGGCAAGCGCTGG
CCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGTAGCTATTAGCCAATTCCGGCAGGGCCC
GCTTTTTAGAAGCTTGATTTCCTTTGAAGATGAAAGACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGG
AACTCGGGGCGATTGGCTGGGAACGTATCCACCCAAATGTCACCGATTTCTTCCTATGCAGGAAATGAGCAGAC
CCATCAATAAGAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAGAGG
GTTGCTCAACGCCCCGCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTGGCGGAGGCGGGGCGAT
GATTGTGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCTTTCCCCGCCCCCTGAGACCTGCAGCACCA
TCTGTCA**ATG**GCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCG
GCCGCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAAGCGGCC
CCAGAACCGACCAACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCAGACTCC
CATGGTTATGACAAGGACCCCGTTTTGGACGTCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATC
CTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAG
AGGCTTGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTTCGACCCCAGCAAGATCCAG
CTGCCAGAGGATGAG**TGA**CCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATT
TGACCTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

FIGURE 232

MAAGLFGLSARLLAAAAATRG LPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE DENLYEKNPDSHG
YDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAERLVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 233

GCGGCGGCTATGCGGCTTGCTCTGCTCGTCTGTTGCTCCTGGGGCCCGGCGGCTGGTGCCTTGCAAAACCCCA
CGCGACAGCCTGCGGGAGGAACTTGTCATCACCCTGCTGCCTTCCGGGACGTAGCCGCCACATTCCAGTTCCGC
ACGCGCTGGGATTGCGAGCTTCAGCGGGAAGGAGTGTCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTG
ATCTCCAAGTATTCTCTACGGGAGCTGCACCTGTCAATTCACACAAGGCTTTTGAGGACCCGATACTGGGGGCCA
CCCTTCTGTCAGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAATCT
TGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGACTCCACCAACACAGTC
ACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTGACCACTACTTTCTGCGCTATGCTGTGCTG
CCGCGGGAGGTGGTCTGCACCGAAAACCTCACCCTCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCTC
TCTGTGCTGCTGAAGGCAGATCGCTTGTTCACACCAGCTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGC
AGAAATGCACGCTGTACTAGCATCTCTGGGAGCTGAGGCAGACCTGTGAGTTGTATTGATGCCTTCATCAGC
GGGCAGGGAAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCTTCACGGAGCCCTGCCCTGGCTTCA
GAGAGCCGAGTCTATGTGGACATCACCACCTACAACCAGGACAACGAGACATTAGAGGTGCACCCACCCCGACC
ACTACATATCAGGACGTCATCCTAGGCACTCGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATC
AACAACCTCTCGAAACCTCAACATCCAGCTCAAGTGGAAGAGACCCCGAGAGAATGAGGCCCCCAGTGCCCTTC
CTGCATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGAGCTGAGCACACTGCTGTACAACACCCAC
CCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCGGCTGTATGTGCACACCTCACC
ATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCCACTACCAGCCTGCCAGGACCGGCTGCAACCCAC
CTCCTGGAGATGCTGATTCAGCTGCCGGCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTG
AAGTGGACCGAGTACACGCCAGATCCTAACCATGGCTTCTATGTCAGCCCATCTGTCTCAGCGCCCTTGTGCCC
AGCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCAGTCTCTGATGGC
TCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCCGACACCGGACTTCAGCATGCCCTAC
AACGTGATCTGCCCTACGTGCACGTGTGGTGGCCGTGTGCTACGGCTCCTTCTACATCTCCTCACCCGAACCTTC
CACATCGAGGAGCCCCGCACAGGTGGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCC
CCACTCTGATTCTTGGCCCTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTTTC
TGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTCAGGGCCTACAGCTGTGTTGT
CCAGTACAGGAGCCACGAGCCAAATGTGGCATTGGAATTTGAATTAACCTAGAAATTCATTTCTCACCTGTAGT
GGCCACCTCTATATTGAGGTGCTCAATAAGCAAAAGTGGTGGTGGCTGCTGTATTTGGACAGCACAGAAAAAGAT
TTCCATCACACAGAAAGGTGGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGT
GTAGTGGATGGAGTTTACTGTTTGTGGAATAAAAAACGGCTGTTTCCGTGGAAAAA

FIGURE 234

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHYRLF PKALGQLISK
YSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDTVTDVDSWKELSNVLSGIFCASLNFIDSTNTVTPT
ASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWKLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNA
RCTSISWELRQTL SVVFD AFITGQKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTY
QDVILGTRKTYAIYDLLDTAMINNSRNLNIQLKWKRPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTHPYR
AFPVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANSVTKVSIQFERALLKWT
EYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSDGSNYFVRLYTEPLLVNLPDPFSMPYNVI
CLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLAKRLANLIRRARGVPPL

FIGURE 235

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAGCACCAGGAGC
 CCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGTGGGCTACCCCTGGTGGTGG
 TTATGGGGGTCTCTGCCCCTGGAGGGCCTTATGGACCACCAGCTGGTGGAGGGCCCTATGGACACCCCAATCCTGG
 GATGTTCCCTCTGGAACCTCCAGGAGGACCATATGGCGGTGCAGCTCCCGGGGGCCCTATGGTCAGCCACCTCC
 AAGTTCCTACGGTGCCCAGCAGCCTGGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCA
 CTCCTGGTTCCAGTCGGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAA
 CTGCAATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCAGGCCG
 CATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGGAAGAACCTCTTCCAGCAGTATGACCG
 GGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCCAATGGGCTACAACCTGAGCCCCA
 GTTCACCCAGCTTCTGGTCTCCCGCTACTGCCCACGCTCTG~~C~~CAATCCTGCCATGCAGCTTGACCGCTTCATCCA
 GGTGTGCACCCAGCTGCAGGTGCTGACAGAGGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCT
 CAGCTTCGAGGACTTCGTCACCATGACAGCTTCTCGGATGCTATGACCCAACCATCTGTGGAGAGTGGAGTGAC
 CAGGGACCTTTCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC
 ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCAAAATAGTGAGG
 ACCGGGGCTGAGGCCACACAGATAGGGGCCCTGATGGAGGAGAGGATAGAAGTTGAATGTCCTGATGGCCATGAGC
 AGTTGAGTGGCACAGCCTGGCACCAGGAGCAGTCTTGTAATGGAGTTAGTGTCCAGTCAGCTGAGCTCCACCC
 TGATGCCAGTGGTGAAGTGTTCATCGGCCCTGTTACCGTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAAC
 GAGCCCATTTTCTCCAAAGTGGAATCTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCT
 GCCACACCCATAAATCCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTG
 GGCATCTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCCTGCCATGCTCTGCTCGGCTTCAGT
 CTCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAATTTGCATTTTTTTTCATTTGGGGCCAAAAG
 TCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 236

MASYFYRQCPCGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYGHPNPGMFPSG
TPGGPYGCAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSHSGYISMKELKQALVNCNWSS
FNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDRDRSGSISYTELQQALSQMGYNLSPQFTQLL
VSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREKDTAVQGNIRLSFEDFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-
83, 83-88, 87-92, 110-115

FIGURE 237

[illegible]

FIGURE 238

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSONFGTNLPQLGQPSSTGPSNSEHPQPALDPRSNDLARV
PLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAAEDRLGEALPEELSYLSSAAALAPGSGP
LPGESSPDATGLSPEASLLHQDSESRRLLPRSNSLGAGGKILSQRPPWSLIHRVLPDHPWGTNLNPSVSWGGGGPGT
GWGTRMPHPHEGIWGINNQPPGTSGWGNINRYPGGSWGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGV
LRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263, 259-264, 269-
274, 270-275, 280-285, 281-286, 305-310

FIGURE 239

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCCCGCGCTGTGCGCG
 CTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCCGAGAGCTCAAGCGCCC
 AGCTCTGCCCCAGGAGCCCAGGCTGCCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCT
 GGGTGGTGTTCATCCCTTGGGGCTGCTGTTCCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACTCT
 CTTAGAGGAGCTGCTCAGCAAATACCAGCACAACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGAGGA
 CAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACAT
 GGTGAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCAGGGGGTGGGGCCCTGGGCCACCAGCCTGCTCTGTTCCCCAG
 CCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGGCTGGCTCAGGGTCTCCTCTGCGCAGGGGAGGATCCCGGCTCTG
 TTCTGTTTTGTTTGTGTTGTTTGGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCATGGCACAAATCGTCA
 TGCCCTGAAACCTTAGACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAGGCATGC
 ACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGTTGCCAGGCTGGTCTTGAA
 CTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTGCTAGGATTATAGGCATGAGTCACCCTGTCTGG
 CTCTGGCTCTGTCTTAACATTCCTGCCAAAACAACACACGTTGGGTTCCTGTGCGAGAGCCTGCCCTCGTTGCCCTC
 ATGTCACTCTTGGTAGCTCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGGCC
 AGGGCTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTCCTTAGCCCG
 TGTGAGCCTCACTTTCCACTTGGAGAGTCCCTCCTCGCGTGGTTGCCATGACTGTGAGATAAGTCGAGGCTGTGA
 AGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGGCTTTGCTAACCGGGAAGGAGCTAACGGTGACAGA
 AGACAGCCAAGGTCAACCCCTCCCGGGTGATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGAC
 CCAAGCTCCAGTGTGGAACTTCCTTCCTGGCTGGTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAG
 GGTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTTTTAAACAAACC
 CACGTCCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATCCAAGTTAGCCGGGCATGGTGGTGCG
 CACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAGGTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGC
 TTGAGCCTGGGAAGTCGAGGCTGCAGTGAGCTGAGATTGCACCCTGCACCTCAGCCTGGGTGACAGAGCAAGAC
 CCTGTCTCAAAA

FIGURE 240

MSCVLGGVIFLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILMLHNKLRGQVQPQAS
NMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGRGGSRLCSVLFCFETGSHSATDAGVQ
WHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 241

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCC
CTTGTCCTCCTCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAG
GAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCAT
CTCCCTTCAGGGACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCA
TTGAAGCCTGTGTCTTCTTGGCCCGGGCTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAG
CAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 242

MSGGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFELLEKLCLLLHLPSTSVTLHHARSQHHVVCNT

FIGURE 243

GGCAAGTGGAACTGGCTTGGTGGATTTTGCTAGATTTTCTGATTTTAACTCCTGAAAAATATCCCAGAT
AACTGTCCATGAAGCTGGTAACTATCTTCCTGCTGGTGACCATCAGCCTTTGTAGTTACTCTGCTACTGCCTTCCT
CATCAACAAAGTGCCCCCTTCCTGTTGACAAGTTGGCACCTTTACCTCTGGACAACATTCTTCCTTTATGGATCC
ATTAAAGCTTCTTCTGAAAACCTCTGGGCATTTCTGTTGAGCACCTTGTGGAGGGGCTAAGGAAGTGTGTAATGA
GCTGGGACCAGAGGCTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCTATCACACTTGGTGTGACATCAAGATAA
AGAGCGGAGGTGGATGGGGATGGAAGATGATGCTCCTATCCTCCCTGCCTGAAACCTGTTCTACCAATTATAGAT
CAAATGCCCTAAAATGTAGTGACCCGTGAAAAGGACAAATAAAGCAATGAATACATTA

FIGURE 244

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59855
<subunit 1 of 1, 93 aa, 1 stop
<MW: 10161, pI: 7.39, NX(S/T): 0
MKLVTIFLLVTISLCSYSAFLINKVPLPVDKLAPLPDNLFPMDPLKLLKTLGISV
EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV

Important features:

Signal peptide:

Amino acids 1-18

FIGURE 245

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGATCCCTCTATGACT
GCAATGTGAGGTGTCCGGCTTTGCTGGCCCCAGCAAGCCTGATAAGCATGAAGCTCTTATCTTTGGTGGCTGTGGT
CGGGTGTGTGCTGGTGGCCCCAGCTGAAGCCAAACAAGAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACC
TTATAGAAACATCAGTGGGCACATTTACAACCAGAATGTATCCAGAAAGGACTGCAACTGCCTGCACGTGGTGGGA
GCCCCATGCCAGTGCCTGGCCATGACGTGGAGGCCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAGCAC
CACCACCATCAAGGTCATCATTGTCTATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCTACATGGCCTTCCTGAT
GCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAACTGCACAATGAGGAGGAGAATGAGGATGC
TCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGC
CCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTTAGAT
GGGCTGGTGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGGCTACTT
CTCCCTTCCTCGGTTCCAGTCTTCCCTTTAAAAGCCTGTGGCATTTTTCCTCCTTCTCCCTAACTTTAGAAATG
TTGTACTTGGCTATTTTGTATTAGGGAAGAGGGATGTGGTCTCTGATCTCTGTTGTCTTCTTGGGTCTTTGGGGTT
GAAGGGAGGGGGAAGGCAGGCCAGAAGGGAATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTC
TCCTGGCTCCACTCTTGCCGCCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTTGAAGATAAAGCTGGGTCT
TTCAGGAACTCAGTGTCTGGGAGGAAAGCATGGCCCCAGCATTTCAGCATGTGTTCCCTTCTGCAGTGGTTCTTATC
ACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGC
TGGGCCCCCTGAGCCCCACTGGGTCTTCAGGGTGCCTGGAAGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCA
CTGGGGCATGGAGTGCCCATGCATACTCTGCTGCCGGTCCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTC
CTCTCCCCAGTGTCCACAGTCACTGAGCCAGACGGTTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGA
ACACCACAGCCCCCTGTACTTGGGTTGCCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGAGAGAAAATTTTG
TCCTCTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAATTGTTTTATTCTCTCA

FIGURE 246

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPMPVPGHDVEAYCLL
CECRYEERSTTTIKVIVIIYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAAASLGGPRA
NTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 247

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAAACTTTCTGAGTTTCAAAAACAACAGA
CTAGTACTCTAAAGAACTCTTTAAAAACAATTAAGTGTAGGATTGCAGTTATGATTGGATATTATTTAATTCTGT
TTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGCTATTAATATTTACCATTGCAGAAGCTTCATTCAAGTGTG
AAAATGAATGCTTAGTGGATCTGTGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCCTAATCAATGCAGAG
TTCCCTCCCTCCGATTGTTCTAAATTAATTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTGTAT
GATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTTTTTCTTGGCACTAAT
CAAGTGAGTGTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTAGTAAATAGAAACCTGTGTTTATTCTCAG
GTATTTTAGAAACAACAGCCATCATTTTATTTTATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTGG
GCTATCAAATATTACTTCATTCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCA
TTTTCTCAGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTATCTTCA
GATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGAATAAAAGTTCATATCTACCC

FIGURE 248

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLPSDCSK

Important features:

Signal peptide:

amino acids 1-29

FIGURE 249

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA
 ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGGACCCAAGTGAGGGGGCCCCGTGTTGGGGTCCCTCCC
 TCCCTTTGCAATCCCACCCCTCCGGGCTTTGCGTCTTCTGCGGGACCCCTCGCCGGGAGATGGCCCGGTTGATG
 CGGAGCAAGGATTCGTCTGCTGCTGCTCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
 TCGCGGGCCAACTCAACTCCATCAAGTCCCTCTGCGGGCGGGAGAGCGCTGGTCAGGCCGCAATCGATCTGCG
 GGCATGTACCAAGGACTGGCATTGCGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCTTGTAGCAGT
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA
 AAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT
 ACTGAAAGCATCTTAACCCCTCACATCCCGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
 TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTACATATAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA
 CAGTGTCTCCATCAGGGGGGAAGTCTGTACCAACAACGCAAGAAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT
 TGCGACTGTGCGAAGGGCTGTCTTGCAAAGTATGGAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG
 TGTGAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
 CATGGTGGAAAATAAGGTTTCAGATGCAGAAGATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACA
 AAGGGAGAAAGAAAACATGAAGTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG
 CACTTGTCTATGTAAATAATGTACACATTTGTGGAAAATGCTATTATTAAGAGAACAGCACACAGTGGAAAT
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCTTCAGATTGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAACAAAATACTCCTAGAATAACTTGT
 TACAAATAGGTTCTAAAAATAAAATTTGCTAAACAAGAAATGAAAACATGGAGCATTGTTAATTTACAACAGAAAAT
 TACCTTTTGATTTGTAACACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT
 TTCCAAATAATTGCAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGACAAATAAATAACAAACAAACAG
 CCACAAATACTTTTTTTTCAAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAACAGTTCC
 TTCAGATTCTACGGAATGACAGTATATCTCTCTTTATCCTATGTGATTCCCTGCTCTGAATGCATTATATTTTCCA
 AACTATACCCATAAATTTGTGACTAGTAAAATACTTACACAGAGCAGAATTTTACAGATGGCAAAAAATTTAAA
 GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTTT
 GATAGAATTAGATTGGTAAATACATGTATTCTATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG
 CACTGGAGTAAGCAAGAAAATTTGGGAAAACCTTTTCGTTTGTTCAGGTTTGGCAACACATAGATCATATGTCTG
 AGGCACAAGTTGGCTGTTCTCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
 CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTCCGTACTATCCTCAAATTTATTTTATATAG
 TGCTGAGATCCTCAAATAATCTCAATTTTCAGGAGGTTTCAAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
 TTTCAATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAAACCTCTGCAGCATCTG
 CTTTATTTGCCAAAGGGCTAGTTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTAA
 ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTTCTTGAACCACTTTACTACTTTTTTTTAACTT
 AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAGGTTATCTTATAGTCGTGACTTTTAACTTTTG
 TAGACCACAATTCACTTTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG
 AGATTGAGTTTGAGCCTGTATATCTATTAAAAATTTCAACTTCCACATATATTTACTAAGATGATTAAGACTTA
 CATTTTCTGCACAGGTCTGCAAAAACAAAATTATAAACTAGTCCATCCAAGAACCAGGTTTGTATAAACAGGT
 TGCTATAAGCTTGTGAAATGAAAATGGAACATTTCAATCAACATTTCTATATAACAATTATATATTTACAAT
 TTGGTTTCTGCAATATTTTCTTATGTCCACCTTTTAAAAATTAATTATTTGAAGTAATTTATTTTACAGGAAATG
 TTAATGAGATGTATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC
 TTTGTAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTTTCTCCTCTAAAAACTGAAAAA
 AAAAAAAAAAAAAAAAAA

FIGURE 250

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLAFGGSKKGKNLGQA
YPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRCNGICIPVTESILTPHIPALDGTRHRDR
NHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRSSDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGL
EIFQRCDCAKGLSCKVWKDATYSSKARLHVCQKI

Signal peptide:
amino acids 1-25

FIGURE 251

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAAGTGTGGGATTAC
 AGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATTTCTTCAAATTCATGGCAAATATTTCC
 CTTCCCTTTAACTTCTTATGTCAGAAATGAGGAAGGATAGCTGCATTTATTTAGTCAGTTTTCATTGCATAGTAAT
 ATTTTCATGTAGTATTTTCTAAGTTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTG
 AAAATACTTGATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCTTTT
 AAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAAATGGCAAACATCACCAGCTCCAGAT
 TTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACCCCAAGTACACAGCAGAATAGTACAAGTCA
 CCCTACAACCTACTACTTCTTGGGACCTCAAGCCCCCAACATCCCAGTCCCTCAGTCCTCAGTCATCTTGACTTCAA
 ATCTCAACCTGAGCCATCCCCAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGT
 TCCTCCTCCTGGTTTGGAGTCCTTTCCCTCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCCCTCCAC
 TGTGAACAAGCTTTTGCAGCTTCCAGCAGGACCATTTGAAAAATATCTCTGTGTCTGTCCACCAGCCACAGCCCAA
 ACACATCAAACTTGCTAAGCGGCGGATACCCCCAGCTTCTAAGATCCCAGCTTCTGCAGTGGAAATGCCTGGTTC
 AGCAGATGTCACAGGATTAAATGTGCAGTTTGGGGCTCTGGAATTTGGGTGAGAACCCTTCTCTCTGAATTTGG
 ATCAGTCCAAGCAGTGAAAATAGTAATCAGATTCCCATCAGCTTGTATTGGAAGTCTTTAAGTGAGCCTTTGAA
 TACATCTTTATCAATGACCAAGTGCAGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTGCAGTCTGAC
 AAGCTCATCACTGAATTTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACCAGAGTTCTGTGCATAACAGGAT
 CCCATACCAAGCCCTGTGAGTTCATCAGAGTCAGCTCCAGGAACCATCATGAATGGACATGGTGGTGGTCTGAAG
 TCAGCAGACACTAGACAGTAAGTATAGCAGCAAGCTACTCTTGTCTATGGCTGGTGCCAAACCAACAGAGGAAGAG
 GATAGCTCACGTGATGTGGAAAACACCAGTTGGTCAATGGCTCATTGTTTAAAAAGCAGCCCTTTTGCTTTTTTG
 TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGTGGTGGTCTCATA
 TTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCATTTTAAAGATGCTTGGGCCAGGCGGG
 GTGGCTGATGCCCATAAATCCCAGTGCTTTGGGGGGCCAAGGCAGGCAGATTGCCAAGCTCAGGAGTTTGAGACC
 ACCCTGGGCAACATGGTGAAACTCTGTCTCTACTAAAAATACGAAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCC
 TGTAATCCCAGCTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCCGT
 CTGAAAAGA

FIGURE 252

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQQNSTSHPTT
TTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPPGLESFPSQAKLRESTPGDSPSTVNK
LLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASKIPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAP
SSENSNQIPISLYSKSLSEPLNTLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRI PYQ
SPVSSSESAPGTIMNGHGGGRSQTLDSKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

Signal peptide:
amino acids 1-24

FIGURE 253

GGGCGCCCGCTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAACATGGAGCTCTCGCAGATGTCGGAGCTCAT
GGGGCTGTGCGGTGTTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCGGTAGCGCGGGGTGGCTGCGCGCGGG
GGAGGAGAGGAGCGGCCGCGCCCTGCCAAAAAGCAAATGGATTTCCACCTGACAAATCTTCGGGATCCAAGAA
GCAGAAACAATATCAGCGGATTTCGGAAGGAGAAGCCTCAACAACACAACCTTACCCACCGCCTCCTGGCTGCAGC
TCTGAAGAGCCACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGCAGA
TGATCGCACCATCCGCATCTGGAGCACCAGGACTTCCTGCAGCGAGAGCACCGCAGCATGAGAGCCAACGTGGA
GCTGGACCAAGCCACCCCTGGTGCCTTCAGCCCTGACTGCAGAGCCTTCATCGTCTGGCTGGCCAACGGGGACAC
CCTCCGTGTCTTCAAGATGACCAAGCGGGAGGATGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCCTAA
AAAGCACAAGGCGCCTGTCTGACATTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACAC
CACTGTCTCTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACCAGATGAACAACACACACGC
TGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCAGATGTGAAGGTTTGGGAAGTCTGCTT
TGGAAGAAGGGGGAGTTCCAGGAGGTGGTGCGAGCCTTCGAACATAAGGGCCACTCCGCGGCTGTGCACTCGTT
TGCTTTCTCCAACGACTCACGGAGGATGGCTTCTGTCTCCAAGGATGGTACATGGAACTGTGGGACACAGATGT
GGAATACAAGAAGAAGCAGGACCCCTACTTGTGAAGACAGGCCGCTTTGAAGAGGCGGCGGGTGCCGCGCCGTG
CCGCTTGGCCCTCTCCCCAACGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCATCTCTACAATACCCG
GCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCAACCTTGTCCTTTGACATCACTGG
CCGCTTTCTGGCCTCCTGTGGGACCGGGCGGTGCGGCTGTTTCACAACACTCCTGGCCACCGAGCCATGGTGGA
GGAGATGCAGGGCCACCTGAAGCGGGCCTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGC
CCAAGAGACCCTGAAGAGCCTGGGTGCCCTGAAGAAGTGACTCTGGGAGGGCCCGGCGCAGAGGATTGAGGAGGA
GGGATCTGGCCTCCTCATGGCACTGCTGCCATCTTCTCCAGGTGGAAGCCTTTCAGAAGGAGTCTCCTGGTT
TTCTTACTGGTGGCCCTGCTTCTTCCCATTGAACTACTCTTGTCTACTTAGGTCTCTCTCTTCTTGCTGGCTGT
GACTCCTCCCTGACTAGTGGCCAAGGTGCTTTTCTTCTCCAGGCCAGTGGGTGGAATCTGTCCCCACCTGGC
ACTGAGGAGAATGGTAGAGAGGAGAGAGAGAGAGAGAATGTGATTTTGGCCTTGTGGCAGCACATCCTCAC
ACCCAAAGAAGTTTGTAAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTGCAAGGATG
GGAGACTGGGATAGCTTCCCATCACAGAACTGTGTCCATCAAAAAGACACTAAGGGATTTCTTCTGGGCCTCA
GTTCTATTTGTAAGATGGAGAATAATCCTCTCTGTGAACCTTGCAGAGATGATATGAGGCTAAGAGAATATCA
AGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGTAGTACTATTGTCCAATGTCATGAAAGTGGTAAAAGTGGGAA
CCAGTGTGCTTTGAAACCAATTAGAAAACACATTCCTTGGGAAGGCAAAGTTTCTGGGACTTGATCATACATTT
TATATGGTTGGGACTTCTCTCTTGGGAGATGATATCTTGTAAAGGAGACCTCTTTTCAGTTTCATCAAGTTTCAT
CAGATATTTGAGTGCCCACTCTGTGCCCAATAAATATGAGCTGGGGATTAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQKQYQRIKKEKPQQH
NFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQREHRSMRANVELDHATLVRFSPPDCRA
FIVWLANGDTLRVPKMTKREDGGYTFTATPEDFPKKHKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTI
NTNQMNNTAAVSPCGRFVASCFTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKD
GTWKLWDTDVEYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVHGEC
IANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHKLRASNESTRQLQQQLTQAQETLKSLGALKK

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 255

ACGGACCGAGGGTTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGCCAGGTGCCCC
GTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGGCGAGCGCGAGAAGCCCCCTTCCTCGGCGCTGCCAACCC
GCCACCCAGCCC**AT**GGCGAACCCCGGGCTGGGGCTGCTTCTGGCGCTGGGCCTGCCGTTCCCTGCTGGCCCGCTGG
GGCCGAGCCTGGGGGCAAATACAGACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCC
AGCTCCGATGGCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTC
CTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCACT
AGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCTGCCTG
CCCATCT**AG**GTCCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCTCTCT
GGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCCTGAGGTCAAGAGA
GGATGGGGCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAAA

FIGURE 256

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVFSLLAALLAVG
LALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

FIGURE 257

[illegible]

FIGURE 258

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTTASTYLFEEATEKRFFFKN
VSILIPENWKENPOYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGGEYIHFTPDLLLGGKKQNEYGPPG
KLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCESAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQF
FPDKVQTEKASIMFMQSIDSVVEFCNEKTHNQEAPSLQNIKCNRSTWEVISNSEDFKNTIPMVTPPPPPVFSL
KISQRIVCLVLDKSGSMGGKDRLNRMNQAAKHFLQLTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGL
PTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMS
KITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTINSNAWMNDTVIIDSTVGKDTFFLITWNS
LPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKM
NKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNMGVYSRYFTAYTENGRYS
LKVRAHGGANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLLEDFSRASGGAFFVVSQVPSLPLP
DQYPPSQITDLDATVHEDKIILTWTA PGDNFDVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKES
FAFKPENISEENATHIFIAIKSIDKSNLTSKVSANIAQVTLFIPQANPDDIDPTPTPTPTPTPDKSHNSGVNISTL
VLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592, 628-632,
811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 259

CGCCGGAGGCAGCGCGGCGTGGCGCAGCGGCGACATGGCCGTTGTCTCAGAGGACGACTTTTCAGCACAGTTCAA
 ACTCCACCTACGGAAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGCACTGCTTGAGAAGCTGCTGGACCGCC
 CGCCCCCTGGCCTGCAGAGGCCCCGAGGACCGCTTCTGTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCA
 GTCTACTGCCATGGAACTTCTTTATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAG
 CCACCGGGGAGGACCTTGAGGGCTCAGACATCCTGAACACTTTGAGAGCTACCTTGCCGTTGCCTCCACCGTGC
 CCTCCATGCTGTGCTTGGTGGCCAACTTCTGCTTGTCAACAGGGTTGCAGTCCACATCCGTGTCTGGCCTCAC
 TGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAAGGTGGACACTTCTCTCTGGACCCGTTGGTT
 TTTTGGCGTCAACATTGTCTGCATGGTGATCCTCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCA
 TGACCGGCTCCTTTCTATGAGGAACCTCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCG
 TGGCCTCATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGGCCACCA
 TCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCCAGGTACTACATGAGGCCTG
 TTCTTGCGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCAGGACTCCCTCAGTGCCCTTCCGGTGGCCTCCA
 GATTTCATTGATTCACACACACCCCTCTCCGCCCCATCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCT
 ACGTCTTCTTCATCACCAGCCTCATCTACCCGCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCT
 CACTGTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCTGTACAACTTTGCTGACCTATGTGGCCGGC
 AGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCCAGGGTTCGTGCTCTCCGGACCTGCC
 TCATCCCCCTCTTCGTGCTCTGTAACTACCAGCCCCGCGTCCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGT
 ACCCCGCACTCCTCAGCTCCCTGCTGGGCTCAGCAACGGCTACCTCAGCACCTGGCCCTCCTCTACGGGCCTA
 AGATTGTGCCCAGGAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGG
 GCTCAGCCTGCTCTACCCTCCTGGTGCACCTCATCTAGAAGGGAGGACACAAGGACATTGGTGTTCAGAGCCTT
 TGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCCATAAGTTTCACTTGGGGACAGAGAG
 CAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCAGTGAGCCACGTCCATGCCCATTCCGTGCAAGGCAGATA
 TTCCAGTCATATTAACGAACACTCCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACA
 GCTGATGGTTAACAATCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCCTAGAGTTATTACAAA
 GCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCTGACAGCGAGATGCAA
 GCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGAAGTCCCTGGCATGGTCAGTCTCAGGC
 CCAAGACTCAAGTGTGCACAGACCCCTGTGTTCTGCGGGTGAACAACTGCCCACTAACCCAGACTGGAAAACCCAG
 AAAGATGGGCCTTCCATGAATGCTTCATTCCAGAGGGACCAGAGGCCTCCCTGTGCAAGGGATCAAGCATGTCT
 GGCCTGGGTTTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTCTTTCA
 GTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGCCTATTCAAAAA

FIGURE 260

MAVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGLQRPEDRFCGTYIIFSLGIGSLLPWNFFITAK
EYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFLLVNRVAVHIRVLASLTVILAIFMVIT
ALVKVDTSSWTRGFFFAVTIVCMVILSGASTVFSSSIYGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSD
VRNSALAFFLTATIFLVLCMGLYLLLSRLEYARYYMRPVLAHVFSGEEELPQDSLAPSVASRFIDSHTPPLRP
ILKKTASLGFCVTVYVFFITSLIYPAVCTNIESLNKSGSLWTKFFIPLTTFLLYNFADLCGRQLTAWIQVPGPN
SKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLALLYGPKIVPRELAEATG
VVMSEFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252, 305-330,
448-472

FIGURE 261

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACACCTGTTTTA
AAGAACCCTAAGCACCAATTAAAGCCACTGGAAATTTGTTGCTCTAGTGGTTGTGGGTGAATAAAGGAGGGCAGAAAT
GGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTACGTGGCCGGAATCATTTCCCTT
GGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGGGTGCTGGCCTTCTCTGTGGAAGTGTCTCT
GGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAAGATATTCTTGAGGGAAAACACCACCAAGCAAGTGA
AACACATAATGTGATTGCATCAGACAAAAGCAGCAGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCA
CACACAGCTGCATGCCATATATTGGTGT'TTCCCTCGTTCTGGGCTTCGTTTTCATGTTGCTGGTGGACCAGATTGG
TAACTCCCATGTGCATTCTACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACCACGCTGGG
TCTGTTGTCCATGCTGCAGCTGATGGTGT'TGCTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTT
AATTGTGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCTGG
CTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGTCATTGGCAGCACCAGTTATGTCCATGGTGACATA
CTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGGCCATGCTTTTCTCTGC
CGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGAATAGGGCACAGCCACAAGCCCGA
TGCCACGGGAGGGAGAGGCCTCAGCCGCTGGAAGTGGCAGCCCTGGTTCTGGGTGCTCATCCCTCTCATCCT
GTCAGTAGGACACCAGCATTAATGTTCAAGGTCCAGCCTTGGTCCAGGGCCGTTTGGCCATCCAGTGAGAACAGC
CGGCACGTGACAGCTACTCACTTCTCAGTCTCTTGTCTCACCTTGCGCATCTCTACATGTATTCTAGAGTCCA
GAGGGGAGGTGAGGTTAAACCTGAGTAATGGAAGGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTA
TAGACATCCCATTGTGTATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAATATTTCTCTTAACCTTATTCTC
AGGGAAGATGGAATTTAGTTTTAAGGAAAAGAGGAGAAGCTTCATACTCACAATGAAATAGTGATTATGAAAATAC
AGTGTCTGTAAATTAAGCTATGTCTCTTCTCTTAGTTAGAGGCTCTGCTACTTTATCCATTGATTTTAAACA
TGGTTCCCAACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTGATAGCACCCTCA
CTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGCAAGACACATTGAAAGCTC
TCTTTTACTCAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATTAAACAGCTCCTTTGGCAGCTGCCT
CTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGGTGGGAGGAGCTTCTAAAGAGGTGACTGGTATT
TTGTAGCATTCTTGTCAAGTTCTCCTTTGCAGAATACCTGTCTCCACATTCTTAGAGAGGAGCCAAGTTCTAGT
AGTTTCAGTTCTAGGCTTTCCTTCAAGAACAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATATTAATTT
TAAGTGATTTTGGATGGTTATTGATATCTTTGTAGTAGCTTTTTTAAAGACTACCAAATGTATGGTTGTCC
TTTTTTTTGTTTTTTTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGG
TCAGCTTTGGCGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTCCT
ATTGATTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCTGCTCTTTCTTTGCTTTTCTTCTAATTTTCCCTC
TAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTTAATATTTGTGTGGGATGAATTTCTATCAGGACAA
CCACTTCTCGAACTGTAATAATGAAGATAATAATATCTTTATTCTTTATCCCCCTTCAAAGAAATTACCTTTGTG
TCAAATGCCGCTTTGTTGAGCCCTTAAATAACCACCTCCTCATGTGTAAATTGACACAATCACTAATCTGGTAAT
TTAAACAATTGAGATAGCAAAAGTGT'TAACAGACTAGGATAAATTTTTTTTTCATATTGGCAAAATTTTGTAA
ACCCTGTCTTGTCAAATAAGTGTATAATATTGTATTATTAATTTATTTTACTTTCTATACCATTTCAAAACACA
TTACACTAAGGGGGAACCAAGACTAGTTTCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTCTATGAC
GCATAAGCTAGCATGCCATGATTTATTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTT
GTGAGCCCTCTGCTGGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATT
GCATACAATTTTACTACCAAGAGAAGGTATAGTATGGAAGTCCAAATGACTTCTTGATTGGATGTTAACAGCT
GACTGGTGTGAGACTTGAAGTTTTCATCTAGTCCTTCAAACTATATGGTTGCCTAGATTCTCTCTGGAACTGAC
TTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

FIGURE 262

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHALYEDILEGKHHQAS
ETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQIGNSHVHSTDDPEAARSSNSKITTTTL
GLVVHAAADGVALGAAASTSQTSLVQVIVFVAIMLHKAPAAFGLVSFLMHAGLERNRIRKLLVFALAAPVMSMVT
YLGLSKSSKEALSEVNATGVAMLFSAFTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLI
LSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 263

CTCCTTAGGTGGAAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCCGGGAAAGACCATACGTCCTCCCGG
GCAGGGGGTGACAACAGGTGTCTATCTTTTTGATCTCGTGTGTGGCTGCCTTCTTATTTCAAGGAAAGAC
GCCAAGGTAATTTTGACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCC
AGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTGG
TTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGAGGGTG
GACCGAAGAAAGGAAAGGTCCCCCTTGCTGTGTGGCTGCACATCAGGAAGGCTGTGATGGGAATGAA
GGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCCTTTAAAAGTAGAGA
AGCTGCTCTGTGTGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGC
TCCGGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCAGGGAAGCCCTTCGGTGGGGGGCCCCGGCT
TTGAGGGATGCCACCGGTTCTGGACGCATGGTGCTGATTCTGGAATGATGATGGTTCGCCGGGGGGCTGCT
TGCGTGGATTTCCCGGGTGGTGGTFTTGCTGGTGTCTCCTCTGCTGTGCTATCTCTGTCTCTGTACATGT
TGGCCTGCACCCCAAAGGTGACGAGGAGCAGCTGGCATTGCCCAGGGCCAAACAGCCCCACGGGGAAG
GAGGGGTACCAGGCCGCTCCTTCAGGAGTGGGAGGAGCAGCAGCCGAACCTACGTGAGCAGCTGAAGCG
GCAGATCGCACAGCTCAAGGAGGAGCTGACAGGAGGAGTGACGAGCTCAGGAATGGGCAGTACCAAG
CCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTCCTGGCC
TTCCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCCTCAAGCTGGCCACAGAGTATGCAGC
AGTGCCTTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCCTTACCCTGCAACCCG
AGGAGAAGCCTGTGAGGAAGGACAAGCGGATGAGTTGGTGGGAAGCCATTGAATCAGCCTTGGAGACC
CTGAACAATCTGACAGAGAACAGCCCCAATCACCGTCTCTTACACGGCCTCTGATTTCATAGAAGGGAT
CTACCGAACAGAAAGGGACAAGGGACATTGTATGAGCTCACCTTCAAAGGGGACCACAAACACGAAT
TCAAACGGCTCATCTTATTTTCGACCATTGACCCCCATCATGAAAGTGAAAAATGAAAAGCTCAACATG
GCCAACACGCTTATCAATGTTATCGTGCCTTAGCAAAAAGGGTGGACAAGTTCCGGCAGTTTCATGCA
GAATTTTCAGGGAGATGTGCATTGACAGGATGGGAGAGTCCATCTCACTGTTGTGTTACTTTGGGAAAG
AAGAAATAAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAAGCTGCCAACTTCAGGAACCTTTACC
TTCATCCAGCTGAATGGAGAATTTTCTCGGGGAAAGGAGACTTGATGTTGGAGCCCGCTTCTGGAAGG
AAGCAACGTCCTTCTCTTTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTA
GGCTGAATACACAGCCAGGGAAGAAGGTATTTTATCCAGTTCTTTTTTCAGTCAGTACAATCCTGGCATA
ATATACGGCCACCATGATGCAGTCCCTCCCTTGGAAACAGCAGCTGGTCATAAAGAAGGAAACTGGATT
TTGGAGAGACTTTGGAGTTTGGGATGACGCTGTGAGTATCGGTGAGCTTCATCAATATAGTGGGTTTG
ATCTGGACATCAAAGGCTGGGGCGGAGGAGTGTGCACCTTTATCGAAGTATCTCCACAGCAACCTC
ATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAGCT
GACCCCCGAGCAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGG
GCATGCTGGTGTTCAGGCACGAGATAGAGGCTCACCTTCGCAACAGAAACAGAAAGCAAGTAGCAAA
AAAACATGAACTCCACAGAGAAGGATGTGGGAGACACTTTTTCTTCTTGTGAATTAAGTGAAGTG
GCTGCAACAGAGAAAGACTTCCATAAAGGACGACAAAAGAATTGGAATCATGGGTGAGAGATGAGAA
AGCCTCCGATTTCTCTCTGTTGGGCTTTTTTACAACAGAAATCAAATCTCCGCTTTGCCTGCAAAAGT
AACCCAGTTGCACCCTGTGAAGTGTCTGACAAAGGCAGAATGCTTTGTGAGATTATAAGCCTAATGGTG
TGGAGGTTTTGATGGTGTTTACAATACACTGAGACCTGTTGTTTTGTGTGCTCATTGAAATATTCATG
ATTTAAGAGCAGTTTTGTAAAAAATTCATTAGATGAAAGGCAAGCATATTTCTCTCATATGAATG
GCCTATCAGCAGGGCTCTAGTTTCTAGGAAATGCTAAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTA
TTATGATACTAGTGAGTACATTAAGTAAAATAAAATGGACCCAGAAAGAAAAGAAACCATATAAATATCG
TGTCATATTTTCCCCAAGATTAACCAAAAATAATCTGCTATCTTTTTGGTTGTCTTTTTAACTGTCT
CCGTTTTTTTTCTTTTATTTAAAAATGCACTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTA
CCACTTTTGCAAGCCTTACAAGAGAGCACAAAGTTGGCCTACATTTTTTATATTTTTTTAAGAAGTACTTT
GAGATGCATTATGAGAACTTTCAAGTCAAAAGCATCAAATGATGCCATATCCAAGGACATGCCAAATG
CTGATTCTGTGAGGCATGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATAACAGA
CGTACAGATACTTTCTCTGAAGAGTATTTTGAAGAGGACCACTGAACACTGGAGGAAAAGAAAATG
ACACTTTCTGCTTTACAGAAAGGAAACTCATTCAGACTGGTGATATCGTGATGTACCTAAAAGTCAG
AAACCACATTTTCTCCTCAGAAGTAGGGACCGCTTTCTTACCTGTTTAAATAAACCAAAGTATACCGT
GTGAACCAAACAATCTCTTTTCAAACAGGGTGCTCCTCCTGGCTCTGGCTTCCATAAGAAAGAAATG
GAGAAAAATATATATATATATATATATATTTGAAAGATCAATCCATCTGCCAGATCTAGTGGGATG
GAAGTTTTTGTCTACATGTTATCCACCCAGGCAGGTGGAAGTAACTGAATTAATTTTTTAAATTAAGC
AGTTCTACTCAATCACCAAGATGCTTCTGAAAATTGCATTTTTATTACCATTTCAAACTATTTTTTAAA
AATAAATACAGTTAACATAGAGTGGTTTTCTTCATTCTGTGAAAATTATAGCCAGCACCAGATGCAT
GAGCTAATTTATCTCTTTGAGTCTTGTCTGTGTTGCTCAGATAAACTCATTGCTTTAAAAGCTTCAA
GAACATTTCAAGCTGTTGGTGTGTTAAAAATGCATTTGATTGATTTGTACTGGTAGTTTATGAAATTT
AATTAACCAACAGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAAATATGATTTGTGGATATGAA

FIGURE 264

MMVRRGLLAWISRVVLLVLLCCAI SVLYMLACTPKGDEEQALPRANSPTGKEGYQAVLQEWEEQHRNYVSSL
KRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDS
FTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNNPAENSPNHRPVTASDFIEGIYRTERDKGTLYE
LTFKGDHKHEFKRLILFRPFSPIMKVKNEKLNMANTLINVIIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY
FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNT
QPGKKVFYPVLF SQYNPGI IYGHDAVPPL EQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGED
VHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTP EQYKMC MQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQ
KTSSKKT

FIGURE 265

GGATGCAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGTCTGCTTCCTCTTCTACGCTGGCATTGCCCTCTTCA
CCAGTGGCTTCTGCTCACCCGTTTGGAGCTACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
TGCCATGGGGGAGCCAAGGGAAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGCGGGTTGTGTGGTGTGTA
TAGATGCTCTGCGATTTGACTTCGCCAGCCCCAGCATTACACGTGCCCTAGAGAGCCTCCTGTCTCCCTACCCCT
TCCTGGGCAAACCTAAGCTCCTTGCAGAGGATCCTGGAGATTACAGCCCCACCATGCCCGGCTCTACCGATCTCAGG
TTGACCCTCTACCAACCATGCAGCGCCTCAAGGCCCTCACCCTGGCTCACTGCCTACCTTTATTGATGCTG
GTAGTAACCTTCGCCAGCCACGCCATAGTGAAGACAATCTCATTAAGCAGCTCACCAGTGCAGGAAGGCGTGTAG
TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGTCTTCTCAAAGCTTTCTTCTTCCCATCCTTCA
ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCACCATGGACAGTGGTGAATGGG
ACGTGCTGATTGCTCACTTCCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCTGAAATGGCCA
AGAACTTAGCCAGATGGACCAGGTGATCCAGGCACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
CTGGGGACCATTGGGATGACCACAAATGGAGACCATTGGAGGGGACAGTACAGCTGGAGGTCTCAGCTGCTCTCTTTC
TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
CCACGCTGGCCCTGCTGCTGGGCCTGCCCATCCCATTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG
GGGGTGAGGACTCCCAGCCCCACTCCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
CCCCATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
TCTCCAAGGCCTCTGCTGACTACAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA
TTGCTGAGCTGCAGCAGTTCCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC
GCATGGCGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCCTGCTGGCATCTCAGTGGGCAATATCCC
CAGGCTTTCCATTCTGCCCTCTACTCCTGACACCTGTGGCCTGGGGCCTGGTTGGGGCCATAGCGTATGCTGGAC
TCCTGGGAACCTATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATTCTCCCTT
TTCTGTGGAAGCCTGGGCTGCTGCTGGGGGTCCAAGAGGCCCCCTGGCAACCCCTGTTTCCCATCCCTGGGCCCCGTC
TGTTACTCCTGCTGTTTCGCTTGGCTGTGTTCTTCTCTGATAGTTTGTGTGAGCTGAGGCCAGGGCCACCCCT
TCCTTTTGGGCTCATTACCTGCTCCTGCTTGTTCAGCTTTCACCTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC
TCACAATGCCCGCCTTGGCACTTCAGCCACAACAAACCCCCACGGCACAATGGTGCATATGCCCTGAGGCTTG
GAATTGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTATCGTTGCCCTGAAGAGACACCTGTTTGGCACT
CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTTCAGGCCAAGAATTTATGGTATGGAGCTTGTGTGG
CGGCGCTGGTGGCCCTGTTAGCTGCGGTGCGCTTGTGGCTTCGCCGCTATGGTAATCTCAAGAGCCCCGAGCCAC
CCATGCTCTTTGTGCGCTGGGACTGCCCCAATGGCATTTGGGTACTGCTGCCTACTGGGCATTGGCGTTCGGGG
CAGATGAGGCTCCCCCGCTCTCCGGTCTGGTCTCTGGGGCATCCATGGTGTGCTGCTCGGCTTGGGCCCTCATGGCCA
CACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTTCCAGCCATCCATTGGCATGCAGCCTTCGTGGGATTCC
CAGAGGGTCATGGCTCCTGTACTTGGCTGCCTGCTTTGCTAGTGGGAGCCAACACCTTTGCCTCCCACCTCCTCT
TTGCAGTAGGTTGGCCACTGCTCCTGCTCTGGCCTTTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC
CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGG
ATGCGCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCCTCAAGTACCTCTTTATCCTTGGTATTAGATTCT
TGGCCTGTGCTTGGCAGCCTCCATCCTTCGAGGCATCTCATGGTCTGGAAGTGTTCGCCCTAAGTTTCATAT
TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTG
CTGTGAGCTCCTGGTTACGGCAGCTATTCTGGCCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT
ACAGAGAGTGTGAGAAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC
TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTCAGGACCACAGTGGAGTA
TGATCCCTAACTCCTGATTTGGATGCATCTGAGGGACAAGGGGGCGGTCTCCGAAGTGAATAAAATAGGCCGG
GCGTGGTGACTTGCACCTATAATCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA
AGACCAGCCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAGTGTAATAAATGATAATAT

FIGURE 266

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACWMASRFSRVVLVLI
DALRFDFAQPQHSVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQVDPPTTTMQRLKALTTGSLPTFIDAG
SNFASHAIVEDNLIKQLTSAGRRVVFMDGDDTWKDLFPGAFSKAFFFPFNVRLDLDTVDNGILEHLYPTMDSGEWD
VLI AHFLGVDHCGHKHGPHEMAKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFL
YSPTAVFPSTPPEEPEVIPQVSLVPTLALLLGLPIPFGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQQVS
RFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRGARAMCTESWARFSLVR
MAGGTALLAASCFCILLASQWATSPGFFPCPLLLTPVAWGLVGAIAYAGLLGTIELKLDLVLLGAVAAVSSFLPF
LWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRLLAVFFSDSFVVAEARATPFLGSGFILLVVLHVEGQLLPPKLL
TMPRLGTSATTNPPRHNGAYALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVA
ALVALLAAVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAWALASGADEAPPRLRVLVSGASMVLPRVAGL
AASGLALLLWKPVTVLVKAGAGAPRTVLTTPFSGPPTSQADLDYVVPQIYRHMQEEFRGRLETKSQGPLTVAA
YQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFQSFLLLHLLAAGIPVTTTPGPFTVPWQAVSAWALMAT
QTFYSTGHQPVFPAIHWHAAFVGFPEGHGSCTWLPALLVGANTFASHLLFAVGCPLLLLPFLCESQGLRKRQQP
PGNEADARVRPEEEEEPLMEMRLRDAPQHFYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFIF
EAVGFIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR
```

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 267

[illegible]

FIGURE 268

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTDFDPLPALQPHGYDQPGTE
PLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQINSEATFAELHIVHYDSYDSLSEA
AERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSV
LWTVFYRRSQISMEQLEKLGTLFSTEEEPSKLLVQNYRALQPLNORMVFASFIQAGSSYTTGEMLSLGVGILVG
CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 269

GTGGCGCTGGCGGTTGCTGTCTAGCTGATTCCTCGGGGTTGGTGGCAGCGGCGGTAGCAGCAATGGACTTTCTCCTG
GGGAACCCGTTTCAGCTCTCCAGTGGGACAGCGCATCGAGAAAGCCACAGATGGCTCCCTGCAGAGCGAGGACTGG
GCCCTCAACATGGAGATCTGCGACATCATCAACGAGACGGAGGAAGGTCCCAAAGATGCCCTCCGAGCAGTAAAG
AAGAGAATCGTGGGGAATAAGAACTTCCACGAGGTGATGCTGGCTCTCACAGTCTTAGAAACCTGTGTCAAGAAC
TGCGGGCACCCTTCCACGTGCTGGTGGCCAGCCAGGACTTCGTGGAGAGTGTGCTGGTGAGGACCATCCTGCCC
AAGAACAACCCACCCACCATCGTGCATGACAAAAGTGTCAACCTCATCCAGTCCCTGGGCTGACGCGTTCCGCAGC
TCGCCCCGATCTGACAGGTGTGGTCACCATCTATGAGGACCTGCGGAGGAAAGGCCTGGAGTTCCCATGACTGAC
CTGGACATGCTGTCAACCATCCACACACCCAGAGGACCGTGTTCAACTCAGAGACACAATCAGGACAGGATTCTG
TGGGCACTGACTCCAGCCAGCAAGAGGACTCTGGCCAGCATGCTGCCCCCTCTGCCCCGCCCCGCCCCATACTCTCCG
GTGACACGCCCCATAGCACCAACCCCGGAACAGATTGGGAAGCTGCGCAGTGAGCTGGAGATGGTGAGTGGGAACG
TGAGGGTGATGTGCGGAGATGCTGACGGAGCTGGTGGCCACCCAGGCCGAGCCCGCAGACCTGGAGCTGCTGCAGG
AGCTCAACCGCACGTGCCGAGCCATGCAGCAGCGGGTCTTGAGTGATAACCTGCTCCGGGGCCCATGCCCAAGGA
GCCCTTCAGAGCCCACTGCCAGTCGAGGCCTGGCTGGAGGCTGGCCACAGTGGAAATTCGCGGAGCCTATTG
TCCCTACCTGCTCTGCTGCATGGGGCCCCATGGCTTTGGCTGGCCACTGAGGGTAGGGTGTGGAGGTGTGGAGG
CCCCCTGAGGAGCTGCGGCGGCCAGGTACGAAGCTGCAACTCTGCGCGCAGTGGGCGAGATCTCATCAGCCCCA
GGCTGCAGGTGAGGCTTCAGGGGATGCTGGGGCCCCACTGCCCTCCGCTGCCTTGCCCTCCATCCTTCCTCTGT
TCCTTCTGGCCGGGCACCAAGCACTGGGGCTCACCTCTGGTTGATCCTCTTGTAAGTGGGAGAGGTGCCTTTTG
TATCCCCAATTAAAGGTAGAAAACC

FIGURE 270

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62813
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23465, pI: 7.57, NX(S/T): 1
MDFLLGNPFSSPVGQRIEKATDGSLSQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEVMLALTVLE
TCVKNCGHRFHVLVASQDFVESVLVRTLTPKNNPPTIVHDKVLNLIQSWADAFRSSPDLTGVVTIYEDLRRKGLE
FPMTDLDMLSPIHTPRGPCSTQRHNQDRILWALTPASKRTLASMLPLCPPRPYSPVTRP
```

Important features of the protein:

Signal peptide:

Amino acids 1-15

N-glycosylation site:

Amino acids 41-45

N-myristoylation sites:

Amino acids 6-12;23-29

FIGURE 271

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCGTCTGCCATGGGGC
TCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCTGATGCTGCCCGTGAAGCCCCCGCAG
GCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGGTGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCT
TCGGGGGCCAACATCACTGCGGAGGCTTCCTGCTGCGAGCCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCC
ACAGAGACCTCCGCACTGGCCTGGTGGTGCTGGGCGCCACGTCCTGAGTACTGCGGAGCCACCCAGCAGGTGT
TTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGACATCTGCCTGCTGCGGC
TGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGGCTGCTGAGGCTGCCAGGGAGAAGGGCCAGGCCCCCACAG
CGGGGACACGGTGCCGGGTGGCTGGCTGGGGCTTCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGG
CCAAGGTCCGAGTGCTGGACCCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCA
CCCGCAGTGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGAACCGGG
CTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCCGACGTGTACACGCAGGTGTCCG
CCTTTGTGGCCTGGATCTGGGACGTGGTTCTGGCGGAGCAGTCCCCAGCCCGGCCCTGCCTGGGACCACCAGGC
CCCCAGGAGAAGCCCGCTTGAGCCACAACCTTGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCG
TGGCTGGGCCCCACGGGAAGCCTGATGTT'CAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACA
TGCAAAGGGCAGAAGCAAACCCAGTAAATGTAACTGACAAAAAAAAAAAAAAAAAAAAAAGAAA

FIGURE 272

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGFLLRARWVVSAAHC
FSHRDLRTGLVVLGAHVLSTAEP TQQVFGIDALTTHPDYHPMTHANDICLLRLNGSAVLGPAVGLLRLPGRRARP
PTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPDVCNSSWKGHILTLMLCTRSGDSHRRGFCSADSGGPLVCR
NRAHGLVSFSGLWCGDKTPDVYTQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:
amino acids 1-30

FIGURE 273

GAAGTTCGCGAGCGCTGGCTATGGGTCCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTGGCGCTCGGGACAG
GAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGACCAGCGTGGCGCGCGCCCTGGCGCCCG
AGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGCGCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCT
ACGACAAGGTACTTTCTTTGTCATGAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTTACTCTCATCA
AACGCTGTCAGTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGGATG
GCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGGGCCCTGATGCGGCTGC
AGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCCGAGGTGTCTTTCAGAGAGTCACTGGCTCTGCCATCACTG
ACCTGTACAGCCCCAAACGGCTCTTTTCTCTCACAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACA
TGGGGGATTATTACCATGCCATTCCATGGCTGGAGGAGGCTGTGAGTCTCTTCCGAGGATCTTACGGAGAGTGGA
AGACAGAGGATGAGGCAAGTCTAGAAGATGCCCTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGAAATGTTT
CGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAATAAGAGGATGGCCAGGAATGTCTTGA
AATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGCTGAGGCTGTATCCAGAGGCCCAATATACCCC
ACCTGCAGACCAGAGACACCTACGAGGGGCTATGTACAGACCTGGGTTCAGAGCCCACTCTCTACAGATCCCTA
GCCTCTACTGTTCTATGAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCACTCCACC
TGGAGCCCTACATTGCTCTCTACCATGACTTCGTGAGTCACTCAGAGGCTCAGAAAATTAGAGAACTTGAGAAC
CATGGCTACAGAGGTGAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAGTACCGCATCAGCAAAAGTGCCCT
GGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCTCAACCACCGCATTGCTGCCCTCACAGGCCTTGATGTCC
GGCCTCCCTATGCAGAGTATCTGCAGGTGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTGGACCATG
CTACGTACCAAGCAGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCT
CGGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGAATGCAGCACTGT
TTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCATGCTGGCTGTCTCTGCTGGTGGAG
ATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGGACAGGAATTCGCGCAGACCCTGCAGCTCCAGCCCTGAAG
ACTGAACTGTTGGCAGAGAGAAGCTGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGCTA
GGAGAGGAGAAAGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTGAGCTTTGTCTGTGCCTCGCAAATCAGAGGCAA
GGGAGAGGTTGTTACAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAAGTCAGAGTAGGATGC
ACAGTACAAAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGGAGTTCAGATACTCTCTGTTGGGAACAGG
ACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTCTTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGG
CAATGAGGACACCTGCAGGAGGGGCTAGCCTGACTCCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGC
AGCCCAAGCAGGGAGTGTCCCCCTCCCAAGCATATCCCAGATGAGTGGTACATTATATAAGGATTTTTTTTAA
GTTGAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAAAAATGTTTATAAATCAAAA

FIGURE 274

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64849
><subunit 1 of 1, 544 aa, 1 stop
><MW: 61126, pI: 6.40, NX(S/T): 2
MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEA
RLRDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGY
EKVEQDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLT
GDDCFQVGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRA
GNVSCALSLSREFLLYSPDNKRMAVNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDT
YEGLCQTLGSQPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEA
QKIRELAEPWLQRSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRRIAALTGLDVRP
PYAEYLQVVNYGIGGHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIY
ANLSVPVVRNAALFWWNLHRSGEGDSDLHAGCPVLVGDKWVANKWIEHYGQEFRRPCSS
SPED
```

Important features of the protein:

Signal peptide:

Amino acids 1-19

Leucine zipper pattern:

Amino acids 34-56;41-63

Ribonucleotide reductase small subunit signature:

Amino acids 340-356

N-glycosylation sites:

Amino acids 242-246;482-486

Cell attachment sequence:

Amino acids 27-30

Tyrosine kinase phosphorylation site:

Amino acids 189-198

N-myristoylation sites:

Amino acids 4-10;135-141;153-159;164-170;241-247;303-309;309-315;
457-463;473-479

FIGURE 275

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCATCCTGGTGATCACC
TTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGAAGCACAGCAAACGTCGAGTGAGAGAC
AAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTCTGGACAGAAGTCAATGCCTTGAAGGAAATTCAAGCCCTG
CAGACAGTCTGTCTCCGAGGCACTAAAGTTTACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCAT
GAGGCCAATGAAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCCCTC
CAAGACTATGGTAAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGACATGGTCACGGAAGGC
AAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGGACCGTGCACAGCCTAACGGTGGCAAGCGA
GAAAACGTGTCTCTGTTCTCCCAATCAGCTCAGGGCAAGTGGAGTGATGAGGCCCTGTGCGCAGCAGCAAGAGATAC
ATATGCGAGTTTACCATCCCTAAATAGGTCTTTTCTCCAATGTGTCTTCCAAGCAAGATTCATCATAACTTTATAGG
TTCATGATCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAAAAAATTGCAACACAAGATCAATGTCCAT
AGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCTTCTCTGGGGTATAGGGGATC
AGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCTAAACAGACTAAAATCTTTCTCTCTAGTCTTTC
TCACTTGTACAAACCCAGTTTGTGTTTTCAAAAAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTT
AGGCTACCTGAAAGATTTTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTTCCCTACATCAGAGACTCT
AGGTGCTATATAATCCAAAACTTTTCAGCCTGTGTCTATTCTGTCCCATGCTGGCAATAATACCTTGTGAGCC
CATTACCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCTGCCATATCAGAACACAAACCCC
TGAAGAGGTTCTGATTTGATTTTTTTTTTTTTCTTCATGCCTACCCTTTTTTTTGAAGTTTCCAGCCGCAATTTGA
AATGAAATGACAAGGTGTATATTTGATCAATTTTCATTCCCACCATTGCATTACAACCTCTAATTTAAATGGGTA
ACCCTAAGGCATATCAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTT
TAGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCC'TTTTTTACATTTTTCGTATATTTAT
TTTTTTTAGCCATCATTATATGTTTAAGTCTATTTATGGGCAACCAATCTTTGGAAGCTGAAAACCTGAATTTAAAG
AATGCTATCTTGAAAAATTGCATACGTCTGTGCAATTTTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAG
ATTGTACAAAATAACTTCATTGCTTAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTTAGAAG
CAAACAATTTTAAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATATCC
CACTTTGCAAAC'TTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTTCATTGCTCAATAATAAAGCCTGAA
TTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 276

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHKKRRVRDKDGLKTQIEKLWTEVNALKETQALQT
VCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGKRSLPGVNDFWLGINDMVTEGKF
VDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGKWSDEACRSSKRYICEFTIPK

FIGURE 277

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCCCTGCTCCCACCCCTAGGAAGCCACCAGAC
TCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCCACGAGCGCTGGCTGAGGGACCGAGCC
GGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAGCGCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCT
ACTGCGCGCGCTTCTCCTACCTCTGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGG
CCCTGGTCTGTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCCTTCCCTGG
CTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCACTGTTTATGGTCTCCTTCATTGGTGTGCTGGCGTCCCTCC
GTGACAACCTGTACCTTCTCCAAGCATTCATGTACATCCTTGGGATCTGCCTCATCATGGAGCTCATTGGTGGCG
TGGTGGCCTTGACCTTCCGGAACCAGACCATTGACTTCTGAAACGACAACATTGGAAGAGGAATTGAGAACTACT
ATGATGATCTGGACTTCAAAAACATCATGGACTTTGTTTCAAGAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACC
GAGATTGGAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACACCTGCT
GCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATCGACAAGGAGCGTTTCAGTGTGC
AGGATGTCTCTACGTGCGGGGCTGCACCAACGCCGTGATCATCTGGTTCATGGACAACACACCATCATGGCGT
GCATCCTCCTGGGCATCCTGCTTCCCGAGTTCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGG
ACATCATCATGGAGCACTCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCA
CGGGATGCTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTCTGGGATAGC
ACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCCACACTCAGTACTGACCAAGCCAGG
GCTGTGTGTGCTGTGTGTAGGTCCCACGCCCTCTGCCTCCCCAGGGAGCAGAGCCTGGGCCTCCCTTAAGAGGC
TTCCCCGAGGCAGCTCTGGAATCTGTGCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCCTGGG
CTACAGGGGAGGGAGAGCCTGAGGCTCTGCTCAGGGCCCATTTTATCTCTGGCAGTGCCTTGGCGGTGGTATTCA
AGGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGAGGAGGGAAGGGCATCTGGGGAA
GGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTTGGCCTCTTCTCAGCCTCCAGGTGCCCTT
GAGCCCTCTTGCAAGGGCGGCTGCTTCTTGAGCCTAGTTTTTTTTTACGTGATTTTTGTAAACATTATTTTTTT
GTACAGATAACAGGAGTTTCTGACTAATCAAAGCTGGTATTTCCCGCATGTCTTATTCTTGCCCTTCCCCAAC
CAGTTTGTTAATCAAACAATAAAAACATGTTTGTGTTTTTAAAAA

FIGURE 278

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAPAIILILLGVVMFM
VSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFLNDNIRRG IENYYDDLDFKNIMDFVQK
KFKCCGGEDYRDWSKNQYHDCSAPG PLACGV PYTCCIRNTTEVVNTMCGYKTIDKERFSVQDV IYVRGCTNAVII
WFMDNYTIMACILLGILLPQFLGVLLTLLYITRVEDIIMEHSVTDG LLGPGAKPSVEAAGTGCCLCYPN
```

Signal peptide:
amino acids 1-44

Transmembrane domains:
amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 279

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACCTTGCTGCCCTCTGACACCTGGGAAGAT
GGCCGGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGGCTGGCAGCCACCTTGATCCAAGCCACCCCTCAGTCCCAC
TGCAGTTCTCATCCTCGGCCCAAAGTCATCAAGAAAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAG
CATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGCCGGGAAAAGCCAGCCGAGGCATCCCTGTGCTGGGCAGCCT
GGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCC
CTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAA
GACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCAC
CCGCCTGGTCCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCCT
GGTGAACGCCCTTAGCTAAGCAGGTCAAGACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTG
TCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAG
CATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTACAGCTCTACCTGGGGGCCAA
GTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGA
CAACATCCCGTTTCCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTGATGGTCCCTGTGGACTCTGTGCTTCTGAGAGTGGCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGA
AAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTTTTTTATAGA
CCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCAGTGAAGCCCTCCGCCCTTTGTT
CACCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAA
CATCAGCTCTGATCGGATCCAGCTGATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCAT
CACTGAGATCATCCACTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAGATCTGGGGTCCCAGTGTCTTTGGT
GAAGGCCTTGGGATTCGAGGCAGCTGAGTCCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCCCTGTG
GAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGGGTCCCAGCTGGGAGT
ATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTGCCTGTGAAAAA

FIGURE 280

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAMREKPAGGIPVLGS
LVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIIVEFHMTTEAQATIRMDTSASGP
TRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISL
SIDRLEFDLLYPAIKGDITQLYLGAKLLDSQGVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAABAVALSPE
EFMVLLDSVLPESAHLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPL
FTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIITHSILLPNQNGKLRSQVPSL
VKALGFEEAESSLTkdALVLTPASLWKPPSPVSQ
```

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 281

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTCCCCGCGTTCT
CTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCCTGCCCTCCTTTCCCTGCCACCGCTGCTTCCTGGC
CCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTC
CTTTTCGTCTCCCTTCTCCCGACTCCGCTCCCGGACCAGCGCCTGACCC'TGGGGAAAGGAATGGTTCCCGAGGT
GAGGGTCTCTCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCTTGGACTCCACGCTCGAGCCCCGCCAGA
CATGTTCTGCCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCT
GATGTACTGCCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTCCA
CTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCG
GGCCCCACCAAAGTCTTGCCAGCACAAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTT
CCCCCTCCGCTGCCCCAACCAAGTGTGTCTCTGTCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAAACCTG
CCCCGAACCAGGCTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGA
GCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGC
TGGGAGAAAGAGAGGCCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGG
CGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTGCATCCTATG
CACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCCGAGTACCCCTGCCGTACCCCGAGAA
AGTGGCTGGGAAGTGCTGCAAGATTTGCCAGAGGACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAG
GTGTCCCAAGGCACCGGGCCGGTCTCGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTTCGCTTTGC
CCTGGAACACGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCA
GAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGC
AAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACTGGAACGTCTTCCCTAG
CCAGACCCTGGAGCTGAAGGTACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTTAACAGTTGCA
GATATGAGCTGTATAATTGTTGTTATTATATATTAATAAATAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAA
AAAAAA

FIGURE 282

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSEGAHVSCYRLH
CPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELFP SRLPNQC VLCSCTEGQIYC
GLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSF
IPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPC
RHPEKVAGKCKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIY LWKLVKDE
ETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPGAEGHGQSRQSDQDITKT
```

Signal peptide:
amino acids 1-25

FIGURE 283

GCGATGGTGCGCCCGGTGGCGGTGGCGGCGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCAACGAGGAGAAGAT
 GACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGCCATGAGGAGCCTGCCGAGCCTGGGCG
 GCCTCGCCCTGTGTGCTGCGCCCGCCCGCCCGCCCGCTCGCCTCAGCCGCCTCGGCGGGGAATGTCACCGGTG
 GCGGCGGGGCGCGGGGCGAGGTGGACGCGTCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCCTA
 GGGCGACGGCTCCACGGCCAGGCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTGCGA
 CTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTGGGCGACTGCTGGACCCTCTCCACCACCTTTCAGGCGC
 CGCTCGGCCCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTCGACCACCTCTCAGGCGCGGACCAGACCCG
 CGCCGACCACCCCTTTCGACGACCACTGGCCCGGCGCGGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGA
 CTCCCCGACCCCGACCCCGGATCTCCCAGCAGCAGCAACAGCAGCGTCCTCCCCACCCACCTGCCACCGAGG
 CCCCCTCTTCGCTCTCTCCAGAGTATGTATGTAAGTGTCTGTGGTTGGAAGCCTGAATGTGAATCGCTGCAACC
 AGACCACAGGGCAGTGTGAGTGTGGCCAGGTATCAGGGGCTTCACTGTGAAACCTGCAAGAGGGCTTTTACC
 TAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCCACATGGAGCTCTCAGCATACCGTGCAACAGGT
 AAGCAACAGAGGGTGGAACCTGAAGTTTATTTTATTTTAGCAAGGGAAGGCTGCTACTCTCAAGGACCA
 TACTGGTTTAAACAAAGGAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTTACTTTAT
 ATGTTATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAGAGTCGCCAA
 TTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAATTTATTGAAGAATAAATCTGCTTCTGGAAGGGCT
 TTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTTATGTTTATTAATATAACCATTGGAGTTTGAGGAAAT
 TTGTTGTTTGGTTTATTTTCTCTCTAATCAAAATTCACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGG
 GGTACCCTAATTTATTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTGGAGACAAAA
 GTAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGAATAATGTACTGT
 TATCTAAGCATTTGCCTTGTACTGCACTGAAAGTAATTATCTTTGACCTTATGTGAGGCACCTTGGCTTTTTGTG
 GACCCCAAGTCAAAAACTGAAGAGACAGTATTAATAATGAAAAAATAATGACAGGTTATACTCAGTGTAACC
 TGGGTATAACCCAGATCTGCTGCCACTTACGAGCTGTGTTCCCTTGGGCAAGTAATTTCTTTCACTGAGCTTGT
 TTCTTCTCAAGGTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAATT
 CTGGTTTGTTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGAACTTTTAGCTCCTTG
 ACAAAGAAGTGCTTTTACTTTAGCACTAAATATTTTAAATGCTTTATAAATGATATTATACTGTATGGAATAT
 TGTATCATATTGTAGTTTATTAATAATGTAGAAGAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTT
 GGGAGGCCAAGGCGGGTGGATCACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCGCTCT
 CTACTAAAAATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGAGGCTGAGGC
 AGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGTGAG
 AGAGGGAGACTCTGTCTTAAAAA

FIGURE 284

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGG LALLCCAAAAA VASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFPRATAPTAQAPRTGPPRA
TVHRPLAATSPAQSPETTP LWATAGPSSTTFQAPLGPSPTTPPAERTSTTSQAPTRPAPTTLSTTTGPAPTPV
ATTVPAPTTTPRTPTPDLPSSSNSSVLPTPPATEAPSSFPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHC
ETCKEGFYLN YTSGLCQP CDCSPHGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 285

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCTGCTCTGGGGG
 AGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCGTGACGGTGCAGGAAGGCCTGTGT
 GTCCATGTGCCCTGCTCCTTCTCTACCCCTCGCATGGTGGATTACCTTGGCCAGTAGTTCATGGCTACTGG
 TTCCGGGAAGGGGCAATACAGACCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAG
 ACTCGGGACCGATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCGTGAGCATCAGAGATGCCAGAAGA
 AGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCT
 GTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCAGGCACCTGGAGTCCGGCTGCCCCCAGAAT
 CTGACCTGCTCTGTGCCCTGGGCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCC
 CCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCCCTCATCCACAGCCCCAGGACCATGGCACCAGCCTC
 ACCTGTGACGGTACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTACCCGCT
 CAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTGTCA
 CTCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGC
 CTGAGCTGGAGAGGCCTGACCCCTGTGCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCCTGGGTGCAC
 CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCC
 CTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCCGGGGAGCTGGAGCCACAGCCCTGGTCTTCTCTG
 TCCTTCTGCGTCACTCTCGTTGTAGTGAGGTCTTGCAGGAAGAAATCGGCAAGGCCAGCAGCGGGCGTGGGAGAT
 ACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTGAGCCTCTCAGGGGCCCTGACTGAACCTTGGGCAGAAGAC
 AGTCCCCCAGACCAGCCTCCCCAGCTTCTGCCCCCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTC
 AGCTTCCAGATGTTGAAGCCTTGGGACTCGCGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATC
 CACAGATGAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCCTCAGGCAAGGGAGAAGTCAGAGGC
 TGATTCTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATGTGCAGAGTGAAAAGC
 ACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCCACTGTGCCCTCCCTTTATTTTTTTAACTAAAAG
 ACAGACAAATTCCTA

FIGURE 286

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREGANTDQDAPVA
TNNPARAVWEETDRDFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNYKHHRLSVNVTALTHRPNILI
PGTLESGCPQNLTCVWPWACEQGTPPMISWIGTSVSPDPSTTRSSVLTLLIPQPDHGTSLTCQVTFPGASVTTN
KTVHLNVSYPPQNLMTVVFQGDGTVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPS
NPGVLELPWVHLRDAAEFTCRAQNPLGSQQVYLNVSLSQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRK
KSARPAAGVGDTGIEDANAVRGASASQGPLEPWAEDSPDPQPPASARSSVGEGLQYASLSFQMKPWDSRGQE
ATDTEYSEIKIHR

Signal peptide:
amino acids 1-15

Transmembrane domain:
amino acids 351-370

FIGURE 287

CGCGAGCTGAGAGGAGCAGGTAGAGGGGCAGAGGCGGGACTGTCTGTTGGGGAGCCGCCAGGAGGCTCCTCAG
GCCGACCCAGACCCCTGGCTGGCCAGGATGAAGTATCTCCGGCACCGGCGGCCCAATGCCACCCCTATTCTGGCC
ATCGGCGCTTTACCCCTCCTCTCTTCAGTCTGCTAGTGTACACCCACCTGCAAGGTCCAGGAGCAGCCACCG
GCGATCCCCGAGGCCCCTGGCTGGCCCACTCCACCCACCGCCAGCCCGGCCCGTGGCATGCCAACACCTCT
ATGGTCACCCACCCGGAATTGCCCACGCAGCCGCAGCACGTTCAGAACTTCCTCCTGTACAGACACTGCCGCCAC
TTTCCCCCTGCTGCAGGACGTGCCCCCTCTAAGTGCAGCGCAGCCGGTCTTCCTGCTGCTGGTGATCAAGTCTCC
CCTAGCAACTATGTGCGCCGCGAGTGTGTCGGCGCACGTGGGGCCGCGAGCGCAAGGTACGGGGTTTGCAGCTG
CGCCTCCTCTTCCTGGTGGGCACAGCCTCCAACCCGCACGAGGCCCCGCAAGGTCAACCGGCTGCTGGAGCTGGAG
GCACAGACTCACGGAGACATCCTGCAGTGGGACTTCCACGACTCCTTCTTCAACCTCACGCTCAAGCAGGTCTTG
TTCTTACAGTGGCAGGAGACAAGGTGCGCCAAACGCCAGCTTCGTGCTCAACGGGGATGATGACGTCTTTGCACAC
ACAGACAACATGGTCTTCTACCTGCAGGACCATGACCCTGGCCGCCACCTCTTCGTGGGGCAACTGATCCAAAAC
GTGGGCCCCATCCGGGCTTTTTGGAGCAAGTACTATGTGCCAGAGGTGGTGACTCAGAAATGAGCGGTACCCACCC
TATTGTGGGGTGGTGGCTTCTGCTGTCCCGCTTACGGCCGCTGCCCTGCGCCGTGCTGCCCATGTCTTGAC
ATCTTCCCCATTGATGATGTCTTCTGGGTATGTGTCTGGAGCTTGAGGGACTGAAGCCTGCCTCCACAGCGGC
ATCCGCACGTCTGGCGTGGGGCTCCATCGCAACACCTGTCTCCTTTGACCCCTGCTTCTACCGAGACCTGCTG
CTGGTGCACCGCTTCCTACCTTATGAGATGCTGCTCATGTGGGATGCGCTGAACCAGCCCAACCTCACCTGCGGC
AATCAGACACAGATCTACTGAGTCAGCATCAGGGTCCCCAGCCTCTGGGCTCCTGTTTCCATAGGAAGGGCGAC
ACCTTCTTCCAGGAAGCTGAGACCTTTGTGGTCTGAGCATAAGGGAGTGCCAGGGAAGGTTTGAGGTTTGATGA
GTGAATATCTGGCTGGCGAACTCCTACACATCCTTCAAAACCCACCTGGTACTGTTCCAGCATCTTCCCTGGAT
GGCTGGAGGAACCTCAGAAAATATCCATCTTCTTTTGTGGCTGCTAATGGCAGAAGTGCCTGTGCTAGAGTTCC
AACTGTGGATGCATCCGTCCCGTTTGAGTCAAAGTCTTACTTCCCTGCTCTCACCTACTCACAGACGGGATGCTA
AGCAGTGCACCTGCAGTGGTTTAAATGGCAGATAAGCTCCGTCTGCAGTTCAGGCCAGCCAGAACTCCTGTGTC
CACATAGAGCTGACGTGAGAAATATCTTTCAGCCCAGGAGAGAGGGGTCTGATCTTAACCTTTCTGGGTCTC
AGACAACCTCAGAAGGTTGGGGGATACCAGAGAGGTGGTGAATAGGACCGCCCCCTCCTTACTTGTGGGATCAA
ATGCTGTAATGGTGGAGGTGTGGGCAGAGGAGGAGGCAAGTGTCTTTGAAAGTTGTGAGAGCTCAGAGTTTCTG
GGGTCTCATTAGGAGCCCCATCCCTGTGTTCCCCAAGAATTGAGAGAACAGCACTGGGGCTGGAATGATCTTT
AATGGGCCCAAGGCCAACAGGCATATGCCTCACTACTGCCTGGAGAAGGGAGAGATTCAAGGTCTCCAGCAGCCT
CCCTCAGCCAGTATGTTTTACAGATTACGGGGGACCGGTGAGCCAGTGACCCCTGCAGCCCCAGCTTCAGG
CCTCAGTGTCTGCCAGTCAAGCTTACAGGCATTGTGATGGGCGAGCCTTGGGGAATATAAAATTTTGTGAAGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65413

<subunit 1 of 1, 372 aa, 1 stop

<MW: 42515, pI: 8.92, NX(S/T): 6

MKYLRHRRPNATLILAIGAFLLLLFSLVSPPTCKVQEQPPAIPALAWPTPPTRPAPAPCHANTSMVTHPDFAT
QPQHVQNFLLYRHCRHFPLLQDVPPSKCAQPVFLLLVIKSSPSNYVRRELLRRTWGRERKVRGLQLRLLFLVGTA
SNPHEARKVNRLLLELEAQTHGDILQWDFHDSFFNLTLKQVLFLQWQETRCANASFVLNGDDVFAHTDNMVFYLO
DHDPGRHLFVGQLIQNVGPIRAFWISKYYVPEVVTQNERYPYCGGGFLLSRFTAAALRRAHVLDIFPIDDVFL
GMCLELEGLKPASHSGIRTSGVRAPSQLSSFDPCFYRDLLLVRFLPYEMLLMWDALNQPNLTCGNQTQIY

Important features:

Type II transmembrane domain:

Amino acids 15-34

N-glycosylation sites:

Amino acids 10-14;64-68;184-188;202-206;362-366;367-371

TonB-dependent receptor proteins signature 1:

Amino acids 1-32

N-myristoylation sites:

Amino acids 308-314;316-322

FIGURE 289A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCAGGAGCGGGGCCCT
GCACACCA**ATG**CCCCCGGGTGGGCAGGGGTGGGCGCCCGCTGCGCGCCCGCTGGCGCTGGCCTTGGCGCTGGC
GAGCGTCTGAGTGGGCCTCCAGCCGTGCGCTGCCCCACCAAGTGACCTGCTCCGCTGCCAGCGTGGACTGCCA
CGGGCTGGGCTCCGCGCGGTTCTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATAT
CACCAGGATCACCAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGACATCTGGAAGACAACCAGGTGAG
CGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACAAGAATAAGCTGCAAGT
CCTTCCAGAATTGCTTTTCCAGAGCACGCGCAAGCTCACCAGACTAGATTGAGTGAAAAACAGATCCAGGGGAT
CCCGAGGAAGCGTTCCGCGGCATCACCAGATGTGAAGAACCTGCAACTGGACAACAACACATCAGCTGCATTGA
AGATGGAGCCTTCCGAGCGCTGCGCGATTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGT
CACCAGCTTCAACCACATGCCGAAGATCCGAACCTGCGCCTCCACTCCAACCACCTCTACTGCGACTGCCACCT
GGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGCGCAGTTTCACTCTGCATGGCTCCTGTGCATTT
GAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTGTGCCAGCCCCCACTCGGAGCCCCCATCCTG
CAATGCCAACTCCATCTCCTGCCCTTCCGCTGACGTCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTT
GATGGAGATTCTGCCAACTTGGCGGAGGGCATCGTCGAAATACGCTTAGAACAGAACTCCATCAAAGCCATCCC
TGCAGGAGCCTTCACCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGATATTGCTCC
AGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACAAGATCACCGAGATTGCCAAGGG
ACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTCAATGCCAACAAGATCAACTGCCTGCGGGTGAACAC
GTTTCAGGACCTGCAGAACCTCAACTTGCTCTCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTT
CGCCCCCTGTCAGTCCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCT
GGCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCGCGCTGCAGCAGCCCGCGCGGACTCGCCAACAA
GCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGGATTACCGCAGCAGGTTAGCAGCGA
GTGCTTCATGGGACCTCGTGTGCCCGAGAAGTGTGCTGTGAGGGCACGATTGTGACTGCTCCAACCAGAAGCT
GGTCCGCATCCCAAGCCACCTCCCTGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGA
GGCCACTGGCATCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTGCG
AGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCTGGAGACCGTGCACGG
GCGCGTGTTCGTTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGAGTAACCTTGATCAGCTGTGTGAGTAATGA
CACCTTTGCCGGCCTGAGTTCCGTGAGACTGCTGTCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGC
CTTCAACCACGCTTGTCTCCCTGTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTG
GCTCGGCAAGTGTTGAGGAAGAGCGGATCGTCAGTGGGAACCTTAGGTGCCAGAAGCCATTTTCTCAAGGA
GATTTCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAGTAGCTGCCAGCTGAGCCC
GCGCTGCCCGGAGCAGTGACCTGTATGGAGACAGTGGTGGCATGCAGCAACAAGGGGCTCCGCGCCCTCCCCAG
AGGCATGCCCAAGGATGTGACCGAGCTGTACCTGGAAGGAAACCACTAACAGCCGTGCCAGAGAGCTGTCCGC
CCTCCGACACCTGACGCTTATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCACTAACAT
GTCTCACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCCTTCAACGGGCTGCG
GTCCCTGCGAGTGCTAACCTTCCATGGCAATGACATTTCCAGCGTTCTTGAAGGCTCCTTCAACGACCTCACATC
TCTTTCCATCTGGCGCTGGGAACCAACCCACTCCACTGTGACTGCAGTCTTCCGGTGGCTGTGCGAGTGGGTGAA
GGCGGGGTACAAGGAGCCTGGCATCGCCCGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCAC
CCCAACCCACCGCTTCCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAG
CCCGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCCTGCCCC

FIGURE 289B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCAGCATGGAGGCACC
 TGCCACCTGAGTGACAGCCACAAGGATGGGTTTCAGCTGCTCCTGCCCTCTGGGCTTTGAGGGGCAGCGGTGTGAG
 ATCAACCCAGATGACTGTGAGGACAACGACTGCGAAAACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTG
 TGTATCTGTCCGCCTAACTACACAGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCCTGAGCTGAACCTC
 TGTGAGCATGAGGCCAAGTGCATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGGAAG
 CTCTGTGAGACAGACAATGATGACTGTGTGGCCCCACAAGTGCCGCCACGGGGCCAGTGCGTGGACACAATCAAT
 GGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCCTTCTGTGAACACCCCCCACCCATGGTCCTACTGCAG
 ACCAGCCCATGCGACCACTACGAGTGCCAGAACGGGGCCAGTGCGTGGTGCAGCAGGAGCCCCACCTGCCGC
 TGCCACCAGGCTTCGCGGGCCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTG
 GAACTGGCCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAACGGCATC
 CTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGTGCGGCTGGTCTATGACAGC
 CTGAGTTCCCTCCAAACACAGTGTACAGTGTGGAGACAGTGAATGATGGGCAGTTTCACAGTGTGGAGCTGGTG
 ACGCTAAACCAGACCCTGAACCTAGTAGTGGACAAAGGAACCTCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCA
 GCAGTGGGCATCAACAGCCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCAGCCAGGGC
 ACGGACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAGGACTTCAAG
 GCCCTCCACACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTGCACCGTGTGCAAGCACGGCCTGTGCCGC
 TCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAGGCTGGACCGGCCCACTCTGCGACCAAGGAGGCCCGG
 GACCCCTGCCTCGGCCACAGATGCCACCATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCC
 GAGGGCTATGGAGGGGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCAT
 GGGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGCGAGCACTGCCAA
 CAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCAGAAAGGTTATGCATCATGTGCCACA
 GCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGGCTGTGGGCCCCAGTGCTGCCAGCCCCACCCGAGCAAGCGG
 CGGAAATACGTCTTCCAGTGACGGACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGC
 CTCGCGTGTTCCTAAGCCCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCCAT
 GTGGGACCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGAAGAGAATATTAAGTA
 TATTGTAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 290

MAPGWAGVGAAVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGI PRNAERLDLDRNNITR
ITKMDFAGLKNLRVLHLEDNQSVS VIERGAFQDLKQLERLRNLNKNLQVLPPELLFQSTPKLTRLDLSENQIQGIPR
KAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEILTLNNNNISRI LVT SFNHMPKIRTLRLHSNHL YCDCHLAW
LSDWLRQRRTVGQFTLCMAPVHLRGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLME
IPANLPEGIVEIRLEQNSIKAIPAGAFTQYKKLRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAKGLF
DGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTI SKGLFAPLQSIQTLHLAQNPFVCDCHLKW LAD
YLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFSSECFMDLVCPEKCRCEGTIVDCSNQKLVR
IPSHLPEYVTDLRRLNDNEVSVLEATGIFKKLPNLRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRV
FRGLSGLKTLMLRSNLISCVSNDTFAGLSSVRLLSLYDNRI TTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLG
KWLRKRRIVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLRALPRGM
PKDVTELYLEGNHLTAVPRELSALRHLTLIDLSNNSISMLTNYTFSNMSHLSTLILSYNRLRCIPVHAFNGLRSL
RVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCSLRWLSEWVKAGYKEPGIARCSSPEPMADRLLLTTPT
HRFQCKGPVDINIVAKCNACLSSPCKNNGTCTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDS
HKDGFSCSCLPGFEGQRC E INPDDCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVP E LNL CQHEAK
CIPLDKGFSCCEVPGYSGLKCE TDNDDCVAHKCRHGAQCVD TINGYTCTCPQGFSGPFCEHPPPMVLLQTS PCDQ
YECQNGAQCI VVQQEPTCRCP PGFAGPRCEKLITVNFVGKDSYVELASAKVRPQANISLQVATDKDNGILLYKGD
NDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHSVELVTLNQTLNLVVDKGT PKSLGKLQKQPAVGINS
PLYLGGIPTSTGLSALRQGTDRPLGGFHGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDS
VVCECRPGWTGPLCDQEARDPCLGHRCHHGKCVATGT SYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHIS
DQGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQPTRSKRRKYVFQ
CTDGSSFVEEVERHLECGCLACS

Signal peptide:
amino acids 1-27

FIGURE 291

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCAGACTCAACTGAGA
AGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCTCCGGCAGGCTTTGAGGATGAAGGCTG
CGGGCATTCTGACCCCTCATTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACACTCGTTGCAAACTGGCAA
AAATATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCTTCAGCCTTGGAAGCTGGATCTGCATGGCATATTATG
AGAGCGGCTACAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCAACA
GCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGCTCAGCCTTGATCACTG
ATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGAGACACAAGGAATGAACCTATTGGCAAGGCT
GGAAGAAACATTGTGAGGGCAGAGACCTGTCCGAGTGGAAAAAAGGCTGTGAGGTTTCTTAAACTGGAACTGGAC
CCAGGATGCTTTGCAGCAACGCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCTCATCTTGTCCCGTTTCCT
CCCAATATTCCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCATTTAAATGTC

FIGURE 292

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFS LGNWICMAYYESGYNTTAPTVLDDGSIDYGIF
QINSAWCRRGKLKENNHCHVACSALITDDLTDALICARKIVKETQGMNYWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:
amino acids 1-19

FIGURE 293

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTACCCAAGGAAAG
TGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTCTCATAGCGACCACCAGAGGA
TGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGC
AAGGAAATCAAAGACGAATGTCCTAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTAC
CAGACCTTCTGTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGT
GGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAAC
TGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCCTGGCTACTACGAC
ATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCAATAAGTCCCCCATGCAGCACTGGAGAAAACAGCTCCCTG
CTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCA
GTGAAATATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGCGACGCC
CAGAAAAACAGCATCTTATTACTCACCCCTATGGCCAGCGGAATTCAGTGCAGGATTTGTTTCTAGTTTCTAGGGTATTT
AATAACGAGAGAGCAGCCAACGCCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATT
GGTGGAGGAGGATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTTGATTGGAGTGGATAT
GGAACTCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTT
TGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCAGTAGCTAGA
ATGTTAATGGCAGAAGAGAAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 294

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVIYQTFCDMTSG
GGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIW
HVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSP
YGQREFTAGFVQFRVFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSSS
REITEAAVLLFYR

FIGURE 295

CAGGCCATTTGCATCCCACTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGTGTCATGTGTTAAAAA
CGCCAAGCTGAATATATCATGCCCCCTATTAAAACTTGTACATGGCTCCCCATTGGTTTTTGGAGAAAAGTTCAAG
CTTTTTACCTTGGTGTCTGCCTGTATCCAGTGTTTCAGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGT
CACTTCCCAGATCTGCTTCTCACCAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATA
GAGGAATACACCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAAACA
TTCAAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTCACCAGCTTTGACTCAGTTGTT
CCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCTGCTGCTCTCCATCAACAGATACGAAAGGAAG
AAAAATCTGACTTTGGCACTGGAAGCCCTAGTACAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTT
CATCTGATCGTGGCAGGTGGTTATGACGAGAGAGTCTTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATG
GTCCAACAGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCCCTCCTC
CACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCCTCTGGAAGCCATGTACATG
CAGTGCCCAGTCATTGCTGTTAATTCGGGTGGACCCCTTGGAGTCCATTGACCACAGTGTACAGGGTTTCTGTGT
GAGCCTGACCCGGTGCACCTTCTCAGAAGCAATAGAAAAGTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGC
CTGGCTGGAAGAGCCAGAGTGAAGGAAAAATTTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACC
AAACTGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTAAATGTCATTTTTATGGATTGTAGACCCAGTTTTGA
AACCAGAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAACTTGAGTCTTGAATGTGAGCCA
CTTTCCTATATACCACACCTCCCTGTCCACTTTTTCAGAAAAACCATGTCTTTTATGCTATAATCATTCCAAATTT
TGCCAGTGTAAAGTTACAAATGTGGTGTCAATCCATGTTTCAGCAGAGTATTTAATTATATTTTCTCGGGATTAT
TGCTCTTCTGTCTATAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCA
AAGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCACAGATTCAATCCACCGAAGTGT
TCACTGTCTGTGTAGGGAATTTTTGTTTGTCTGTCTTTGCCTGGATCCATAGCGAGAGTGCTCTGTATTTTTT
TTTAAGATAATTTGTATTTTTTGCACACTGAGATATAATAAAAGGTGTTTATCATAAAAAAAAAAAAAAAAAAAAA

FIGURE 296

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLARRRKKILFYCHFPDLLLLTKRDSFLKRLYRAPIDWIEEYTTG
MADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLDDLVPKGKKFLLLSINRYERKKNLTLA
LEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVEHYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCV
LYTPSNEHFGIVPLEAMYMQCPVIAVNSSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRAR
VKEKFSPEAFTEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 297

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCATGTTGGACTTCGCGATCTTCGCCGTTACCTTC
 TTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGACAAGCTGCAGGAATCCAGGGATTACT
 CCAACTGAAGAAAAAGATGGTAATCTTCCAGATATTGTGAATAGTGGAAGTTTGCATGAGTTCTTGGTTAATTTG
 CATGAGAGATATGGGCCTGTGGTCTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACGTGTGATGTA
 CTGAAGCAGCATATCAATCCCAATAAGACATCGGACCCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTATCAA
 TCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGGTGACTGATTCTCTGAAG
 AGTAACTTTGCCCTCCTCCTAAAGCTTTTCAAGAAGATTATTAGATAAATGGCTCTCCTACCCAGAGACCCAGCAC
 GTGCCCCCTCAGCCAGCATATGCTTGGTTTTGCTATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAA
 GATGATCAGGAAGTCATTTCGCTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGAT
 GGGTCACCTTGATAAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTTTTAAGG
 AACATCATAAAGAAGCGAAAAGGAAGGAAGTTCAGTCAACATATTTTCATTGACTCCTTAGTACAAGGGAACCTT
 AATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGGCCAGTTGCATAATAACTGCAAAATTGTGTACC
 TGGGCAATCTGTTTTTTAACCACCTCTGAAGAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGGA
 AATGGTCCTGTACTCCAGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAAACTGTTTCGAACT
 GCCAACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATTATTCTCTAGAGAG
 ACCCTCGTCCCTTATGCCCCCTGGTGTGGTACTTCAGGATCCTAATACTTGGCCATCTCCACACAAGTTTGATCCA
 GATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCCCTCACTTGGATTCTCAGGCACACAGGAGTGTCCAGAG
 TTGAGGTTTGCATATATGGTGACCACAGTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAG
 GGACAGGTTATTGAAACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGA
 TATTAAAATTTTATACATTTAAAATCATTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAAAAATCTATGTTG
 AATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTACTTAA

FIGURE 298

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVSFWFGR
RLVVS LGTVDLKQHINPNKTS DPFETMLKSLRLRYQSGGGSVSENHMRKKLYENGVTDSLKSNFALLLKLSEELL
DKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHGTWVSEIGKGFLDGSLDKNMTRKKQYE
DALMQLESVLRNI IKERKGRNFSQHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLTTSSEEVQK
KLYEEINQVFGNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP
NTWPSPHKFDPDRFDDELVMKTFSSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLSVEGQVIETKYELVTSS
REEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 299

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGACCGCCGCCCTT
GTCCCCGAGGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACGCTCCTGGCGCATCTGGTGGT
CGTCATCACCTTATTCTGGTCCCCGGGACAGCAACATACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTA
TGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCTCTGTCACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTT
CCTCTCAGGAGTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGC
CCTGTCCCTTCTTCATATTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTGTCTTCTGCAGTGCCCTTCC
AGCTGTCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCCTTCTGATTACCTTCATGACG
GGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTT
TTCCCCCTCGGAAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATT
GTATTTAGTGCCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACAATTAAA
AAAAAAAAA

FIGURE 300

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACPLTFTPEEYDKQDIQLVAALSVTLGLFAVELAGFLSGV
SMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 301

CTGGGACCCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGACTCGCTGCTGC
TTCGTGTTCCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATGGTCCCTCCCGGCTCAGAGGAC
CCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCC
CGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCTGGCCCCGCCTGGGGAGGCCTGGGGGCATTCTTGGGCAGCCC
CCCAACCGCCCGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCC
AACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTC
CACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAGAGTTC
CACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTA
GAACGGGGCCCGCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCA
GCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTATCGGCTG
GTCCAGAAGGTGTGCCCAGATTACAACCTACCATAGTGATACCCCCTACTACCCATCTGGGTTGACCCGGGGCAGGC
CACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGG
GTTGGGCCCTCAGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTG
GGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCCTGTGGGCAG
GCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGTTCTTGCCATCCTGAGGAAAGATA
GCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAG
GAGCCAGTCAGCAGGGTGGGGTGGGGCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTC
GTGTGCTGAGCATGGCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCT
CCAGCCAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATGGCACA
CCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCACACTAAGGCCACAGCCCATCCGCGTGCTGTGTGTC
CCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCGAGAGGGGTCCCTCAACAGTCAGCC
TCACCTGTCAGACCGGGGTTCTCCCGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGC
CGGGCCGCAGAGCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGA
AACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

FIGURE 302

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSLLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEA
WGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVP
PSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAF
YSTDYRLVQKVC PDYNYHSDTPYYPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 303

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCCCTTTATGTCT
TCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTTCTGGTTGGTGTCTCTACTGA
TTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACAAAGATGGACCAACACAGAAATATCTGCTGA
TCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCA
GTGAAGGTTTGAAGAGTATAAACCCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGG
GCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCA
TTCATGGAGATTCTCCTCAATCTTCCTTTATTAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGTATTCT
GGGGCATTGTATTTTTTGATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGC
TGGTGTGAGCCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCA
TGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGA
ACTTTCTCTTTACAACCAGCGCTCCAGATAAACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTA
GAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTGGTGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 304

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658

><subunit 1 of 1, 257 aa, 1 stop

><MW: 28472, pI: 9.33, NX(S/T): 0

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKGPTQKYLLIFG
AFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIHG
DSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGT
WAFLAAGGSCRSLKLCLLCQDKNFLLYNQSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 305

[illegible]

FIGURE 306

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSIPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 307

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAAGAAAAATTTTGTG
GGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAAATTGAGTCAACTAGTGAATTCAAAACA
ACTTGAAGCTCAATTTCTGGAATCTCCCTCCTCCTTCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCAGTC
TGCAGGCATTTAAATCCTTCCTGAGATCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTT
TAGACAATGAAGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGGCTT
ACCATTTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCTGACCTGGCGAGGAGGGTGA
AGATTGGACATTCGTTTGAAGAACCGCCGATGTATGTACTGAAGTTCAGCACTGGGAAAGGCGTGAGGCGGCCGG
CCGTTTGGCTGAATGCAGGCATCCATTCCCGAGAGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGA
TTGTATCTGATTACCAGAGGGATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTTCCTGTGG
CCAATCCTGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATCCTGGAA
GCTCCTGCATTGGTGTCTGACCCAAATAGAAACTGGAACGCTAGTTTTTGCAGGAAAGGAGCCAGCGACAACCCCTT
GCTCCGAAGTGTACCATGGACCCACGCCAATTCCGAAGTGGAGGTGAAATCAGTGGTAGATTTTCATCCAAAAAC
ATGGGAATTTCAAGGGCTTCATCGACCTGCACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCA
AAAAGGCCCCAGATGCCGAGGAACCTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTCGGGCA
CTGAGTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGGCGTATGACA
ACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGCTTCTCCTGCCAGCTAACCAGA
TCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGACCATCATGGAGCATGTGCGGGACAACCTCTACTAGG
CGATGGCTCTGCTCTGTCTACATTTATTTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTT
CCTACCTGTGTGAGTCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAG
TCGTGTGTCTGGCGGTGTCCCTGCAAGAACCTGGTTCTGCCAGCCTGCTCAATTTTGGTCTCTGTGTTTTGTATG
AGCCTTTTGTCTGTTTTCTCCTTCCACCCTGCTGGCTGGGCGGTGCACCTCAGCATCACCCCTTCTGGGTGGCAT
GTCTCTCTCTACCTCATTTTTAGAACCAAAGAACATCTGAGATGATTCTCTACCTCATCCACATCTAGCCAAGC
CAGTGACCTTGCTCTGGTGGCACTGTGGGAGACACCATTGCTCTTAGGTGGGTCTCAAAGATGATGTAGAATTT
CCTTTAATTTCTCGCAGTCTTCTGGAAAATATTTTCTTTGAGCAGCAAATCTGTAGGGATATCAGTGAAGGT
CTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGTAGACAGAGTTTTGCTCTTGTGCCCAGGCTGGAGTGTGA
TGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAGCAATTTCTCCTGCCTCAGCCTCTTGAGTAGC
TTGGTTTATAGGCGCATGCCACCATGCCTGGCTAATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGT
CAGGCTGGTCTCAAACCTCCCAACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTG
AGCCACTGTGCCGGGCCCCGTCCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCTTCACTGTGC
TGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCACTGTGTGACCAGGATGGCGGGAGGG
GATCTGTGTCACTGTAGGTACTGTGCCCAGGAAGGCTGGGTGAAGTGACCATCTAAATTGCAGGATGGTGAATTT
ATCCCCATCTGTCTAATGGGCTTACCTCCTCTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTAC
AGGTCTAAATCACTCATCTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTGTGCTGTGGTGTATCCT
GTGTTTCCCTGTCTGCTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
TTTTGTATCCTGGACCACAAGTTCTAAGTAGAGCAAGAATTCATCAACCAGCTGCCTCTTGTGTTTCACTTTCACCT
CAGCACGTACCATCTGTCTTTTGTGTTGTGTTGTTGTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTT
TCTTAACCTCCTGCCTAGGATTTGTACAGCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAA
AAAAAAAAA

FIGURE 308

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNRPVDVLVPSVSLQA
FKSFLRSQGLEAYVTIEDLQALLDNEDDEMOHNEGQERSNNFNFGAYHSLEATYHEMDNIAADFPDLARRVKIG
HSFENRPMYVLKFSTGKGVRPAPVWLNAGIHSREWISQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANP
DGYVYTQTQNRLLWRKTRSRNPGSSCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDVFIQKHGN
FKGFIDLHSYSQLLMPYPYGYSVKKAPDAEELDKVARLAALASVSGTEYQVGPTCTTVYPASGSSIDWAYDNGI
KFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDNLV

Signal peptide:
amino acids 1-16

FIGURE 309

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGCCTGAGTCCAAGAT
TCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTATCTCTTCACCTTCAAGTCCC
CTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGC
CACAAAGAGACAGATGAAGATGCAGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGC
AACAAATTCCAATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCAC
CAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGG
GGTCAGCATAGTCACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAGTTCAG
CACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGAGTCCAGCACACCTCCAGTGGGGCCAGCACAGTCCCAACTCTGGGTCCAGTGTGACCTCCAGTGG
AGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAG
CACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAG
GGCCAGCACTGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTTCAG
AACGACCTCCAATGGGGTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCACAGCCACCAACTCTGACTCCAG
CACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCAC
CAATTCTGAGTCCAGCACACCTCCAGTGGGGCCACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGG
GGCCAACACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAG
CACAACTCCAGTGGGGTCCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTGAGGCCAGCACAGCCACCAACTCTGAGTCTAGCACAGTGTCCAGTGG
GATCAGCACAGTCCCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCACACAGCCACCAACTCTGGGTCCAG
TGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGAATGCACACAACTTCCCATAGTGCATCTACTGCAGT
GAGTGAGGCAAAGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCCTCATCACCTGGTCTCGGTTGTGGCGGC
CGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGT
CTACCACCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGGAATCATGGAGCCCCCAGAGGCCAG
GTGGAGTCTTAAGTGGTTCTGGAGGAGACAGTATCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCC
CTGAGCAGCCCCGGAAGCAAGTGCCGATTCTTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCCTTT
CATTCATCCCAGGAGACCCCTCCAGCTTTGTTTGGATCCTGAAATCTTGAAGAAGGTATTCCTCACCTTTCT
TGCTTTTACCAGACACTGGAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACAC
ACACGACAAAGAGAAGCTGTGCTTGCCCCGGGTGGGTATCTAGCTCTGAGATGAACTCAGTTATAGGAGAAAAC
CTCCATGCTGGACTCCATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 310

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATIS
GSSVTSNGVSIIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESS
TPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTS
SGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGA
GTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTA
TNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNS
ESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESS
TVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGS
LVPWEIFLITLVSVVAAGLFLAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAP
HRPRWSPNWFRRPVSSIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 311A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGCGCGCGCTACGAAGAGGACGGGGACAGGCGCGCTGCGAACCGA
 GCCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCCGCCCGCTCGTCCCGCTCG
 TGCCCGCCCCCGCTCCCCGCGCGCGAGCGGGAGGAGCCCGCCACCTCGCGCCCGAGCCCGCGCTAGCGCGCGC
 CGGGCATGGTCCCTCTTAAAGGCGCAGGCCGCGGCGGGCGGGCGGGTGTGCGGAACAAAGCGCCGCGCGGGG
 CCTGCGGGCGGCTCGGGGGCCGCGATGGGCGCGGGCGGGCCCGCGGCGGGCGGGCGCTGCCGGGCGGGCCCTCG
 CGGCGCTAGGGCGGGCTGGCCCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGGCGCGC
 GCGGCGCGGGCGGGCCCGGCGGGCGGAGCGCGCGGGCATGGCGCGCGCGGGCGCGCCTGGCTCAGCGTGC
 TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG
 GCCCACGGCGCCGCGCAGCCCCGAGGGCTGCGGCTCCGGGCGAGCGCGCGGCTTCCAGGCCGCGGGCGCGCG
 GCGATGCGCGCGGGCGCAGCTCTGGCCGCCCGGCTCGGACCCAGATGGCGGCGCGCGACAGGAACCTTCTCT
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATGGTCCAAGACAA
 TTCCTGGGAAAGTTCAGTTCTTCTCAAGTGAGGGTCTTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG
 GTGTGGACGACTCTACCGCCCCCAGAAGAAGTCTTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACTTCTGAGGAGTT
 TGAACAGCAGCGAGCCCTCTTCTTGGGCGAGCAGGCCTGGGCACACGGAAGAAATGGGAAAACCTGGCCCTGG
 AGCCTGGTGAGAACTTCTGCATGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTCCGAGAATGGTGCCGC
 ACATTGGCAAGTGTCTCCGGGAGATGTACACCCCATGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTGTG
 CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCGAGCTTTTTTATGAGAATTACGAGCAGAACAAAAAGGGGT
 ACATTAGAGATCTCCATAACAGTAAAATTACCAAGCTATCACATTACACCCCAACAAAAACCCACCTACCAGT
 ACAGGCTCCACAGTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGACAATACAGCTGCACCGCGAAA
 TTGTCTGATGAGCAAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCTTCA
 TGAGGTTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACTTGTATTCCGCAG
 TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCCCAGAGGGAAGCCTTGGACGACATTGTCTATGCAAGTCA
 TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATATTGACTTCAAAGAGATCCAGTACGGCTACCGCC
 GGGTGAACCCCATGTATGGGGCTGAGTACATCTGGACCTGCTGCTTCTGTACAAAAAGCACAAAGGGAAGAAAA
 TGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC
 TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTTCTCTCAAACCTCCCTGAAGA
 AGCTCGTCCCCTTTTCAGCTCCCTGGGTGCAAGAGTGAGCACAAAGAACCACAAAGATAAAAAGATAAACATACTGA
 TTCCCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAAACTTTGAGAAGACGTGTCTTATCCCCAATC
 AGAAGCTCAAGCTCGTGGTCTGCTTTTCAATTCTGACTCCAACCTGACAAGGCCAAACAAGTTGAAGTATGA
 GAGATTACCGCATTAAGTACCCTAAAGCCGACATGCAGATTTTGCCTGTGTCTGGAGAGTTTTCAAGAGCCCTGG
 CCCTGGAAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTCTTCTTTCGCGACGTGACCTCGTGTTTACTA
 CAGAATTCCTTCAGCGATGTGAGCAAAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCCAGT
 ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCCTTTACTCAGAAAACCTGGCTCT
 GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA
 TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTTCAACAAGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC
 AGGAAGTAGGAGTAGTCCACGTCCACCATCCTGTCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT
 GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA
 GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAATGTCCAGCTTTGCTGGAAAAGACGTTTT
 TAATTATCTAATTTATTTTCAAAAATTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC
 AAGTGGTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTTCCTTTGAA
 CACATCTTCTGCTGAACATTATGTAGCAGACCTGCTTAACCTTTGACTTGAAATGTACCTGATGAACAAAACCTTT
 TTTAAAAAATGTTTTCTTTTGAACCTTTTGTCTCAGTCCATATGGCAGAAAACGTGAACATTCTGCAAGATAT
 TATTGTAACAAAACACTGTAACCTCTGGTAAATGTTCTGTTGTGATTGTTAACAATCCACAGATTCTACCTTTGT
 GTTTTGTTTTTTTTTTTTACAATTGTTTTAAAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
 GCTGTTTCATCATTGTCTTCAGGAGAGCTTTCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC
 CACGTAGGTTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG
 CAGTGGCGCAATCTGGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATCCCCTGCCTTTGCCCTCCGAGT
 AGCTGGGATTACAGGCACACACCACGCCAGNTAGTTTTTTTTGTATTTTAGTAGAGACGGGTTTACCAT
 GCAAGCCAGCTGGCCACGTAGGTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG
 TGGTAGTTCAATCGGCCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTGGGCATTTCTCTTCTTGACCTT
 CTCTTTAAAGGTAATAATGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT
 GAAACATACACACATACCCCTAATCAAAACGTTGGGGAAAAATGTATTTGGTTTTGTTCTTTTCATCCTGTCTG
 TGTATGTGGGTGGAGATGGTTTCATTCTTTCATTACTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAA

FIGURE 311B

TTTATTTAATATCTGTTGTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG
GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCCAAAGATTTCTTTTGGAAAACGCTTTTCCCTCC
TTAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCCTTGACAATTTTGGTGCTCATGTGTTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTTGGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAATTAAACACGAAAAA

FIGURE 312

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGARG
DARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEGS
TSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLENFLRSLN
SSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYTTHE
VEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYYIRDLHNSKIHQAITLHPNKNPPYQYRL
HSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQREEILEW
LTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQYGYRRVNP
MYGAEYILDLLLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKRINQESGSL
SFLSNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTCLIPNQNVKL
VVLLENSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQFNNESSLFFC
DVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFTQKTGFWRNYGF
GITCIYKGD LVRVGGFDVSIQGWGLEDDVLEFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLD
PKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:
amino acids 1-23

FIGURE 313

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCC
TACGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACA
GGTGGGAGGCTGGAACATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCA
ACAAATGGATGATGTGATATATGCAATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCAT
GGTCAATTAACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCT
TTGGAATCATGGTGTGTCATGGAAAGGGATTTACTTTTATACTGACTCTGTTTTGGGGAAGCTTTT
TTGGAAGCATTTTTCATGCTGAGTCCCTTTTTTACCTTTTGATGTTTGTAACCCATCTTGGTATC
GCTGGATCAACAACCGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCA
TGTTTGGTGTAAGAGTGATTATAACTGGGGATGCATTTGTTCTGGAGAAAAGAAGTGTCATTA
TCATGAACCATCGGACAAGAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCT
ACCTCAGATTGGAGAAAATTTGCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTTGGTTGGG
CCATGCAGGCTGCTGCCTATATCTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTTCG
AAGACATGATTGATTACTTTTGTGATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAG
GGACTGATCTCACAGAAAACAGCAAGTCTCGAAGTAATGCATTTGCTGAAAAAAATGGACTTC
AGAAATATGAATATGTTTTACATCCAAGAACTACAGGCTTTACTTTTGTGGTAGACCGTCTAA
GAGAAGGTAAGAACCCTTGATGCTGTCCATGATATCACTGTGGCGTATCCTCACACATTCTCTC
AATCAGAGAAGCACCTCCTCCAAGGAGACTTTCCAGGGAAATCCACTTTCACGTCCACCGGT
ATCCAATAGACACCCTCCCCACATCCAAGGAGGACCTTCAACTCTGGTGCCACAAACGGTGGG
AAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAGGGGAGAAGAATTTTTATTTTACCGGAC
AGAGTGTCATTCCACCTTGCAAGTCTGAACTCAGGGTCCTTGTGGTCAAATTGCTCTCTATAC
TGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCATATATTTGTACAGTCTTGTTAAGT
GGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGAGAATATTTGGTGGACTGGAGA
TCATAGAACTTGATGTTACCGACTTTTACACAAACAGCCACATTTAAATTCAAAGAAAAATG
AGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTGGAATGTTCTAAACCTT
TCTAAGCTCAGATGCATTTTTCATGACTATGTGCAATATTTCTTACTGCCATCATTATTTGT
TAAAGATATTTTGCCTTAATTTTGTGGGAAAAATATTGCTACAATTTTTTTTAACTCTCTGAA
TGTAATTTTCGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTTGGGCCAGAATA
TTATTAAACAATCATCAGGCTTTTAAA

FIGURE 314

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSIFML
SPFLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTR
MDWMFLWNCLMRYSYLRLEKICLKASLKGVPFGFGWAMQAAAYIFIHRKWDDKSHFEDMIDYF
CDIHEPLQLLIFPEGTDLTENSKSRSNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLD
AVHDITVAYPHNIPQSEKHLQGDFFPREIHFHVHRYPIDTLPTSKEDLQLWCHKRWEEKEERL
RSFYQGEKNFYFTGQSVIPPCKSELRVLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITI
VIFVLQERIFGGLEIIEELACYRLLHKQPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

FIGURE 315

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGA
CCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTTCATAGTGTGAGATCAACCCACAGG
AATATCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTG
GCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTG
CTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGTTCTTTCAGGAATCAGTTCCA
TGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCG
AGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAAA
CATCACTCCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCAGATTTACGATGAGGA
GGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCCATCGTGGGATA
TGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCCCACAGCCAA
GTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAG
CCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCAT
CCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCA
GCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGT
TGTGATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTG
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCT
GGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAATGTAACCCATAGAAA
AGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCA
GGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGACAAAATGTAGGGTGGTATGT
GGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACAATGTGACTTTGTCTCCCAACAATGG
GTATTGGGTCTCTCAGACTGACAACAGAACATTTGTATTTACATTTCAATCCCCATTTTATCAG
CCTCCCCCCCCAGCACCCCTCTACACGAGTAGGGGTCTTCTGACTATGAGGGTGGGACCAT
CTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGCTGACATGTGAGTTTGAAGG
CTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAGGGGACTCCCATATTCAT
ATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGCCCCACACCACAGACC
CAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGCCCCAGCTTCTCTCCGGAGCCTGCGC
ACAGAGAGTCACGCCCCCACTCTCTTTAGGGAGCTGAGGTTCTTCTGCCCTGAGCCCTGCA
GCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAGTCAGAAGCC
ATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAATCCATC
CAGCTAAGCGATCTTGAACAAGTCACAACCTCCAGGCTCCTCATTTGCTAGTCACGGACAGT
GATTCTGCTTCCAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTTTGA
GGGCACAGTGTGTTGCTAATGATGTGTTTTTATATTATACATTTTCCCACCATAAACTCTGTTT
GCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACAC
CTGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTTTCACTGATTCTATAAGCCAG
CATTACCTGATACAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCA
TATCCCTCATTAACACAGACACAAAAATTCTAAATAAAATTTTAAACAAATTAACCTAAACAAT
ATATTTAAAGATGATATATACTACTCAGTGTGGTTTTGTCCACAAATGCAGAGTTGGTTTAA
TATTTAAATATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAA
AAAAAAA

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAV
VHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEAT
WELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLY
DVEISIIVQENAGSILCSIHAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALCGVVM
GMIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAP
QEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRRDDVDRGKNNVTLSPNNGYW
VLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLL
RPYIQHAMYDEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 317

GCACCTGCGACCACCGTGAGCAGTCAATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTTC
TGGGCTTGTCCTGGCTCTGTGCTGCTGCTGCCCAAGGCCTTCCTGTCCCGCGGGAAGCGGCA
GGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCACCA
GGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGGCATT
TGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTGATGGG
GCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATTTAAGGT
AAGTAGAATCATCCTAATCATATTACATCAATGAAAATCTAATATGGCGATAAAAAATCATTGT
CTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTAAATCCTGC
CTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAGTTTCACATAAGAATGTTTACTCAA
TGTTTAAGTGTTTTGCCCAAATTCACAACTAACAAGGCAGAACTAGGACTTGAACATGGAT
CTTTTGCTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

FIGURE 318

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGRFPPMMHHHQAPSDGQTP
GARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFYILYILFKVSRIILILHQ

FIGURE 319

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAG
GAAAAGAGTTTGTGGGAACCTGGGTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCT
GGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAATTA
CTATAGCACATTGTCATTTACAACGACAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAA
CAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAATCTCC
ATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGGAGTGT
GGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAACTGTAGATAAAAT
TGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTAGATCCTCA
CTCAGTTAAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGG
AACACGAAGAAGTAAACTCTAGGTCAAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGA
GGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTT
AATTAATGCCACATGGCTTGTGAGTGTGCTCACTGTTTTACAACATATAAGAACCCTGCCAG
ATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAAT
AATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCTCTTGACAGAGCTTTC
TAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGATGCATCCTATGAGTT
TCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAATGATGGTTACAGTCA
AAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACTTGCAATGAACCTCAAGC
TTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGC
ATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGC
TGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTGTTTATACTAGAGT
TACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTAAAGAGACAAAAGCCTCATGGAA
CAGATAACATTTTTTTTTTGTTTTTTGGGTGTGGAGGCCATTTTTTAGAGATACAGAATTGGAGA
AGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAACTGTTTGCTTGATGCATGTATTTT
CTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCAGATCAACTCTGTCATCTGTGA
GCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATACAATATTACATTACAGCCTGTA
TTCATTTGTTCTCTAGAAGTTTTGTCAGAATTTTGACTTGTTGACATAAATTTGTAATGCATA
TATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTTCAGCAAATATCCA
TTTTCAAGGTGCAGAACAAAGGAGTGAAAGAAAATATAAGAAGAAAAAAATCCCCTACATTTTA
TTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGTGGAATATTAGAAATGATCATATTTCATTAT
GAAAGGTCAAGCAAAGACAGCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACATA
GTTAAGGAAGTCCAGAAAGAAGCCAAGATATATCCTTATTTTTCATTTCCAAACAACACTATG
ATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCTATAATAATTATACAACTTCATGCAATG
TACTTGTTCTAAGCAAATTAAGCAAATATTTATTTAACATTGTTACTGAGGATGTCAACATA
TAACAATAAAATATAAATCACCCA

FIGURE 320

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTDK
LYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFH
STEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQS
LRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIK
PSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVYTNVHRVCLPDASYEFQPGDVMFVTG
FGALKNDGYSONHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLV
SSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 321

CCGGGCTCCTGGGTGAGGCCGGCAAGTTTGGAGCGTGGTCAGACAATAGGGGCGTGGCTACGG
CTCGCGGAGCGCAACCAACGCTCTAGACCAGACCTGGGCTCGAGACCATAACTGTTTGGCTTT
AACAGTACGTGGGCGGCCGAATCCGGGAGTCCGGTGACCCGGGCTGTGGTCTAGCATAAAGG
CGGAGCCCAGAAGAAGGGCGGGGTATGGGGAGAAGCCTCCCCACCTGCCCCGCAAGGCGGCA
TCTGCTGGTCTCTGCTGCTCCTCTCTACCCTGGTGATCCCCTCCGCTGCAGCTCCTATCCA
TGATGCTGACGCCCAAGAGAGCTCCTTGGGTCTCACAGGCCTCCAGAGCCTACTCCAAGGCTT
CAGCCGACTTTTCCTGAAAGGTAACCTGCTTCGGGGCATAGACAGCTTATTCTCTGCCCCAT
GGACTTCCGGGGCCTCCCTGGGAACTACCACAAAGAGGAGAACCAGGAGCACCAGCTGGGGAA
CAACACCCTCTCCAGCCACCTCCAGATCGACAAGATGACCGACAACAAGACAGGAGAGGTGCT
GATCTCCGAGAATGTGGTGGCATCCATTCAACCAGCGGAGGGGAGCTTCGAGGGTGATTTGAA
GGTACCCAGGATGGAGGAGAAGGAGGCCCTGGTACCCATCCAGAAGGCCACGGACAGCTTCCAC
ACAGAACTCCATCCCCGGGTGGCCTTCTGGATCATTAAGCTGCCACGGCGGAGGTCCCACCAG
GATGCCCTGGAGGGCGGCCACTGGCTCAGCGAGAAGCGACACCGCCTGCAGGCCATCCGGGAT
GGACTCCGCAAGGGGACCCACAAGGACGTCTAGAAAGAGGGGACCGAGAGCTCCTCCCACTCC
AGGCTGTCCCCCGAAAGACCCACTTACTGTACATCCTCAGGCCCTCTCGGCAGCTGTAGGGG
TGGGGACCGGGGAGCACCTGCCTGTAGCCCCATCAGACCCTGCCCCAAGCACCATATGGAAA
TAAAGTTCTTTCTTACATCTAAAAA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68879
><subunit 1 of 1, 242 aa, 1 stop
><MW: 27007, pI: 8.68, NX(S/T): 2
MGEASPPAPARRHLLVLLLLLSTLVIPSAAAPIHDADAQESSLGLTGLQSLQGF SRLFL
KGNLLRGIDSLFSAPMDFRGLPGNYHKEENQEHQLGNNTLSSHLQIDKMTDNKTGEVLIS
ENVVASIQPAEGSFEGDLKVPRMEEKEALVPIQKATDSFHTELHPRVAFWI IKLPRRRSH
QDALEGGHWLSEKRHRLQAIRDGLRKGTHKDVLEEGTESSSHSRLSPRKTHLLYILRPSR
QL

Important features of the protein:

Signal peptide:

Amino acids 1-30

N-glycosylation sites:

Amino acids 97-101;112-116

N-myristoylation sites:

Amino acids 80-86;132-138;203-209;216-222

FIGURE 323

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCC
 TGCCCCGATGAGCCCCCGCGTGCCTCCCCGACTATCCCCAGGCGGGCGTGGGGCACC GGCC
 CAGCGCCGACGATCGCTGCCGTTTTGCCCTTGAGGAGTAGGATGTGGTGAAAGGATGGGGCTTC
 TCCCTTACGGGGCTCACAATGGCCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTAC
 GCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGG
 GACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTG
 ACTTACTTTTCTGTGGTTTATCCGGTCATGATTGCTGTTTGGTGTTCCTTATCATTTGTGGG
 ATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCAATGGTACTTTGGAAGT
 TTGCTTGTCAATTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTTATG
 GTTCCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTATGGATTACCT
 AGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTA
 GTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCTCTGCTGTGTT
 AGAGAATTTCCAGGATGTTCCAAACAGGCCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG
 GGTTGTGGGAAGAAAATGTATTCCTTTTTTGAGAGGAACCAAACAACCTGCAGGTGCTGAGGTTT
 CTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGG
 GCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAAC
 TCTCAGCACCTGTCTGTCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAA
 CACACATCCATGGCAAACAGCTTTTAATACACACTTTGAGATGGAGGAGTTATTAAAAAGAAATG
 TCACAGAAGAAAACCACAACTTGTTTTTATTGGACTTGTGAATTTTTTGAGTACATACTATGTG
 TTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA
 TGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGATGC
 CCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAAC
 ACAGTTATGTTTTGAGGCAGCATGGTTTTGATTAGCATTTCCGCATCCATGCAAACGAGTCACA
 TATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGTATATAAAGTACT
 AATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTACTCAGCGATCTATTC
 TTCTGATGCTAAATAAATATATATCAGAAAACCTTCAATATTGGTGACTACCTAAATGTGAT
 TTTTGCTGGTTACTAAAATATTCTTACCACCTAAAAGAGCAAGCTAACACATTGTCTTAAGCT
 GATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTTCAGTTCT
 GATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTTA
 GCCTTTTCTGTAAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAACTGTTA
 TTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGA
 ATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTTCAGAA
 AGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTTGACACTAAACACTTTTTTAAAA
 AGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGA
 AAATAGTGTCTTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAG
 AGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTT
 TTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCAATTTTACTGTATTTTGTGTAT
 TTTGTTTATTTCTCAGAATATGGAAAGAAAATTAATAATGTGTCAATAAATATTTTCTAGAGAG
 TAA

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVV
HPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWS
DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGC
SKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDR
REPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 325

AGCAGTGCATTGCTGGAGCGAGGAGAAGCTCACGAATCAGCTGCAGGTCTCTGTTTTGAAAAA
GCAGAGATACAGAGGCAGAGGAAAAGGGTGGACTCCTATGTGACCTGTTCTTAGAGCAAGACA
ATCACCATCTGAATTCAGAAGCCCTGTTTCATGGTTGGGGATATTTTCTCGACTGCATGGAAT
CAGAAAGAAGCAAAAGGATGGGAAATGCCTGCATTCCCCTGAAAAGAATTGCTTATTTCTTAT
GTCTCTTATCTGCGCTTTTGTGACTGAGGGGAAGAAACCAGCGAAGCCAAAATGCCCTGCCG
TGTGTACTTGTACCAAAGATAATGCTTTATGTGAGAATGCCAGATCCATTCCACGCACCGTTC
CTCCTGATGTTATCTCATTATCCTTTGTGAGATCTGGTTTTACTGAAATCTCAGAAGGGAGTT
TTTTATTACGCCCATCGCTGCAGCTCTTGTTATTACATCGAACTCCTTTGATGTGATCAGTG
ATGATGCTTTTATTGGTCTTCCACATCTAGAGTATTTATTTCATAGAAAACAACAACATCAAGT
CAATTTCAAGACATACTTTCCGGGGACTAAAGTCATTAATTCACTTGAGCCTTGCAAAACA
ATCTCCAGACACTCCCAAAAGATATTTTCAAAGGCCCTGGATTCTTTAACAATGTGGACCTGA
GGGGTAATTCATTTAATTGTGACTGTAACTGAAATGGCTAGTGGAATGGCTTGCCACACCA
ATGCAACTGTTGAAGACATCTACTGCGAAGGCCCCCCAGAATACAAGAAGCGCAAAATCAATA
GTCTCTCCTCGAAGGATTTTCGATTGCATCATTACAGAATTTGCAAAGTCTCAAGACCTGCCTT
ATCAATCATTGTCCATAGACACTTTTTCTTATTTGAATGATGAGTATGTAGTCATCGCTCAGC
CTTTTACTGGAATGCATTTTCTTGAATGGGACCATGTGGAAAAGACCTTCCGGAATTATG
ACAACATTACAGGCACATCCACTGTAGTATGCAAGCCTATAGTCATTGAACTCAGCTCTATG
TTATTGTGGCCAGCTGTTTGGTGGCTCTCACATCTATAAGCGAGACAGTTTTGCAAATAAAT
TCATAAAATCCAGGATATTGAAATTTCTCAAATCCGAAAACCCAATGACATTGAAACATTCA
AGATTGAAAACAAGTGGTACTTTGTTGTTGCTGACAGTTCAAAAGCTGGTTTTACTACCATTAC
AAATGGAACGGAACGGATTCTACTCCCATCAATCCTTACACGCGTGGTACAGGGACACTGAT
GTGGAATATCTAGAAATAGTCAGAACACCTCAGACACTCAGAACGCCTCATTTAATTCTGTCT
AGTAGTTCCAGCGTCCTGTAATTTATCAGTGGAACAAAGCAACACAATTATTTCACTAACCA
ACTGACATTCCTAACATGGAGGATGTGTACGCAGTGAAGCACTTCTCAGTGAAAGGGGACGTG
TACATTTGCTTGACAAGATTCATTGGTGATTCCAAAGTCATGAAATGGGGAGGCTCCTCGTTC
CAGGATATTCAGAGGATGCCATCGCGAGGATCCATGGTGTTCAGCCTCTTCAAATAAATAAT
TACCAATATGCAATTCCTGGAAGTGATTACTCCTTTACTCAAGTGTATAACTGGGATGCAGAG
AAAGCCAAATTTGTGAAATTTTCAGGAATTAATGTTTCAGGCACCAAGATCATTACACATGTG
TCCATTAATAAGCGTAATTTTCTTTTGTCTCCAGTTTTAAGGGAAATACACAGATTTACAAA
CATGTCATAGTTGACTTAAGCGCATGAGACACCAATTCCTGTGGCTGCCATCAGAAATTTTCT
ACAGTACATGACCCGGATGAACTCAATGCATGATGACTCTTCTTATCACACTTGCAATGAAT
GCCTTTCAAACATTGAGACTGCTAGAACCAAGCACTACCAGTATCTCCATCCTTAAGTGTCCA
GTCCAGTGATGTGGGAAGTTACCTTTTATAAGACAAAATTTAATTGTGTAAGTGTCTTTGCA
GTGAAGATGTGTAAATAAGCGTTTAAATGGTATCTGTTACTCCAAAAGAAATATTAATATGTA
CTTTTCCATTTATTTATTTCATGTGTACAGAAACAAGTCCCAAATAAAATGTTTACATTTTCTT
TCATA

FIGURE 326

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68882
><subunit 1 of 1, 557 aa, 1 stop
><MW: 63818, pI: 8.61, NX(S/T): 3
MESERSKRMGNACIPLKRIAYFLCLLSALLLLEGKKPAKPKCPAVCTCTKDNCENARS
IPRTVPPDVISLSFVRSGFTEISEGSFLFTPQLLLFTSNSFDVISDDAFIGLPHLEYL
FIENNNIKSISRHTFRGLKSLIHLSLANNNLQTLPKDIFKGLDSLTVNVDLRGNSFNCDCK
LKWLVEWLGHTNATVEDIYCEGPPEYKKRKINSLSSKDFDCIITEFAKSQDLPYQSLSID
TFSYLNDEYVIVIAQPFTGKCIFLEWDHVEKTFRNYDNITGTSTVVCKPIVIETQLYVIVA
QLFGGSHIYKRDSFANKFIKIQDIEILKIRKPNDIETFKIENNWFVVDSSKAGFTTIY
KWNGNGFYSHQSLHAWYRDTDVEYLEIVRTPQTLRTPHLILSSSSQRPVIYQWNKATQLF
TNQTDIPNMEDVYAVKHFSVKGDVYICLTRFIGDSKVMKWGGSSFQDIQRMPSRGSVMVFQ
PLQINNYQYAILGSDYSFTQVYNWDAEKAKFVKFQELNVQAPRSFTHVSINKRNFLFASS
FKGNTQIYKHVIVDLISA
```

Important features of the protein:

Signal peptide:

Amino acids 1-34

Transmembrane domain:

Amino acids 281-306

N-glycosylation sites:

Amino acids 192-196;277-281;422-426

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 310-314

Tyrosine kinase phosphorylation sites:

Amino acids 228-235;378-385

N-myristoylation sites:

Amino acids 172-178;493-499

Amidation site:

Amino acids 33-37

FIGURE 327

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCTCTGATAAAGCCC
CTACCAGTGCTGATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCCTTAAAAAAAAAAGTGCTTGA
AAGAGAAGGGGACAAAGGAACACCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTC
CAGAAGGATGCTCCATTCCTGCTTCTCACCTGCCTCTTCATCACAGGCACCTCCGTGTCACC
CGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGCCCTGGAGGAACATGACCA
CCAGTTGGATGAGTCTCAAGGTCCTCCTCTATGTGACAACCATGTGAATGGGGAGTGGTACCA
CTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAAC
CCACGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAAGGCGACGGCATTTGTGCAACGCCA
GGCTTGTGCCAGCTTCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAGTCAAGGCTTG
CCCTGGAGGCTACTATGTGTATCGTCTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGG
TCATTTTTTATGACATCTGCGACGAGGACTGCCATGGCAGCTGCTCAGATACCAGCGAGTGCAC
ATGCGCTCCAGGAACCTGTGCTAGGCCCTGACAGGCAGACATGCTTTGATGAAAATGAATGTGA
GCAAAACAACGGTGGCTGCACTGAGATCTGTGTGAACCTCAAAAACCTTACCCTGTGAGTG
TGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAA
TAACAATGGTGGCTGCAGCCACTCTTGCCCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCC
CCGGGGCCTGGTGTCTGTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAAATCAAA
TGCCATTGAAGTGAACATCCCCAGGGAGCTGGTTGGTGGCCTGGAGCTCTTCTGACCAACAC
CTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACATCCTCTTCTCTCTCAAGACATGTGG
TACAGTGGTTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGACAGGTCTACCCAA
GCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTGAC
CTGCGAGTTTCCACGCCTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCC
ACTGGAAATCATGAGCCGAAATCATGGGATCTTCCCATTCACCTCTGGAGATCTTCAAGGACAA
TGAGTTTGAAGAGCCTTACCGGAAGCTCTGCCCACCCCTCAAGCTTCGTGACTCCCTCTACTT
TGGCATTGAGCCCGTGGTGCACGTGAGCGGCTTGGAAAGCTTGGTGGAGAGCTGCTTTGCCAC
CCCCACCTCCAAGATCGACGAGGTCCTGAAATACTACCTCATCCGGGATGGCTGTGTTTCAGA
TGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGGTCCCTGTCTT
CAAGTTTGTGGGCAAAGACCACAAGGAAGTGTCTTCTGCACTGCCGGGTCTTGTCTGTGGAGT
GTTGGACGAGCGTTCCCGCTGTGCCCAGGGTTGCCACCGGCGAATGCGTCTGTGGGGCAGGAGG
AGAGGACTCAGCCGGTCTACAGGGCCAGACGCTAACAGGCGGCCCGATCCGCATCGACTGGGA
GGACTAGTTTCGTAGCCATACCTCGAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTC
CCCCACCGCCCTCTAAGAACATCTGCCAACAGCTGGGTTCAGACTTCACACTGTGAGTTCAG
ACTCCCAGCACCAACTCACTCTGATTCTGGTCCATTCACTGGGCACAGGTCACAGCACTGCTG
AACAATGTGGCCTGGGTGGGGTTTTCATCTTTCTAGGGTTGAAAACCTAAACTGTCCACCCAGAA
AGACACTCACCCCATTTCCCTCATTTCTTTCTTACACTTAAATACCTCGTGTATGGTGAATC
AGACCACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAACAG
TTACTGAAATTATGACTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTT
GAAATTTCAATTCAAATGCAGACTAATTATAGGGAATTTGGAAGTGTATCAATAAAACAGTAT
ATAATTTT

FIGURE 328

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFT
GMAGDAMPTFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPG
GYYVYRLTKPSVCFHVYCGHFYDICEDEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQN
NGGCSEICVNLKNSYRCECGVGRVLRSDGKTCEDEVEGCHNNNGGCSHSCLGSEKGYQCECPRG
LVLSEDNHTCQVPVLCKSNAIEVNIPRELVGGLLEFLTNTSCRGVSNNGTHVNIILFSLKTCGTV
VDVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVTCEFPRLYTISEGYVPNLRNSPLE
IMSRNHGIFPFTLEIFKDNEFEPEPYREALPTLKLRLDSLYFGIEPVVHVSGLESLVESCFATPT
SKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRVLVCGVLD
ERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

Important features of the protein:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 329

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCT
 GCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACC
 TGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACC
 GGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCG
 ATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCA
 TCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGGTGATTC
 TGGATAAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTG
 ACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAG
 GGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCA
 CAGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTA
 GGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAA
 TCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCC
 TGGTCTCCCTGCACTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGG
 AGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGACAAACAGCACGTCT
 GTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCCACTGCTTCAGGAAACATA
 CCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGCAGCTTCCCATCCCTGG
 CTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCC
 TCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCT
 TTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGA
 ATGGAGGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGT
 GCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCCG
 AAGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCCCCTGATGTACCAATCTGACCAGT
 GGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAAGGAT
 ACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTGTAATGCT
 GCTGCCCCCTTTCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCTGGGGATCCCCAA
 AGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCATTTCTT
 GGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCCTCGCAGCCCAGAGGCGCCAGAGGAAG
 TCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACT
 GAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGC
 AGGCTGTCTTGTAAGCCAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCA
 GCCCTGTCCGTCTTCACCCATCCCCAAGCCTACTAGAGCAAGAAACCAGTTGTAATATAAAAT
 GCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCAATTGTTATTACAGCTATGG
 CCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAAAAA

FIGURE 330

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL
CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSA
CFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPGCLSGSLVSLHCL
ACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCAGSILDPHWVLTAAHCFRKHTDVFNWK
VRAGSDKLGSPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTP
ATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
QGDSGGPLYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 331

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGGC
TCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTTCTCAAGGAGGACG
AGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTTCGAAATCA
ATGTTCCAAAGCCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATCTACC
TGATCCTGCTCACCCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGCGCGGC
TCCGGGTCTTGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGTCCTTCT
CCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTGCAAGTCC
TGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGTAGACAACCT
TCACTCAGAAACCAGGGATGTTTCAAGATCAAAGGTGAACAAGGCGCCCCAGGTCTTCAAGGTC
ACAAGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCCCGGGACCACCTGCTGAGAAGGGAG
CCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGGCCACCGGGAG
TCAAGGGAGAGGCGGGCTCCAAGGACCCCAGGGTGTCTCAGGGAAGCAAGGAGCCACTGGCA
CCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATTGGCCCCAAAAGGGG
AAACTGGAACCTAAGGGAGAGAAGGAGACCTGGGTCTCCAGGAAGCAAAGGGGACAGGGGCA
TGAAAGGAGATGCAGGGGTCTATGGGGCTCCTGGAGCCCAGGGGAGTAAAGGTGACTTCGGGA
GGCCAGGCCCACAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGATCAAGGACAACCTGGAC
TGCAGGGTGTTCGGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGCCAAGGGTGAGCCTGGCA
GTGCTGGCTCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGAGTCCAGGAGCCACAGGCC
TGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGAAGAAAAGGAGAATCAGGAG
TTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGGGCTGGCAGGTCCCAAGGGAG
CCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAGGATCTTCTGGGGAGCAAGGAG
TAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCCGTCAGGATTGTCGGCAGTAGTA
ACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGGGACAATTTGCCATGACGAGTGGC
AAAATTCTGATGCCATTGTCTTCTGCCGATGCTGGGTACTCCAAAGGAAGGGCCCTGTACA
AAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAATGTTTCAAGTGTGGGGCACGGAGAGTA
CCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCATGACTGCAGCCACGAGGAGGACGCAG
GCGTGGAGTGCAGCGTCTGA~~CCCCGAAAC~~CCTTTCACTTCTCTGCTCCCAGGTGTCTCGGG
CTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGTTCCCTGGGGACAACCTGAGCAGCCTCTGG
AGAGGGGCCATTAATAAAGCTCAACATCATTGA

FIGURE 332

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886
><subunit 1 of 1, 520 aa, 1 stop
><MW: 52658, pI: 9.16, NX(S/T): 3
MRNKKILKEDELLSETQQAAAFHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGLL
VVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVRVS
HEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRDGAT
GPSGPQGPVGKGEAGLQGPQGAPGKQGATGTPGPQGEKSGKGDGGLIGPKGETGTKGEKGD
GLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPGAQGDQGPGLQGVPGPPGAV
GHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKSGKGDGLQGGQGRKGESGVPGPAGVKGEQ
GSPGLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGRAEVYYS
G TWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLDNVQCRGTESTLWSCTKNSWG
HHDCSHEEDAGVECSV
```

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

FIGURE 333

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCTG
CCTCTGGCATATGCACACACTCACACATTCTGTCTCACACCCGTACACACACATACCATGTTCT
CCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCCTGAAGCTCTGGC
TGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCCAACTG
CTGTCACTGCATGCTCTGCCAAGGAGGAGGGAACTGCAGTGACAGCAGGAGTAAGAGTGGGAG
GCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTCAGCGAGCCTAGAGAGGGGCAGACTA
TCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGAAGACCGG
GGCACTTGTGGGTTGCAGAGCCCCCTCAGCC**ATG**TTGGGAGCCAAGCCACACTGGCTACCAGGT
CCCCTACACAGTCCCGGGCTGCCCTTGTTCTGGTGCTTCTGGCCCTGGGGGCCGGGTGGGCC
CAGGAGGGGTTCAGAGCCCGTCTGTCTGGAGGGGGAGTGCTTGGTGGTCTGTGAGCCTGGCCGA
GCTGCTGCAGGGGGGGCCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGCGAGTGGCATT
GCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGCACCAGTGGGGCC
ATCTACTTCGACCAGGTCTTGGTGAACGAGGGCGGTGGCTTTGACCGGGCCTCTGGCTCCTTC
GTAGCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGGTGTACAACCGCCAA
ACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCTCAGCCTTTGCCAATGATCCT
GACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGACCCTGGGGACCGAGTG
TCTCTGCGCTGCGTCCGGGGGAATCTACTGGGTGGTTGGAAATACTCAAGTTTCTCTGGCTTC
CTCATCTTCCCTCTCT**AG**AGGACCCAAGTCTTTCAAGCACAGAATCCAGCCCTGACAACCTT
CTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAGACTCCCTCTGGCTCCTATC
CCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAAGAGAAGAGTAGAGCTGTGGC
ATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTACCCCTCCAGCCACCTGCTGCATC
TGTTCTCTGCTGCTGCTCCTCCGGTTCCCCCACCCAGCTTCTCTGCTCAATGCTGATCAGGGACAGG
TGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCAGATGGACAAGCCTCAGCGTACCCTG
CAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATCTCAGCCAGCACCGTCAGAAGCTGAG
CCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCACAGGCAGAAGGGTGGGAAGGGCCTGGA
GTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTGTCTAGACTGAACATGGTACACATTCTG
CATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCTGGCTGTCTTCTATGCTGGATCCAGAT
GGACTCTGGCCCTTACCTCCCCACCTGAGATTAGGGTGAGTGTGTTTGCTCTGGCTGAGAGCA
GAGCTGAGAGCAGGTATACAGAGCTGGAAGTGGACCATGGAAAACATCGATAACCATGCATCC
TCTTGCTTGGCCACCTCCTGAAACTGCTCCACCTTTGAAGTTTGAACCTTTAGTCCCTCCACAC
TCTGACTGCTGCCTCCTTCCCTCCAGCTCTCTCACTGAGTTATCTTCACTGTACCTGTTCCAG
CATATCCCCACTATCTCTCTTTCTCCTGATCTGTGCTGTCTTATTCTCCTCCTTAGGCTTCCT
ATTACCTGGGATTCCATGATTCATTCCTTCAGACCCTCTCCTGCCAGTATGCTAAACCCTCCC
TCTCTCTTTCTTATCCCGCTGTCCCATTTGGCCAGCCTGGATGAATCTATCAATAAAACAACT
AGAGAATGGTGGTCAGTGAGACACTATAGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGA
TCGGGTGTTACAGGTACAAGTAGGTATGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAA
AATTAAAAA

FIGURE 334

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLPLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECLVVCEPGRAAAGGPGGAA
LGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVYSF
RFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAATSSVLLPLDPGDRVSLRLRRGNLL
GGWKYSSFSGFLIFPL
```

Signal peptide:
amino acids 1-32

FIGURE 335

[illegible]

FIGURE 336

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRSK
VEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVDWNTPKKGRRSQW
VRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFPGIR
PYLATLAGNFRMPVLRREYLMMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGGAESLSSMPGKN
AVTLNRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSGRWVQKKFQKYIGFAPCIFH
GRGLFSSDTWGLVPYSPKITTVPGEPIITPKLEHPTQQDIDLYHTMYMEALVKLFDKHKTKFG
LPETEVLEVN
```

Important features of the protein:

Transmembrane domain:

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 337

GGGCGGCGGGATGGGGGCGGGGGCGGGCGGGCGCCGACTCGCTGAGGCCCGACGCGAGGGCCGGGCCGGGCCCA
GGGCCGAGGAGCGCGGCGGCCAGAGCGGGGCGCGGAGGCGACGCCGGGGACGCCCGCGGACGAGCAGGTGGCG
GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGGA
CGGCTGTCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGCGCCATGGGCCTGCTGGCCTTCTCTGAAGACCCA
GTTCCGTGCTGCACCTGCTGGTGGGCTTTGTCTTCGTGGTGGTGGTCTGGTTCATCAACTTCGTCCAGCTGTGCAC
GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA
ACTGGTCATGCTGCTGGAGTGGTGGTCTTGACGGAGTGATACACTGTTACGGACCAGGCCACGGTAGAGCGCTT
TGGGAAGGAGCACGCAGTCATCATCCTCAACCACAACCTTCGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA
GCGCTTCGGAGTGCTGGGGAGCTCCAAGGTCCTCGCTAAGAAGGAGCTGCTCTACGTGCCCCCTCATCGGCTGGAC
GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG
GCGCCTGTCGGACTACCCCGAGTACATGTGGTTTCTCCTGTACTGCGAGGGGACGCGCTTACGGAGACCAAGCA
CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG
CTTCACCACCGCAGTCAAGTGCCCTCCGGGGGACAGTCGCAGCTGTCTATGATGTAACCCTGAACCTCAGAGGAAA
CAAGAACCCGTCCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCTCT
GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAAGTGTACCAGGAGAAGGACGCGCTCCA
GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGGAGGCCGTGGACCTCCTGAA
CTTCCTGTCTGGGCCACCATTCCTGTCTCCCCCTTTCAGTTTTGTCTTGGGCGTCTTGGCCAGCGGATCACC
TCTCCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCCTTTGGAGTTCGCAGACTGATAGGAGAATCGCT
TGAACCTGGGAGGTGGAGATTGCAGTGAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
CAGTCTCAAAAAAAAAAAAAAAAAACAAAAAACCAGAAATTCTGGAGTTGAACTGTGTAGTTACTGACATGAAAA
ATTCAGTAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
TTTCAGGCTAATGAAAAAAGATGAAGGAAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA
CATATGCATGATGAGAGTCCAGAAAGGAGAGGAGAGAAAGGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCA
AATCAAAGTGTCAAATGACAAAGAATCTTGAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTTG
ATCAGATTAAACAGCTCATTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
AACCTTCAACTGTAATTATTGGACTTTTGGAGTCTTAGATGGTCTGACCTCTTTGTCTTCAGGGACAGTTTTTCA
ATTTAATCCCTAATAACAATTAGTCAAGCTTCCTTGACCTGTAGGAAGGCCTGTCTTTAGGCCGGGCACAGTGGC
TTACACCTGTAATCCAGCACTTTGGGAGGCCAGACGGGTGGATCATTGGGGTCAGGCTGATCTCAAACCTCCT
GAGTTCAGGTGATCTGCCCGCCTCAGCCTCCCAAAGTGTTGTGATTGCAGGCGTGAGCCACTGCGCCTGGCCGGA
ATTTCTTTTAAAGCTGAATGATGGGGGCCAGGCACGATGGCTCACGCCTGTGATCCCAAGTAGCTTGGATTGTA
AACATGCACCACCATGCCTGGCTAATTTTTTGTATTTTTTAGTAGAGACGTGTTAGCCAGGCTGGTCTCGATCTCCT
GACCTCAAGTGACCACCTGCCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTTGA
GCATCTTGTGATGTGCTTATTGGCCATTGTATATCTTCTATCTTCTTTGGGGAAATGTCTGTTCAAGTCCTTTG
CCTTTTTAAATTTTTTATTATTTATTTATTTATTTATTTTGTAGACAGGGTCTTGTCTGTTGCCAGGCTGGAGTA
CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT
AGCTGTATTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATTGA
TGCCAGGCTGGTCTTGAACCTCCTGAGCTCAAGTGATCTGCCTGCTTCAGCCTCCCAAAGTGCTGGGATTACAGA
CATGAGCCACTGCACCTGGCAAACCTCCCAAATTC AACACACACACACAAAAACACCTGATTCAAATGGGCA
GAGGGGCGGGTGTGGCCCCAACTACCAGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG
CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCTGTCTC

FIGURE 338

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFVVFVVSGLVINQVQLCTLALWPVSKQLYRRLNCRSLAYSLWSQLVM
LLEWWSCTECTLFQTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKKEL
LYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSM
EVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAADVDTLNFGRGNKNPSLLGILYGKKYEAD
MCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQGMFPGEQFKPARRPWTLNFLSWA
TILLSPLFSFVLGVFASGSPLLILTLGFGVGAASFGVRRRLIGESLEPGRWRLQ

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 339

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCAG
CCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTTGC
TTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCGGCT
TACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGGGATA
GCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCCTGGGATCTGCCTATACCTTCTTTTCTC
TAACCTGGCATAACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAAAGTATT
TAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGTACATGTG
GTGTTCTCTTGTTCGTTCTCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCTTTCTCTT
TGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTCATCCTGCAG
ATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCATCTTGTTTAAAT
GCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTATCTTTATGTGC
GTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGCTGCGTGAGGGTC
AAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCTCATGTTTTAGAGA
CTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCAGATGGTGTAGGGCC
CAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGATGCAGGTCCTGATTC
AGTAGGCCCAGGTTGGGCATCTCTAACAAACTCCCACGTGATGCTGATGCTGGTCCTATGAAC
TATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGCTCACACCTATGATCCCA
GCATTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATTTCAAGACTAGCCTGGCCA
ACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTGGGCATGGTGGCACATGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTGAACCTGGGAGGCGGAGGTTG
CAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGACAGAGTGAGACTCTATGTCCAA
AAAAAAAAAAAA

FIGURE 340

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHS LQCPGAATRH IHL CVCF SFALALGHFLLISLVGKGLSLSCGVGGRQAGLR LIRPWVRRE
GKINFY TNGDSWGLR PASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWSGP
CPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 341

CGCCATGGCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCGACG
CTGTTGGCGCTGCTCGTGTGCGCCGCGCGGGGTCGCGGCGGCCGGGACCACGGGGACTGGGAC
GAGGCCTCCCGGCTGCCGCCGCTACCACCCGCGAGGACGCGGCGCGCGTGGCCCGCTTCGTG
ACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGCCGG
CCCTTCGCCGACGTCCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCCCTAT
TTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTACACTG
ACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTTGATCCACAAAGTCCCCTT
TGTGTTACATAATGCTGTCAGGAACGTGACCAAGGTGAATGAAACAGAAATGGATATTGCA
AAGCATTGTTATTATTGACACCCCTGAGATGAAAACCTGGCCTTCCAGCCATAATTGGTTC
TTTGCTAAGTTGAATATAACCAATATCTGGGTCTGGACTACTTTGGTGGACCAAAAATCGTG
ACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAATTTAGCAACAC
TTATGAAGTTTCTTAAAGTGGCTCATACACACTTAAAAGGCTTAATGTTTCTCTGGAAAGCGT
CCCAGAATATTAGCCAGTTTTCTGTC

FIGURE 342

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269
><subunit 1 of 1, 220 aa, 1 stop
><MW: 24075, pI: 7.67, NX(S/T): 3
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR
FVTHVSDWGALATISTLEAVRGRPFADVLSLSLDGPPGAGSGVPHYFYLSPQLSVSNLQEN
PYATLTMTLAQTNFCKKHGFDPOSPLCVHIMLSGTVTKVNETEMDIAKHSLFIRHPEMKT
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTVQ
```

Important features of the protein:

Transmembrane domain:

Amino acids 11-29

N-glycosylation sites:

Amino acids 160-164;193-197;216-220

N-myristoylation sites:

Amino acids 3-9;7-13;69-75;97-103

FIGURE 343

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGAT
TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAGCCACAG
GAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATT
AAAATCTGTTTTTTGTTCTCTTGTAAC TAGCCTTTACCTTCCTAACACAGAGGATCTGTCACT
GTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGT
CCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAAC
TGTCTCACGTCTGGAGGCACTGACTCGGGCAGTG CAGGTAGCTGAGCCTCTTGGTAGCTGCGG
CTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGA CAAGCCCGAAGATTCATAGGCG
ATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGG
GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCATCTAACCTTTT
CATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCT
TGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTTTTATGTGACAGGA
CTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTG
TGCCAAATTATGGGTCAGAAAAGATGGAGGTGTTGGGTATCACAAGGCATCGAGTCTCCTGC
ATTCAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACTCGGGACTCACCTCTG
GGGCCATCAGACAGCCGTTTTCCGCCCCGATCCACGTACCAGCTGCTGAAGGGCAACTGCAGGC
CGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAGCCAGGGGCAGCCGTCTG
GGAAGGAGCAAGCAAAGTGACCAATTTCTCCTCCCCCTCCTTCCCTCTGAGAGGCCCTCCTATGT
CCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATGGCTCAGTGTTGGCCCAGGA
GGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCGAACACGGAAATGCCTCCAGT
AAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCTCAATTTAAATCATGTTCTAGT
AATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTTCAAATGATCTCCAAGGGCCCT
TATACCCCAGGAGACTTTTGATTTGAATTTGAAACCCCAAATCCAAACCTAAGAACCAGGTGCA
TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTTTGGGAGGCCGAGGCG
GGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTC
TACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATCCCAGCTACTCGGG
AGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT
TCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTATGGTTATTT
GTAA

FIGURE 344

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVMFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS
PCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

Signal peptide:
amino acids 1-15

FIGURE 345

CCGCGCCGCGCAGCCGCTACCGCCGCTGCAGCCGCTTTCCGCGGCCTGGGCCTCTCGCCGTCA
CATGCCACACGCCTTCAAGCCCGGGGACTTGGTGTTTCGCTAAGATGAAGGGCTACCCCTCACTG
GCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCCAACAAGTACCCCAT
CTTTTTCTTTGGCACACAGAAACAGCCTTCTGGGACCCAAGGACCTGTTCCCTACGACAA
ATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGGGAGAT
CCAGAACAACCCCCACGCCAGCTACAGCGCCCCCTCCGCCAGTGAGCTCCTCCGACAGCGAGGC
CCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGGGGGTCA
GGCCGTACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCAGACTCAGA
CAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGATGTCGGTCTCGAA
ACGAGCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCGAAGAGGAGAA
CTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCTGAGAAGAAAGC
AGCGGTCCGGGCGCCACGGAGGGGCCCTCTGGGGGGACGGAAAAAAAAGAAGGCGCCGTCA
CTCCGACTCCGACTCCAAGGCCGATTTCGGACGGGGCCAAGCCTGAGCCGGTGGCCATGGCGCG
GTCGGCGTCCCTCCTCCTCCTCTTCTCCTCCTCCTCCTCCGACTCCGATGTGTCTGTGAAGAAGCC
TCCGAGGGGCAGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGGGCGGAAACCGAAGCC
TGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGGTGGACCGCATCAGTGA
GTGGAAGCGGCGGGACGAGGCGCGGAGGCGCGAGCTGGAGGCCCGGCGGCGGCGAGAGCAGGA
GGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGAGCGGAGGCGCGAGCGGGC
CGACCGCGGGGAGGCTGAGCGGGGCAGCGGCGGCAGCAGCGGGGACGAGCTCAGGGAGGACGA
TGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGGTCCCCCGTCTCCTCTGACTC
CGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGCGAAGAAGCCGCAGTCTCAAG
CACAGAGCCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAGTGCGGCCCGAGGAGAAGCAACA
AGCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCCGAGGGCTTCTCGATGGACAGGAA
GGTAGAGAAGAAGAAAGAGCCCTCCGTGGAGGAGAAGCTGCAGAAAGCTGCACAGTGAGATCAA
GTTTGCCCTAAAGGTGACAGCCCGGACGTGAAGAGGTGCCTGAATGCCCTAGAGGAGCTGGG
AACCTTGACAGGTGACCTCTCAGATCCTCCAGAAGAACACAGACGTGGTGGCCACCTTGAAGAA
GATTCGCCGTTACAAAGCGAACAAGGACGTAATGGAGAAGGCAGCAGAAGTCTATACCCGGCT
CAAGTCGCGGGTCTTCGCCCCAAAGATCGAGGCGGTGCAGAAAGTGAACAAGGCTGGGATGGA
GAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAGGAGCTGGCCGGGGAGGAGGCCCCCAGGA
GAAGGCGGAGGACAAGCCAGCACCGATCTCTCAGCCCCAGTGAATGGCGAGGCCACATCACA
GAAGGGGGAGAGCGCAGAGGACAAGGAGCACGAGGAGGGTCCGGGACTCGGAGGAGGGGCCAAG
GTGTGGCTCCTCTGAAGACCTGCACGACAGCGTACGGGAGGGTCCCGACCTGGACAGGCCTGG
GAGCGACCGGCAGGAGCGCGAGAGGGCACGGGGGGACTCGGAGGCCCTGGACGAGGAGAGCTG
AGCCGCGGGCAGCCAGGCCAGCCCCGCCCCGAGCTCAGGCTGCCCTCTCCTTCCCCGGCTC
GCAGGAGAGCAGAGCAGAGAACTGTGGGGAACGCTGTGCTGTTTGTATTTGTTCCCTTGGGTT
TTTTTTTTCTGCCTAATTTCTGTGATTTCCAACCAACATGAAATGACTATAAACGGTTTTTTA
ATGA

FIGURE 346

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPKNKYPIFFFGTHETAFLGPKDLFPYDK
CKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDEDRGVM
AVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLQASVSPSEEEN
SESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPVAMAR
SASSSSSSSSSSSDSDSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEVDRISE
WKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGDELREDD
EPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRVRPPEEKQQ
AKPVKVERTRKRSEGFSDMRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELG
TLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKEAVQKVNKAGME
KEKAEKLAGEEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHEEGRDSEEGPR
CGSSEDLHDSVREGPDLDPRGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

FIGURE 347

GTGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA
ACACCATTTGAAAGAGAACATTGTTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA
TTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCACTTTGAAGCA
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTCAAATAGCTGTATTCCCTTTTTGGGTTTCATC
AGAAGGACTGGATTTTCAAACCTCTTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT
CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAGATTATTTGGCCTGCTGCAAAGGAACGGGTGGA
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCTATAACAA
AACTCACATATATGTGTGTGGAACCTGGAGCATTTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCCTCAGCAGCC
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCATT
CACTCGATCCCTTGGGCCCTACTCATGACCACCACTACATCAGAACTGACATTTTCAGAGCACTACTGGCTCAATGG
AGCAAAATTTATTGGAACCTTTCTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTTCG
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGCT
AGGAGGACAACGCAGCCTGATAAAACAAGTGGACGACTTTTCTTAAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
AGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTGTGTGTATAGCATGGCTGACAT
CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGACAGCCATCGTTGGGTGACAGTATGATGGGAGAAT
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA
TGATGTCATCAGTTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTTCATTGCAGAAGATGGCCAGTACGA
TGTAATGTTTCTTGGAACAGACATTTGGAACCTGTCCTCAAAGTTGTGTCAGCATTTCAAAGGAAAAGTGAATATGGA
AGAGGTAGTCTGGAGGAGTTGCAGATATTCAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA
GCAACAATTGTACATTGGTTCCCAGATGGATTAGTTTCAGCTCTCCTTGCACAGATGCGACACTTATGGGAAAGC
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCCTGGGATGGAATGCATGCTCTCGATATGCTCCTAC
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAATCACCCAGTGTGGGACATCGAAGACAG
CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC
TAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTGAGGGATGAGCATCGAGAGGAGTTGAAGCCCGA
TGAAAGAATCATCAAAACGGAATATGGGCTACTGATTGCAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG
CAAAGCCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCTTGAAGATGAACAGATGGA
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
CTACATCCAAATCCTTAGCAGCCCAAACCTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG
GAGACAGAGAAACAAGGGGGGCCCAAAGTGAAGCAGCATGAGGAAATGAAGAAGAAACGAAATCGAAGACATCA
CAGAGACTGGATGAGCTCCCTAGAGCTGATGAGCCAGTAGTTTCTTACTTAATTTAAAGAAAAGAATTCCTTACC
TATAAAAACATTGCCCTTCTGTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTGTCTAAGG
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAAATTCATTGTAACAGTTTTT
CCAAGAACAAATCTTGCAAGCAAAGTATAAGAATTATCTTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA
TGTTTTGAGTTTGGGAATTTATTGTGATGTAAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGTATAAGGT
GCTTTATTCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT
CATTCCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTGAGACACAAATTAAGACAACCTCCCATATC
AACAGGAACCTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCCAGGATTTCT
ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTTAATAAAACAAGGAAAAACA
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTAGAAGACAGAAGGAAAGACAGCCAT
AAATCTGGCTTTGGGGAAAACCTCATATCCCATGAAAAGGAAGAACATCACAAATAAAGTGAGAGTAATGTAA
TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAAATCTAGATTATAACA
AACTGCTAGCAAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTATAACC
AATGATATTTTCAGTATATATTTTCTCTTTTAAAAAATATTTATCATACTCTGTATATTATTTCTTTTACTGC
CTTTATTCTCTCCTGTATATTGGATTTTGTGATTATATTGAGTGAATAGGAGAAAAACAATATATAACACACAGA
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATATTTGTGTAATAACAGAACGAGTGTAAAATTTTAAC
AACGGAAGGGTTAAATTAACCTCTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAATT
GTAGTATTGTTTTTGTAAATTTAACAATAAATAAGCCTGCTACATGT

FIGURE 348

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKD LLLSN SCIPFLG
SSEGLDFQ TLL LDEERGR LLLGAKDHI FLLSLVDLNKNFKKIYWPA AKERVELCKLAGKDANT
ECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFPDPQQ
PFASVMTDEYLYSGTASDFLGKDTAFT RSLGPTH DHYI RTDISEHYWLN GAKFIGTFFIPDT
YNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLICSIPGS
DGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGPYAHKES
ADHRVWQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPD DVISFIKRHSVMYKSVYPVAGGPTFK
RINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVV SISKEKWNMEEVVLEELQIFKHSS
IILNMELSLKQQQLYIGSRDGLVQLSLHRC DTYGKACADCC LARDPYCAWDGNACSR YAPT SK
RRARRQDVKYGDPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQATIKWYIQRSG
DEHREELKPD ERIIKTEYGLLIRSLQKKDSGMY YCKAQEHTFIHTIVKLTLNVIENEQMENTQ
RAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRNKGGPKWKHMQEM
KKKRNRRHHRDLDELPRAVAT
```

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 349

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACCGCGGGGAGCAGA
 CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC
 CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTGTCTGGAGTGGGGAGCAGAAGGCGTGGCTGGCAAGA
 GTGGCCTGGAGAAAGAGGTTTACGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCATGGGCATC
 GGGTGAGGTGGGGGGGCGACAGGTGTATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
 AGCCATTGAGGGTGTCTAGGAGCTACAGAGGGGAGGGAAAGGTATTTAAGTAACAGTGTGGCACAATAGTTAA
 GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTCCTTCTGTTGCTTCTAGTTCTGTAGCCCCAGGT
 AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCTCATCACTAAAGTAGGGCCAATAATAGCACCACCTCAT
 AGGGAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
 TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCGGGGCACAGGTGAGCC
 AGGTGAAGGGGGCTGCCCGGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGCGGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTCTC
 CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
 CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGCTGGTATTTCTGCTATCAGGCAGGGCGTGAGGATG
 AGCTGACAAATCACGGAGGGTGAGTGGCTGGAGGTGATAGAGGAGGAGATGCTGACGAATGGGTCAAGGCTCGGA
 ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCAGAGAGCAGCC
 AAGACAGTGACAATCCCTGCGGGGAGAGCCACAGCATTCTGGCACAGGCCCTGTACAGCTACACCGGACAGA
 GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCCGGGCCCCAAGATGGAGTAGATCAG
 GCTTCTGGAGGGGAGAATTTGGGGGCGGTGTTGGGGTCTTCCCTCCCTGCTGGTGGGAAGAGCTGCTTGGCCCC
 CAGGGCCACCTGAACCTCTGACCTGAAACAGATGCTGCCGTCCCTTCTCTTCCAGCTTCTCCCCACCTGCAC
 CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTCTCTGG
 ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCGGCTAAAGCCCCGATCCTGGCCACC
 CAGATCCCTCACCTGAGAGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGCTGTCCCTATCTTCAAGCTGTGAGA
 CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCCCTCACCTCAAGGGT
 GGAACCTTGCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTTCCATTGTTCTATCATCTTAGGACC
 GGAACCTACTACCTTCTCTTCTGTGATGACCTATCTAGGGTGGTGAATGCCTGAAATCTCTGGGGCTGGAAACC
 ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTTCCCCACCCTGGCTCCATGACCCACCCACTCTGGATG
 CCAGGCTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
 CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCTCTGTG
 CTAAGAGGGGAGGGGGCCTACGGTGTCTATTGCTTTAGGGGCCCCACCGGGCAGGGGCTGCTCCAGCTGCCAC
 GCTCTATCATATGGAGCGAGGTGTTGGGAAGGCGGGGAGGCGAGCCTGTTGACGGCAGGGGAAGGAGAAGAGAC
 TGAGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
 AGCTGGGGGGCAGTGCTGTCCAGTGGAGGGGAGGGCTTTACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG
 TCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTTGCTTCTGTTCAGCTGTGTCCAGC
 TTTTCCCTTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC
 AGTTTACTCTGGGGGTTTCCAGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA
 TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG
 TCAACAAATGAGAGACCAGGAGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCAGCCAGTGC
 AGTCCCGGCTGTGTTTTCTTACCTGGTGATCAGAAGTGTCTGGTTTGCTTGGCTGCCCATTTGCCTCTTGAGTGG
 GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTGGCTCTGCAGAAGCTCTGGGGTTCCCTTCAAGTG
 CACGAGGGGTAGGCTGTCTGCTGAGTCCCTCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
 TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCCTGGGCTGCCCTCCCCCAGACCCCTGACCACCCCTG
 GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT
 TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG
 GCCCTCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCTTCTC
 AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCACTT
 TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCACCTGCCCCACCTGCCCA
 CAGAGAACACAGTGGTCTCCCTGTCCGGGGGCGGCTTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAG
 GCCTCTGTGCTGCGGTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACGTGTGTGATGATGGGAGGGGGCTC
 CGTCTGCAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCT
 TCATGTTTTGTTTCTTACGTTCTTTCAGCATGCTCCTTAAACCCAGAACCCCAATTTCCCAAGCCCCATTT
 TTTCTGTCTTTATCTAATAAACTCAATATTAAG

FIGURE 350

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRAQ
VSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELSDF
EECEETGELFEPPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEWVKA
RNQHGEVGFVPERYLNFPDLSLPESQSDSNPCGAEP TAF LAQALYSYTGQSAEELSFPEGAL
IRLLPRAQDGVDDGFWRGEFGGRVGVFP SLLVEELLGPPGPPELSDPEQMLPSPSPPSFSPPA
PTSVLDGPPAPVLP GDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

FIGURE 351A

[illegible]

FIGURE 351B

[illegible]

FIGURE 352

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIVF
PEKLNQSVLPQSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEPGT
YLTGTINGDPESVASLHWDGGALLGVLYQYRGAEHLQPLEGGTPNSAGGPGAHILRRKSPASG
QGPMC NVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAAAKA
FKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHFDTAIL
FTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHDNSKPCI
SLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGK
DYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGG
RCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRPVPRNNGGKYCEGRTRFR
SCNTEDCPTGSALTFREEQCAAYNHRDLEFKSFPGPMDWVPRYTGVAPQDQCKLTCQARALGY
YYVLEPRVVDGTPCSPDSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDGSGCSKQSGSFR
KFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTLMPSPTDVVLPGA
VSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPTPSTPRPTPDWLH
RRAQILEILRRRPWAGRK
```

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 353

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCCC
GGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCTGC
TCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGACAG
CGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAGTGTG
TGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCCCCAAG
ACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCGCCT
GCGCCGTGCATCGGGATGAAGTGACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTG
CCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGTCTCCTGGA
CCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGAAGTTGAGA
TTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGTGGCACCCCTGC
TTTGCTGTCTTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCCAGGGCCACCA
CGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATCGGGCCC
CCTCAGTGACCTCGGCCACGCACAGCGGTACAGGCTGAACGACTACGTGTGAGTCCCCACAG
CCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGG
TTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATAATGTGAATGCGAGGA
AATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAAAGCTCTCTATACCAA
GACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATATTTATGTGGGTGATTGA
TAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGTTGGTTTGTGATCCAGGAA
TAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAA

FIGURE 354

MASTAVQLLGFLLSFLGMVGTLITTTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQ
CQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTLFI
LAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQDEA
PYRPHYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 355

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGC
AGGCGGCAGGGCGGGCGGCCAGGATCATGTCACCACCACATGCCAAGTGTTGGCGTTCTCTCC
TGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGG
ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGA
GGCAGAGTTCAGGCTTCACCGAATGCAGGGCCCTATTTACCATCCTGGGACTTCCAGCCATGC
TGCAGGCAGTGCAGAGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCCTGGTAT
CCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAAACATGA
CACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTGTCTGTGT
TTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTG
GGATGGTGCAGACTGTTTACAGACCAGGTACACATTTGGTGC GGCTCTGTTCTGGGCTGGGTG
CTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAG
AAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTGCCTACAAGCCTG
GAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAGATATACGATGGAG
GTGCCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTATGTGTAAATGCTCTA
AGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAAACAAGGAGATCCCA
TCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCTCGATTTTCTCTTTG
GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACAGCTGAG
TTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAA
CTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAG
ACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTATTTCCCAGCTTATCCCCAAG
AAAACCTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTTGTCTC
CCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATT
TGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAAGTTACCAAACCA
AAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTGTTGACATCTTCTTATTACAGC
AACACCATTTCTAGGAGTTTCCTGAGCTCTCCACTGGAGTCCTCTTTCTGTGCGGGTCAGAAA
TTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTTAAGTCCTAAATATAGTTAAATATA
ATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG
AAGGAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAA
GTACAAATTCATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGG
ATCACTTGAGCCAGAAAGTTTCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAA
ATACAGAGAGAAAAAATCAGCCAGTCATGGTGGCATAACCTGTAGTCCCAGCATTCGGGGAG
GCTGAGGTGGGAGGATCACTTGAGCCAGGGAGGTTGGGGCTGCAGTGAGCCATGATCACACC
ACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAATAAAAAATAAATAATGGA
ACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

FIGURE 356

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTEC
RPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFI
VSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGMVQTVQTRYTFGAALFVGWVAGGLTLIGG
VMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQ
SYPSKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 357

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGG
 AGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGG
 CTGTTTCTTGGTGGTGTGGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGA
 GTGTGGCCCTTCATTGAAAACAACATCGTGGTTTTTGAAGCTTCTGGGAAGGACTGTGGATG
 AATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTT
 TCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCT
 TTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAAGGTGAAG
 GCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGCTCATCCCT
 GTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAA
 AAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGA
 GGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA
 CCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCGTCTACTCC
 AGAAGTCAGTATGTCTAGTTGTGTATGTTTTTTTAACTTTACTATAAAGCCATGCAAATGACA
 AAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTACTGTTCTTAACTGC
 CTAATCTTAATTACAGGAACGTGCATCAGCTATTTATGATTCTATAAGCTATTTTCAGCAGAA
 TGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGG
 TTCAAGCATCTACTCTTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTT
 ACTACTGTAATTTCTCCACGACATAGCATTTATGTACATAGATGAGTGTAACATTTATATCTCA
 CATAGAGACATGCTTATATGGTTTTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAAT
 AGAACTCACTATTGCTTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGTTACTATTAATTG
 TTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAAGATTAAAATGAAGGCTTTAA
 TCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTTAGCCTAGGAGTTAGAA
 ATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTTCTTGTGTATTAAATTAACATT
 TTTAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCAAAGCTGCTTTTCCAGGGCTATACTC
 AGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTTAGGAAAGTGAAAATATTTTT
 GTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT
 TAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATAT
 GTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTC
 ACCTGCTCCTATGTGGGTACCTGAGTCAAATTTGTCATTTTTGTTCTGTGAAAAATAAATTTTC
 CTTCTTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATT
 CCAAATTTGATGAACTGACAATCCAATTTGAAAGTTTGTGTGCGACGTCTGTCTAGCTTAAAT
 GAATGTGTTCTATTGCTTTATACATTTATATTAATAAATTGTACATTTTTCTAATT

FIGURE 358

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMQWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQ
CKIYDSLIALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIF
IITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCN
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 359

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCCCTCGCCCTCCTGCTCGCGCCCC
GCCGCCATGGCTGCCTCCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGCTC
CTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAAAAA
CGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGAATTC
CTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGCAGCAG
TGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATCACCTAT
TGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCACTATGAT
GAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCGTCAACTAC
GATGACTACTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCTCTTCATGT
ATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGATCTTTTCTACC
TACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTTTGATATTTTCAT
GGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTTAAAAAGA

FIGURE 360

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLLMLQKREAPVPTKTKVAVDENKAKEFLG

SLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYDYYQRHYDED

SAIGPRSPYGFRRHGASVNYDDY

Signal peptide:

amino acids 1-30

FIGURE 361

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAGA
TTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCCTC
AGCTGCACCTCCTCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGCTTT
CTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCTGGAG
GACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGGAAAGC
AAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTCTTCCAG
ATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCACGTAGAC
TGTCAAGATCTGCTGAATCCCAACCTTCTTGCCAGGCATCCACTGCGCAAAAAGGATTGTGTCC
GGAGCACGGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTTCAAGCCGGCCACTCTCC
TACTGGCTGACAGGATGCCGCCTGAGATGAACAGGGTGCGGGTGACCCGTGGAGTCATTCCA
AGACTCCTGTCTCTCACTCAGGGATTCTTCATTTCTTCTTCCTACTGCCTCCACTTCATGTTAT
TTTCTTCCCTTCCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAATGGTTTTCTTGG
CTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTATTTGTAAACTGAGG
ACCACAATAAAGAAATCTTTATATTTATCG

FIGURE 362

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKIN
ENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNP NLLAGIHCAKRIVSGARGMNNW
VEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

FIGURE 363

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCAC
CAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGAAAGAAACACCTGAGCA
GAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTCAAT
TTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGACTTGG
GGTGAAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGACACACGCTGTTG
GCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCAACCCAT
GTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGACCTGTTGC
ATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATGCAGACTCC
AGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGTTGCACCCTC
CCCACCACACCCTGCACCAGACTGTACAGCCCAAGCCAGCAAGCACAGCCCTGAAGCCAGGT
ACCGCCTGGACTTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGAGGGTGAAGAGT
ACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGCTGCTGGTGGCCG
TGGCCTTACCCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGGAGCTACCGCCTCA
TCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGGGGCTGATGAGGACG
GGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTTCAAGCCTGGACCCACGTGGCCTCCAGGAGG
CACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGGCACCCACTGTGTCTGC
AGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTGTTTTCCATGATGAGGCCT
GGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGCCAGGGCCTTCTCTGAAGG
AGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAGTCTGCTCTCAGCGAATATG
TGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAGGCTGGGTGCCATCAGGGCCC
GGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCTTCATGGATGCCCACTGCGAGT
GCCACCCAGGCTGGCTGGAGCCCCCTCCTCAGCAGAATAGCTGGTGACAGGAGCCGAGTGGTAT
CTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTATTACCCCTCAAAGGACCTGCAGC
GTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAACCTTTGCCAGAGCATGTGAGGAAGG
CCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTGGTGCCCCGAGAGGTGGTGGCCATGG
ACAGACATTACTTCCAAAACACTGGAGCGTATGACTCTCTTATGTGCTGCGAGGTGGTGAAA
ACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTGGCTCTGTTGAAATCCTTCCCTGCTCTC
GGGTAGGACACATCTACCAAATCAGGATTCCCATTCCCCCTCGACCAGGAGGCCACCCCTGA
GGAACAGGGTTTCGATTGCTGAGACCTGGCTGGGGTCATTCAAAGAAACCTTCTACAAGCATA
GCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGAAGCCAGACTGCATGGAACGCTTGACGCTGC
AAAGGAGACTGGGTTGTGCGACATTCCACTGGTTTTCTGGCTAATGTCTACCCCTGAGCTGTACC
CATCTGAACCCAGGCCAGTTTCTCTGGAAAGCTCCACAACACTGGACTTGGGCTCTGTGCAG
ACTGCCAGGCAGAAGGGGACATCCTGGGCTGTCCCATGGTGTGGCTCCTTGACGTGACAGCC
GGCAGCAACAGTACCTGCAGCACACCAGCAGGAAGGAGATTCACTTTGGCAGCCCACAGCACC
TGTGCTTTGCTGTGAGGAGGAGCAGGTGATTCTTCAGAAGCTGCACGGAGGAAGGCCTGGCCA
TCCACCAGCAGCACTGGGACTTCCAGGAGAATGGGATGATTGTCCACATTCTTTCTGGGAAAT
GCATGGAAGCTGTGGTGCAAGAAAACAATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAG
CCCGCCAGCAGTGGCGATTTGACCAGATAAATGCTGTGGATGAACGATGAATGTCAATGTGAG
AAGGAAAAGAGAATTTTGGCCATCAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATT
TCATGAAGCTGATCCTTTTGTGTGTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAA
GAATATAGGAAGTTTCTCCTTTTTCACACCTTATTTCAATTGACTGCTGGCTGCTTA

FIGURE 364

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLMLGCVLMMVAMLHPPHHTLHQTVTQAASKHSPEARYRLDFGE
SQDWVLEAEDEGEYEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPRRQ
DKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHPQDS
LPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVARLEGV
KLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSFVIDVI
DWKTFQYYPSKDLQRGVLDWKLDFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMDRHYFQN
TGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQYQNDQSHSPLDQEATLRNRVRIA
ETWLGSFKETFYKHSPEAFSLSKAEKPDCEMERLQLQRRLLGCRTFWFLANVYPELYPSEPRPS
FSGKLHNTGLGLCADCAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSPQHLCFAVRQ
EQVILQNCTEEGLAIHQHWDFFQENGMIVHILSGKCMEEAVVQENNKDLYLRPCDGKARQQWRF
DQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 365

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGG
AGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGC
AGCCGGGAGCCATGCGACCCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGC
TGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAA
AGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAG
CAGGAGTGCCTGGTTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCC
CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCT
GGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA
TTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCT
CACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTG
AATG TTCAGGACCTCTTCCCATTTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGA
ATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTG
GATTAGTGGATGTTGCTATCTGGGTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTA
CTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTT
CATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCAC TTAAATGACATTTTAAATAAG
TTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCA
CACTGTTTTTTAAATCTAGCATTATTCAATTTTGCTTCAATCAAAGTGGTTTCAATATTTTTTT
TAGTTGGTTAGAATACTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTG
TGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATATAAAAGCTACCAATCTTTG
TACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAATAAAAATTATTTCCAACA

FIGURE 366

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAAGVP
GRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAEC
TFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPENSTI
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 367

GTAAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCGCTGCCCTCACTCCCGGCCAGGATGGC
ATCCTGTCTGGCCCTGCGCATGGCGTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTGCT
CACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCCGTC
GGGAGAAGGCCCCGTGGAGAGCACCAAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCCCAGC
CCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGCGGCGG
GTCGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTGCGTGCT
GCTGGCGCTCGTGGTCTGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAAGGGGCCG
CGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 368

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVVESTSPGREPVD TGP
PAPT VAPGPEDSTAQERLDQGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 369

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGGC
GGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCACG
GCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGAAC
TCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCAGCTGGAGCGACG
ACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGACCAAG
TGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCCCCGGGT
ATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAACGCCATCA
TCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGGACCCAGCC
TAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCTAAGTAGCCCCCAGAGGCG
CTGGGAGTGTTGCCACCGCCCTCCCTGAAGTTTGCTCCATCTCACGCTGGGGGTCAACCTGG
GGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCATCGACTGTCAGC
ACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAGACTCGCACGTGC
CCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGTGCCAGGGCCCTAC
TGTCCTTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCTTCCACCTGGCTGTTCATCGG
GTAGGGCGGGGCCGTGGGTTAGGGGCGCACCACTTCCAAGCCTGTGTCCACAGGTCCTCGG
CGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACCTACATAAATAACTGGCACAAAGTAAGTCC
CCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTGGGTGAGTATGTGTGGGG
CACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGGCTCCCGAGGAGGTGGAACCTCAACC
CAGCTCTGCGCAGGAGGGCGGCTGCAGTCCTTTTCTCCCTCAAAGGTCTCCGACCTCAGCTGG
AGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCCACCCCATCCCAGGTCTGTGG
TCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCCATGGAGGGGCTGACTGCCCCA
CATTGCCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGCCCTGACCTGGACTTCAGGGGA
GGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCTAGATCAGTGGGGGCACTGCAGGT
GGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTACCTCTGCAACCACACCCATGTGGTG
GTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGGCCTGGGACACACAGAGCCACCCCGG
CCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGAAGGGGTGCTCGTAAGCCAACACCAGC
GTGCCGCGGCCTGCACACCCCTTCGGACATCCCAGGCACGAGGGTGTCTGTGGATGTGGCCACAC
ATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCTGGGGCCCCCAGGGAGGGAGGCAGGGGGT
GGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCCCCGCAGCCTGGTATCGCCAGCCTTAAGGT
GTCTGGAGCCCCCACACTTGGCCAACCTGACCTTGGAAGATGCTGCTGAGTGTCTCAAGCAGC
ACTGACAGCAGCTGGGCCTGCCCCAGGGCAACGTGGGGGCGGAGACTCAGCTGGACAGCCCTT
GCCTGTCACTCTGGAGCTGGGCTGCTGCTGCCTCAGGACCCCTCTCCGACCCCGGACAGAGC
TGAGCTGGCCAGGGCCAGGAGGGCGGGAGGGAGGGAATGGGGGTGGGCTGTGCGCAGCATCAG
CGCTGGGCAGGTCCGCAGAGCTGCGGGATGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 370

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMKE

LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIERHL

APGSWGGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

FIGURE 371

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGA CTGCCCGGGCTGCCGCCC
CCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCCTC
TCGGCCACGGCTGGGTTCGGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGCTGG
CAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCCGCGGCCCGGACCTGAGGCGTTCGC
CTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGCGCCGC
CCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGATCAAGG
ATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTCTGGTCAG
AAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGTTATGCGAA
TTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAGCAGGGAAAC
TGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCAGAAAAAGAATATGAAGGTG
AAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCGTCATTATGAAA
AGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGATGAAAGAGAATG
TTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTTACTAAATTTAAAA
CAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAAAAAGAATGATTTTG
AACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAATCCCTAAGATTATTTA
AAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCAACTTTTGGCTATACCC
TACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGACTATATGCAGAAAAATAT
TCCATGACTTGATATGCTGACGACTGTGCAGGAAGAAAACGAGCCAGTGATTTACAATAGAG
CAAGGTAAATGAATACCTTCTGCTGTGTCTAGCTATATCGCATCTTAACACTATTTTATTAAT
TAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGCCACATTTTGGGAGCTTTTCT
ACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACATGTTTATAAAGTAAAAAA

FIGURE 372

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRGA
APAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGAPG
IVVGVSVDGKEVWSEGLGYADVENRVPCPETVMRIASISKSLTMVALAKLWEAGKLDLDIPV
QHYVPEFPEKEYEGEKVSVTTROLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAFEQEK
EGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKNDPLFF
KPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 373

GACTACGGGGAGAGAGAGAGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAA
GAGCAAAGATGTTTCAAACCTGGGGGCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGG
CCCAGTTTGGAGGCCTGCCCCGTGCCCCCTGGACCAGACCCTGCCCTTGAATGTGAATCCAGCCCTG
CCCTTGAGTCCACAGGTCTTGCAGGAAGCTTGACAAATGCCCTCAGCAATGGCCTGCTGTCT
GGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACATCCTGAAGCCTGGAGGAGGT
ACTTCTGGTGGCCTCCTTGGGGGACTGCTTGGAAAAGTGACGTCAGTGATTCTTGGCCTGAAC
AACATCATTGACATAAAGGTCACTGACCCCCAGCTGCTGGAACCTTGGCCTTGTGCAGAGCCCT
GATGGCCACCGTCTCTATGTCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCCTG
GTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTTAGCTGTG
AGAGATAAGCAGGAGAGGATCCACCTGGTCCTTGGTGACTGCACCCATTCCCCTGGAAGCCTG
CAAATTTCTCTGCTTGATGGACTTGGCCCCCTCCCCATTCAAGGTCTTCTGGACAGCCTCACA
GGGATCTTGAATAAAGTCCTGCCTGAGTTGGTTCAAGGCAACGTGTGCCCTCTGGTCAATGAG
GTTCTCAGAGGCTTGGACATCACCTGGTGCATGACATTGTTAACATGCTGATCCACGGACTA
CAGTTTGTCAATCAAGGTCTTAAGCCTTCCAGGAAGGGGCTGGCCTCTGCTGAGCTGCTTCCCAG
TGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACAGTTGCCTTCTCTCCGAGGAACCT
GCCCCCTCTCCTTTCCCACCAGGCGTGTGTAACATCCCATGTGCCTCACCTAATAAAATGGCT
CTTCTTATGCA

FIGURE 374

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76533
><subunit 1 of 1, 256 aa, 1 stop
><MW: 26713, pI: 5.62, NX(S/T): 0
MFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNVNPALPLSPTGLAGSLTNALSNGLL
SGGLLGILENLPLLDILKPGGGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGL
VQSPDGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRDKQERIHVLGDC
THSPGSLQISLLDGLGPLPIQGLLDSLTGILNKVLPPELVQGNVCPLVNEVLRGLDITLVH
DIVNMLIHGLQFVIKV
```

Important features of the protein:

Signal peptide:

Amino acids 1-19

Transmembrane domain:

Amino acids 79-97

N-myristoylation sites:

Amino acids 46-52;49-55;58-64;62-68;66-72;80-86;81-87;
82-88;85-91;86-92;89-95;202-208;233-239

FIGURE 375

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTTT
AAATATGTCAAGATCCAGACTTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTGTG
TTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGTAAA
TTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTTGGTGGC
AGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGAATTGA
TTCTCACAGGCGCACCATGGCAGTTTTTGTCTGTTGGAGACTTGGACTCTATTTATGGGACAGA
AGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTATATCCTGT
TCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTAAAAACAAC
CTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCAAAACATCAA
ATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATAGTCTGAGGAA
GGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATGTTTAAATAGTA
AAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACACAACCAAATTAAT
GCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTTTCCATCACATTTA
GGACTCCACTGCAGTATACAGCACACCATTTTTCTGCTTTAAACTCTTTCCTAGCATGGGGTCC
ATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACATGTCCAGAACCAGAAC
CAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAAGAAAAGTTTGGAGTTG
AAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCTCAGCAAAAACAAGAGGT
TTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGAAGGAGATTGCTGAAGATA
TAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCCCTTTTACAGTAATGAATGT
GGCCTCCATAGTCCATAGTGTTTCTCTGGAGCCTCAGGGCTTGGCATTATTATGCAGCATCATG
CTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGCAGAAGTAGCAATGAGACATCT
TCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGACAAAACATCCATCACAGATGA
CATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAATAAACATCAATAGATATCTAAAAA

FIGURE 376

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVAA
LLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYPVP
APCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 377

CGCGGATCGGACCCAAGCAGGTGCGCGGCGGCGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCG
 ACCCCCGTGTGCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCC**ATG**GCCAGGCCCGGC
 ATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCGCTCGGGGGGCATCGGCGCGGCC
 GTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAAC
 ATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGACTTTGATCCCTACAGA
 TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC
 GGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCGCTGACACCCTGCTCTCAGGCAGC
 ACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAA
 GCCTACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCATTAAATCAATAGCATG
 TCTGGCCACCGAGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC
 ACTGCGCTGACAGAGGGACTGAGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACG
 TGCATCTCTCCAGGTGTGGTGGAGACACAATTCGCCCTTCAAACCTCCACGACAAGGACCCTGAG
 AAGGCAGCTGCCACCTATGAGCAAAATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTT
 ATCTACGTCCTCAGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGGAG
 CAGGTGACCT**AGT**GACTGTGGGAGCTCCTCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTG
 CCTCTGGATTTTAGGTGTTGATTTCTGGATCACGGGATACCACTTCCTGTCCACACCCCGACC
 AGGGGCTAGAAAATTTGTTTGAGATTTTATATCATCTTGTCAAATTGCTTCAGTTGTAAATG
 TGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTTACTTGTTAACTTGTTCTTG
 TGCCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTT
 GTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG
 GAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCCTCCTCTGCCTGCCCC
 ACTGCACCCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCAGTCTTGGCTTCTTGT
 CCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCTGGC
 CCAGTGGATTTATGGTGATCATTAAGAAAGAAAAATCGCAACCAAAAAAAAAAAAA

FIGURE 378

MARPGMERWRDRLALVTGASGGIGA A VARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGT
LIPYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALS
ICTREAYQSMKERNVDDGHIININSMGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQT
HIRATCISP GVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ
MRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 379

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGTT
TCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCCGCTTATTAGC
TCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCACG
GCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACTCCCT
CTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAGATGAA
GAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTCAAGTCTTGATTTGTGGCTTACCT
CAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTTTGCTTCTTCAGAAATGTTTTTTTACAATCTC
AAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGATTTTGGACTCATTGTTGGGATT
GATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTTACGTGAGCA
AATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGAACACAGTGGA
TGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATTGCTGTCCTTCT
GGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATATTGTTGTGAATGG
CTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAACCACAAATAAAAG
AACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGCTGCTGCTCCATCCACTG
TGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGACAGAGCAATACTTTAC
AATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTGATGAACTCTAATTCTGTACATA
AAAATTTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATGCTGTACTATGTCCTTAA
AGAGAATTTGGTAACCTGGTTGATGTGGTAAGCAGATAGGTGAGTTTTGTATAAATCTTTTGT
GTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTGATTTCTATAACACATTTAT
TTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAATCATTCTGTCAATTGTTCTC
AATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAAATGTGCTTATTGTACTATATTTTGT
ATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAATAATGTTTTGAAATCATGACCC
AAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGAAGGTTAATTATTGTATATTTTAA
AAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAGCAGCCACTGTCCATTACCTATCGT
AAACATTGGGGCAATTTAATAACAGCATTAAAATAGTTGTAAACTCTAATCTTATACTTATTG
AAGAATAAAAGATATTTTTTATGATGAGAGTAACAATAAAGTATTCATGATTTTTTCACATACAT
GAATGTTTCATTTAAAAGTTTAAATCCTTTGAGTGTCTATGCTATCAGGAAAGCACATTATTTCC
ATATTTGGGTAAATTTTGCTTTTATTATATTGGTCTAGGAGGAAGGGACTTTGGAGAATGGAA
CTCTTGAGGACTTTAGCCAGGTGTATATAATAAAGGTACTTTTTGTGCTGCATTAAATTGCTTG
GAAAGTGTTAACATTATATTATATAAGAGTATCCTTTATGAAATTTTGAATTTGTATAACAGA
TGCATTAGATATTCATTTTATATAATGGCCACTTAAAATAAGAACATTTAAAATATAAACTAT
GAAGATTGACTATCTTTTCAGGAAAAAAGCTGTATATAGCACAGGGAACCTAATCTTGGGTA
ATTCTAGTATAAAAACAAATTATACTTTTATTTAAATTTCCCTTGTAGCAAATCTAATTGCCAC
ATGGTGCCCTATATTTCATAGTATTTATTCTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCT
AGATTTAGACTATATAGAATTTAGATATTGTATTGTTGCTCATTATAATATGCTACCACATGT
AGCAATAATTACAATATTTTATTAAAATAAATATGTGAAATATTGTTTCATGAAAGACAGATT
TCCAAATCTCTCTTCTCTCTGTACTGTCTACCTTTATGTGAAGAAATTAATTATATGCCA
TTGCCAGGT

FIGURE 380

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
NKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNLVP
VTTNKRTNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

FIGURE 381

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACC
ATCATGTCCCTCCCACCCCTCCTTTGACTGCGGGCCGTTCAAGGTGCAGAGTCTCAGTTGCCCGG
GAGCACCTCCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCCAGTTCTGGTT
TCATGCCAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTT
TTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTCAGTAGCCACCAG
CCACCTGTGGCCGTTGAGTGCTTGAAATGAGGAACTGAGAAAATTAATTTCTCATGTATTTTT
CTCATTTATTTATTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGG
ATACATGTATACAATATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACAT
TTATTTTTTATTCTTTTTTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCC
ATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAA
GTAGCTGGGACTACAGGCATGCACCACAAATGCCCAAATAATTTTTGTATTTTTAGTAGAGACG
GGGTTTTGCCATGTTGCCCAGGCTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTTGCCTCG
GCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCTGGCCTAAACATTTATCTTTT
CTTTGTGTTGGGAACCTTTGAAATTATACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTG
CTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGT
ACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACCTC
CATGAGATCCACTTTTTTAGCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTG
CCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAATGACAGGA
TTTCGTTCTTAATTTCAATTAAAATAACCACACATGGCAAAAA

FIGURE 382

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQ
PVKGHGTLGESPMFVKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

FIGURE 383

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAG
CCTGGAGCATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTTCAAGTAGCACCTCTATCAG
TTATGGCTAAATCCTGTCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATC
GCTTTCTGACATCCATTCCAACAGGAATACCAGAGGATGCTACAACCTCTCTACCTTCAGAAC
ACCAAATAAATAATGCTGGGATTCCTTCAGATTTGAAAACTTGCTGAAAGTAGAAAGAATAT
ACCTATAACCACAACAGTTTTAGATGAATTTCTACCAACCTCCCAAAGTATGTAAAAGAGTTAC
ATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAAAAATTCCTATCTGG
AAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCATTCCGAG
ACAGCAACTATCTCCGACTGCTTTTCCCTGTCCCGTAATCACCTTAGCACAATTCCCTGGGGTT
TGCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCAT
CTCTTCAAGGTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATG
GTTTAGGTGACAAAGTTTTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATT
CCCTGACTGCTGCACCAGTAAACCTTCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATA
ACCACATCAATCGGGTGCCCCCAAATGCTTTTCTTATCTAAGGCAGCTCTATCGACTGGATA
TGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTTGATGATTTGGACAATATAACAC
AACTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGT
TACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAAAGGTTT
GTGGGATGGCTATTAAGGATCTCAATGCAGAAGCTGTTTGATTGTAAGGACAGTGGGATTGTAA
GCACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCAAGGACAGTGGCCAG
CTCCAGTGACCAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG
GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCATA
TCTCTTGGAACCTTGCTCTACCTATGACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATA
GCCCCGCATTTGGATCTATAACAGAAACAATTGTAACAGGGGAACGCAGTGAGTACTTGGTCA
CAGCCCTGGAGCCTGATTCACCCCTATAAAGTATGCATGGTTCCCATGGAAACCAGCAACCTCT
ACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTTCGAATGTACAACC
CTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACCTTTGG
CTGCCATCATTTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGT
ATGTTTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAA
AGGATGACTATGCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAAACTT
CTTTTCAGATGTTACCAATAAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAATACACACCA
TATTTCCCTCCTAATGGAATGAATCTGTACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAA
GCTACAGAGACAGTGGTATTCCAGACTCAGATCACTCACACTCATGATGCTGAAGGACTCACA
GCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATGGT

FIGURE 384

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTL
YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLK
IPYLEELHLDDNSVSAVSIIEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIST
ISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKL
YLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDLNDITQLILRNNPWYCGCKMKW
VRDWLQSLPVKVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQ
GQWPAPVTKQPDIKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWL
KLGHSPAFGSITETIVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFDETPVCJETETAPL
RMYNPPTTLNREQEKEPYKNPNLPLAAIIGGAVALVTIALALVCWYVHRNGSLFSRNCAYSK
GRRRKDDYAEAGTKKDNSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSES
SSNRSYRDSGIPDSHSHS

Important features of the protein:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645

Amidation site.

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 385

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCCAGGCTTCTTGG
CAGCCCTGCCGGGGCCACTTGTCTTCATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAG
GGCGTGCAGAGGCAGTCTGGGCTTGCCAGAGCTCAGGGTGTGAGCCTGTGACCAGCAGTGA
GCAGAGGCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACC
GCTGTGGTCCCTCCTCACTGCCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCT
GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCT
GGATGGCATGGTGGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGGAGAAGTGGGC
CCAGGAGCCCCCTGCTGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGC
TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCA
GCTGACCCCTCCAGCCCCGGGTTTTGGAAGCTCCCACATGCCTGGATCCACACTGATGCCTCCTT
GGTGTACCCACGTTCCGGGCCCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGT
GCAGCTGCTGGGAACCGGGACGGACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAG
CCTCATGACCAAGCCCCGGCTGCTCAGGCTACTGCCTGTCCCACCAACTGCTCTTCTTCCTCTG
GGCCAGAATGAGGGGATGCACACAGGGACCACTCCAACAGAGCCAGGACTATATCAACCTCTT
CTGCGCCAACATGATGGACTTGAACCGCAGAGCTGAGGCCATCGGATACGCCTACCCCTACCCG
GGACATCTTCATGGAACATCATGTTCTGTGGAATGGGCGGCTTCTCCGACTTCTACAAGCT
CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAAACAGCAGGAAGGATGCTTCGGGGAGCCTGA
TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTTTTCGAGGAGAGTGAA
GAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGTTGCTCAGGCTGGAGTACAGTGGCGCAA
TCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGCAATTCTCTTGCCTCATCCTCCCGAG
TAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAATTTTTTATATTTTTTTAGTAGAGAC
AGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGATCTCAAGAGATCCGCCACCTC
AGGCTCCCAAAGTGTGGGATTATTAGGTGTGAGCCACCGTGTCTGGCTGAAAAGCACTTTCAA
GAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTCATGGGGGCTCTCTCCCC
TAGATGGCTGCTCCTCCCACAACACAGCCACAGCAGTGGCAGCCCTGGGTGGCTTCCTATACA
TCCTGGCAGAATACCCCCCAGCAAACAGAGAGCCACACCCATCCACACCGCCACCACCAAGCA
GCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCCTTTAGTCCTCA
TCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAA
GCCACCCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGGGGCCGGG
AGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAAAAA

FIGURE 386

MSARGRWEGGRRACRGSGLGLARAQGAERVTSSEQRPAMASLGLLLLLLLLLTALPPLWSSSLPG
LDTAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPL
SLRVGMLGEKLEAAIQSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQ
DSFSEERSDVCLVQLLGTGTDSSSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQ
GPLQQSQDYINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS
WQKQQEGCFGEFDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLP
PGFKQFSLILPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

FIGURE 387

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGC
TGCTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGG
GAGGGAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGG
TGAAGCCTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTT
TCCTTAAGACAGATGGGAGTTTTGTGGTTTCATGATATACCTTCTGGATCTTATGTAGTGGAAG
TTGTATCTCCAGCTTACAGATTTGATCCCGTTTCGAGTGGATATCACTTCGAAAGGAAAAATGA
GAGCAAGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAA
TGAAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTC
TAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAG
TGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATT
CCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTG
GCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAAAGGAGGTAAGTCAG
GCCGTCCAGAGCTGGCATTTCACACAAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAA
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCCGACGTTGATCTCTTACAACGTGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGT
ATGAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTTATAGAAAATGCCATTAATAAA
TTATATGAACTACTATACATTATGTATATTAATTAAAACATCTTAATCCAGAAATCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 388

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPQDWIS
AARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVS PAYRFD PVRVDITSKGKMRARYVNYI
KTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMLVPLLI FVLLPKVVNTSDPD
MRREMEQSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:

Signal sequence:

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

FIGURE 389

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCCTCC**ATG**GCGTGGAGCCTTGGGAG
 CTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTCAG
 AATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGGGAA
 CCTGACTTTCACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATACTAC
 CTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTCAGGGC
 TGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCTGTGGATGACACCAT
 TATTGGACCCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTTTCTTAGC
 CCCTAAAATTGAGAATGAATACGAACTTGGACTATGAAGAATGTGTATAACTCATGGACTTA
 TAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCAGTATGACTT
 TGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTTATTGTGTTCAAGTTCGAGGGTTTCTTCC
 TGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACCCATGACGAAAC
 GGTCCCCCTCCTGGATGGTGGCCGTATCCTCATGGCCTCGGTCTTCATGGTCTGCCTGGCACT
 CCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTACGCCTTCTCCCCTAG
 GAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCATAACACACTTCTGTT
 TTTCTCCTTTCCATTGTGCGATGAGAATGATGTTTTTGACAAGCTAAGTGTCATTGCAGAAGA
 CTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGACCCCGCCTGGGCAGGG
 GCCCCAAAGCT**TAGG**CTCTGAGAAGGAAACACACTCGGCTGGGCACAGTGACGTACTCCATCTC
 ACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGACCATCTGAGCCAGCCCCA
 CATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACATTTTAAAGGCTGTCTTGGA
 AAAATACTCCATTTGGGAACTCACTGCCTTATAAAGGCTTTCATGATGTTTTCAGAAAGTTGGC
 CACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAAGATCATGTTTTAATTGTGAGA
 AACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCACCTTAGAGGTCGAGGCAGGCGG
 ATCACTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAATATGGTGAAACCCAGTCTCTACTAA
 AAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTATAATCCCAGCTACTCGAGTGCCTGA
 GGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGAGGTTGCAGTGAGCCGAGATAGCGGC
 ACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAATTGTG
 AGAAACAGAAATACTTAAATGAGGAATAAGAATGGAGATGTTACATCTGGTAGATGTAACAT
 TCTACCAGATTATGGATGGACTGATCTGAAAATCGACCTCAACTCAAGGGTGGTCAGCTCAAT
 GCTACACAGAGCACGGACTTTTGATTCTTTGCAGTACTTTGAATTTATTTTCTACCTATAT
 ATGTTTTATATGCTGCTGGTGTCCATTAAAGTTTTACTCTGTGTTGC

FIGURE 390

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQ
DKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHSDWVNITFCPVDDTIIGPPGMQVEVLADS
LHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCV
QVRGFLPDRNKAGEWSEPVCETTHDETVPSSWMVAVILMASVFMVCLALLGCFSLWCVYKKT
KYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESQKQNPGDSCSL
GTPPGQGPQS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

FIGURE 391

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGA
AGCACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGG
TCCAGACGAGGGGCATCAAGCACAGAATCAAGTGAACCGGAAGGCCCTGCCCAGCACTGCCC
AGATCACTGAGGCCCAGGTGGCTGAGAACCGCCCGGAGCCTTCATCAAGCAAGGCCGCAAGC
TCGACATTGACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCG
ATGGCATCCACTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCT
GCATCAATGCCACCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACC
AGCAGGTGCTCTGGCGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGG
AGAGGGGCGCAGGACTTCGGGTCAACATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGA
TCTGGCTCATGGTGAAATAAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAA
TCCTGGCAAGTGACCCAGCTCTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCAGGAGC
GGCGATGCACTCGCACTGCAAATGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCT
GATAGATGGGGGACTGTGGCTTCTCCGTCACTCCATTCTCAGCCCCCTAGCAGAGCGTCTGGCA
CACTAGATTAGTAGTAAATGCTTGATGAGAAGAACACATCAGGCACTGCGCCACCTGCTTCAC
AGTACTTCCCAACAACCTCTTAGAGGTAGGTGTATTCCCGTTTTACAGATAAGGAAACTGAGGC
CCAGAGAGCTGAAGTACTGCACCCAGCATCACCAGCTAGAAAGTGGCAGAGCCAGGATTCAAC
CCTGGCTTGTCTAACCCAGGTTTTCTGCTCTGTCCAATTCCAGAGCTGTCTGGTGATCACTT
TATGTCTCACAGGGACCCACATCCAAACATGTATCTCTAATGAAATTGTGAAAGCTCCATGTT
TAGAAATAAATGAAAACACCTGA

FIGURE 392

MRKHLSSWWLATVCMLLFSHL SAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQG
RKLDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNK
LHQQVLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

FIGURE 393

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA
TGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCCCT
CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGCCAA
TTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTGAGAG
ATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTCCTTTG
CTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTACCCTGCTTCTC
TGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCAC'TTTGGGCCCTGCCAAGTGAAGGGG
GTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGAT
AACATCACGAGTGCCTCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGC
TGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAAGTGT'TTTCAAAAACCACCACAAT
AGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC'TTTGTTCTCATC
GTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGG
CGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGCC
CTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGCTCTTGAATGTCTAGA
CCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCA'TTCAAACAGTCTCCCTTCC
TATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCTTGGCCCAGGATTATT
GTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAGGTGCCTCTGGATGCTGT
GAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAAC'TCTATTTAATTAATGTCAGTATTT
AACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGGCAGCAGAATATTGTGCCCC
ATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAGTGGATGGGTGCTTAGTAAGT
ACTTAATAAACTGTGGTGCTTTTTTTTGGCCTGTCTTTGGATTGTTAAAAAACAGAGAGGGATG
CTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACTGTCTTCTGATATCTGCAGGGAC
AGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAAAGTAAACGATAAAATGTGGATTAAA
GTGCCCAGCACAAAGCAGATCCTCAATAAACATTTCA'TTTCCCACCCACACTCGCCAGCTCAC
CCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTTATCCTAGTCATTCTTCCCTAATCT
TCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGACATTGCACCTGGATGTACTATCCAATC
TGTGATGACATTCCCTGCTAATAAAAGACAACATAACTCCAAAAAAAAAAAAAAAAAAAAAAAAA
AAAA

FIGURE 394

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPLLATASQMQMVVLPCLGFTLLLWSQVSGAQQQEFHFGPCQVKG
VVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYKTVFKNHHN
RTVEVRTLKSFSSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKA
LGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 395

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT
TTCCTGATGATTTATAGACTCAAAGAAAACTCATGTTTCAGAAGCTCTCTTCTCTTCTGGCCTC
CTCTCTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCA
AGCTGGAAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTTATTTTT
TGAAATTTCACTTTCAGATTCAGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCAT
GATGCTGAGGTTTGGGT

FIGURE 396

MFRSSLLFWPPLCLLSLFLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGT
CEGLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

FIGURE 397

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTG GGGACGGGCAGTTCCCTG
 TGTCTCTGGTGGTTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT
 CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG
 TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG
 GGGAAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTTAGAAACACAAAT
 TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCTGACAGCTCC
 AGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCT
 GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA
 CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTT
 CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA
 TCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT
 GTTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA
 CCCAGCAAATTTGATTTTGTATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA
 AAAAAATCGTGATTAACTTTATCACCCCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA
 TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA
 CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA
 AATTTTTTTGTGACTCTGAAGAAAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAG
 CAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT
 TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT
 ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATACACCCC
 TCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA
 AGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAAACTGGCAGGCTGTGTATTCTTCGCT
 GTCCAGCTTCGACCAGGATTCTAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA
 GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC
 CTATCTCATGCAATTCATGGAGGAATGGGGTTATATGTGCAGATGGAAAAC**TGAT**GGCCAACA
 CTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA
 GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTCTGAGTGTCTGTGAGAA

FIGURE 398

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYF
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQI
GPPEVALTTDEKSISVVLTAPEKWKRNPECLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV
FLFSVMGYSIYRYIHVGKEKHPANLILYGNFDRFFVPAEKIVINFITLNISSDDSKISHQD
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGETSLTQQESLS
RTIPDPKTVIEYEYDVRTTDCAGPEEQELSLQEEVSTQGTLLSQALAVLGPQTLQYSYTP
QLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEE
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 240-260

N-glycosylation sites.

amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,
304-307, 523-526

Tyrosine kinase phosphorylation site.

amino acids 385-392, 518-526

N-myristoylation sites.

amino acids 53-58, 106-111, 368-373, 492-497

Tissue factor

amino acids 1-278

FIGURE 399

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG
CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA
ATCCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACCTAGTGTTGCAACAGGGGAC
TATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAG
GCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAAT
TACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATC
GGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATATATTCTTAATGCAAAT
ATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATA
ATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGT
AAGAAGAATGAGGAGACAGTAGAAGTGAACCTTCAACAACCACTCCCCTGGGAAAACAGATACATG
GCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAA
CAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTG
ACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGC
CCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCT
CTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGG
AGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAGGTT
CTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT
CAAAACCATTGCAGAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATG
GGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCC
AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCAGTGAGAAC
TCTCAAGACCTCTTCCCCCTTGCCCTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCAT
CTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTC
AGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCAT
GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTG

TAG

FIGURE 400

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLI PGDLRDLRVEPVTTSVATGDYS
ILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGF
PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKK
NEETVEVNFTTTPLGNRYMALIQHSTIIIGFSQVFEPHQKKQTRASVVI PVTGDSEGATVOLTP
YFPTCGSDCIRHKGTVVLCPTGTGVPFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH
ERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKIAEMGP
VQWLATQKKAADKVVFLLSNDVNSVCDGTGCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLH
KYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKKQVSAGKRSQACHDGCCSL

Important features of the protein:

Signal peptide:

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201
and 283 - 287

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

FIGURE 401

GGGAACAGGGAACTATCAGCCCGTCGGCCTCCGGGCCCTGCATTCTCTAGCCATGGACCG
GGACCTTTTTCGGGCAGTCGCTAAATTGCCACGGGTCGTCTTTGCTCTCTCTACTTTCGGAG
CGAACAGCAGGACAATCCACACTTCCGTAGCCTCCTGGGGTCGGCCGCCGAGCCAGCCCG
GGGCCCGCCGCCCCAGCACCCGTTGCAGGGCAGAAAAGAGAAGAGAGTTGACAAACATCGA
GATACAGAAATTTCATCTCCAAAAAGCGGATCTGCTTTTTTGCACTTTTCCTGGAAATCAGA
TGCACCTGCAACTTCTGAAATTAATGAAGACAGTGAAGATCATTATGCAATCATGCCACC
TTTAGAGCAATTTCATGGAGATACCTAGTATGGATCGGAGAGAGCTGTTTTTCCGAGATAT
TGAGCGTGGTGATATAGTGATTGGAAGAATTAGTTCTATTTCGGGAATTCGGTTTTTTTCAT
GGTGTGATCTGTTTTAGGAAGTGGTATCATGAGAGATATAGCCCACTTAGAAATCACAGC
TCTTTGTCCCTTAAGAGATGTGCCTTCTCACAGTAACCATGGGGATCCTTTATCATATTA
CCAACTGGTGACATCATTCGAGCTGGAATCAAGGATATTGACAGATACCATGAAAAGCT
AGCAGTATCTCTGTATAGCTCTTCTCTTCCACCACACCTATCTGGTATTAAATTAGGTGT
AATTAGCTCTGAAGAGCTTCCCTTTATACTACAGGAGAAGTGTTGAGCTAAATAGCAATTC
TTTGGAGTCCTATGAAAATGTCATGCAGAGTTCCTTGGGATTTGTTAATCCAGGAGTAGT
TGAATTCCTTCTAGAAAACTAGGAATAGATGAATCTAATCCACCATCTTTAATGAGAGG
CCTACAAAGCAAAAATTTCTCTGAAGATGATTTTGCTTCTGCATTGAGAAAAAACAATC
CGCATCTTGGGCTTTAAATGTGTGAAGATCGGAGTTGACTATTTTAAAGTTGGACGCCA
TGTGGATGCTATGAATGAATACAATAAAGCTTTGGAAATAGACAAACAAACGTGGAAGC
TTTGGTAGCTCGTGGAGCATTATATGCGACAAAAGGAAGTTTGAACAAAGCAATAGAAGA
TTTTGAGCTTGCATTAGAAAACGTCCAACTCACAGAAATGCAAGAAAATACCTCTGCCA
GACACTTGTAGAGAGAGGAGGACAGTTAGAAGAAGAAGAAAAGTTTTTAAATGCTGAAAG
TTACTATAAGAAAGCCTTGGCTTTGGATGAGACTTTTAAAGATGCAGAGGATGCTTTGCA
GAACTTCATAAATATATGCAGAAATCTTTGGAATTAAGAGAAAAACAAGCTGAAAAGGA
AGAAAAGCAGAAAACAAAGAAAATAGAAACAAGTGCAGAAAAGTTGCGTAAGCTCTTAAA
AGAAGAGAAGAGGCTAAAGAAGAAAAGAAGAAAATCAACTTCTTCTTCAAGTGTTTCTTC
TGCTGATGAATCAGTGCTTTCATCATCATCCTCTTCTCTCTGCTCACAAAAGGCATAA
GAAACATAAGAGGAACCGTTCAGAGTCTTCTCGCAGTTCAGAAAGGCATTTCATCTAGGGC
ATCCTCAAATCAGATAGATCAGAATAGGAAAGATGAGTGCTACCCAGTTCAGCTAATAC
TTCAGCATCTTTTCTTAACCATAAACAAGAAGTGGAGAACTACTGGGGAAGCAGGATAG
GTTACAGTATGAAAAGACACAGATAAAAGAGAAAGATAGATGCCCTCTCTCTTCATCTTC
ACTTGAAATACCGGATGATTTTGGAGTGTAATCTTATTTTAAAGTTAACTATAAA
ACAGCCTCAGGCAGGTCTTTCAGGAGATATTCCAGAAGAGGGCATTGTTATCATAGATGA
CAGCTCCATTTCATGTTACTGACCCTGAAGACCTTCAAGTGGGACAAGATATGGAGGTGGA
AGACAGTGGTATTGATGATCCTGACCACGGGTAGGCTTAGGTTTATGTGTGTGTATGTGT
CTTAGTTTTTAAACAAAAAATTAAGTAAAAAACTAAAAATAGAAAAATGCTTAGAG
AATAAGGATATAAAGAATATTTTGTGCAGTTGAACAATGAGTGCTTAAGCTAAATGTCA
TCACAAAAGAGTAAAAAATTTTACAAAATTAAGTGTAAAGTTAAAGCTCTAGG
AAGCTAAGGTCAATTTATTATTGGAGAAATAAATTTATTTTATGAATTTACTGT

FIGURE 402

MDRDLLRQSLNCHGSSLLSLLRSEQQDNPHFRSLLGSAAEPARGPPPQHPLQGRKEKRVD
NIEIQKFISKKADLLFALSWKSDAPATSEINEDSEDHYAIMPPLEQFMEIPSMRRELFF
RDIERGDIVIGRISSIREFGFFMVLICLGSGIMRDIAHLEITALCPLRDVPSHSNHGDPL
SYYQTGDIIRAGIKDIDRYHEKLAVSLSYSSSLPPHLSGIKLGVISSEELPLYRRSVELN
SNSLESYENVMQSSLGFVNPGVVEFLLEKLGIDESNPPSLMRGLQSKNFSEDDFASALRK
KQSASWALKCVKIGVDYFKVGRHVDAMNEYNKALEIDKQNVREALVARGALYATKGSLNKA
IEDFELALENCPTHNRNARKYLCQTLVERGGQLEEEKFLNAESYYKKALALDETFKDAED
ALQKLHKYMQKSLELREKQAEKEEKQKTKKIETSAEKLRLKLLKEEKRLKKRRKSTSSSS
VSSADESVSSSSSSSSSGHKKRHHKRNRSSESRSSRRHSSSRASSNQIDQNRKDECYPVP
ANTSASFLNHKQEVERKLLGKQDRLQYEKTKIIEKDRCPSSSSSLEIPDDFGVYSYLFKKL
TIKQPQAGPSGDIPEEGIVIIDDSSIHVTDPEDLQVGQDMEVEDSGIDDPDHG

Important features of the protein:

Signal peptide:

Amino acids 1-23

Transmembrane domain:

Amino acids 138-155

N-glycosylation sites:

Amino acids 288-292;508-512;542-546

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 300-304;472-476;473-477;517-521;598-602

N-myristoylation sites:

Amino acids 218-224;222-228;271-277;348-354

Amidation site:

Amino acids 52-56

Cell attachment sequence:

Amino acids 125-128

FIGURE 403

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTTC
CAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATA
GGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTT
ATGACAAACTTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAG
AGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCC
CGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCA
CTGCCTACTTTGTGATTCAACCTTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCTGGAGCTC
ACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAAGAAGTACA
TGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTCCAGACTTTG
ACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCCAACTGCACTG
GCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAAATTTGAGAGGC
TCCATCCACTGGTGATCAAGACGGGAAAGCCCCCTGTTGGAGGAAGAGATTCAGCATTTTTTGT
GCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAGTGGTGGCGCTGCT
TTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAACAGATCACAAATGT
TACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATGCCTCTTTAAACAAGT
GCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAGATGCCTGACCTATTTA
TCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCAGTGCCGAAGACATTGTC
AGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCGACACCACCCACTGGAAGG
TCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGATGGAACCGCTTTCTCAGAAC
TGTAGGAAATAGAACTGTGCACAGGAACAGCTTCAGAGCCGAAAACCAGGTTGAAAGGGGAA
AAATAAAAACAAAAACGATGAACTGCAAAAA

FIGURE 404

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIIVVYK
VLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPLHG
GDEDRPFPDFDPWWTNDCEQNESEPI PANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKTGKP
LLEEEIQHFLLCQYPEATEGFSEGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFVFTHL
PFPKASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRHRCQSVAMPIEPGD
IGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

FIGURE 405

TGCCGGGCTGCGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGGCTCCACTCGTCTGCCCCCTGGACTCCC
 GTCTCCTCCTGTCTCCTCCGGCTTCCCAGAGCTCCCTCCTTATGGCAGCAGCTTCCCGCGTCTCCGGCGCAGCTTCT
 CAGCGGACGACCCTCTCGCTCCGGGGCTGAGCCCACTCCCTGGATGTTGCTGAAAC'TCTCGAGATCATGCGCGGG
 TTTGGCTGCTGCTTCCCCGCGGGGTGCCACTGCCACCGCCGCGCCTCTGCTGCCGCGGTCCGCGGGATGCTCAG
 TAGCCCGCTGCCCCGGCCCCCGGATCCTGTGTTCTCGGAAGCCGTTTGCTGCTGCAGAGTTGCACGAAC'TAGTC
 ATGGTGCTGTGGGAGTCCCCGCGGCAGTGCAGCAGCTGGACACTTTTGGAGGGCTTTTGTGGCTGCTGCTGCTG
 CCCGTCATGCTACTCATCGTAGCCCGCCCGGTGAAGCTCGCTGCTTTCCCTACCTCCTTAAGTGACTGCCAAACG
 CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTTCTCTGTGACACCAACACCTGTAAA
 TTTGATGGGGAATGTTTAAAGAAATTGGAGACACTGTGACTTGCGTCTGTGAGTTCAAGTGCAACAATGACTATGTG
 CCTGTGTGTGGCTCCAATGGGGAGAGCTACCAGAATGAGTGTTACCTGCGACAGGCTGCATGCAAAACAGCAGAGT
 GAGATACTTGTGGTGTGTCAGAAAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGC
 TCTGGAGAACTAGTCAAAAGGAGACATCCACCTGTGATATTTGCCAGTTTGGTGCAGAATGTGACGAAGATGCC
 GAGGATGTCTGGTGTGTGTAAATATTGACTGTTCTCAAACCAACTTCAATCCCCCTCTGCGCTTCTGATGGGAAA
 TCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGTGAGAAACAGGAGAAAATTGAAGTCATGTCTTTGGGT
 CGATGTCAAGATAACACAAC'TACAACTACTAAGTCTGAAGATGGGCATTATGCAAGAACAGAT'TATGCAGAGAAT
 GCTAACAAATTAGAAGAAAGTGCCAGAGAACACCACATACCTTGTCCGGAACTTACAATGGCTTCTGCATGCAT
 GGGAAAGTGTGAGCATTCTATCAATATGCAGGAGCCATCTTGCAGGTGTGATGCTGGTTTACTGGACAACACTGT
 GAAAAAAGGACTACAGTGTCTTATACGTTGTTCCCGGTCCTGTACGATTTTCAGTATGTCTTAAATCGCAGCTGTG
 ATTGGAACAATT'CAGATTGCTGTCTATCTGTGTGGTGGTCTCTGCATCACAAGGAAATGCCCCAGAAGCAACAGA
 ATTCACAGACAGAAGCAAAATACAGGGCACTACAGTTT'CAGACAATACAACAAGAGCGTCCACGAGGTTAATCTAA
 AGGGAGCATGTTTACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATACAGTATTATAGACAAAAGAATAA
 GACAAGAGATCTACACATGTTGCCTTGCATTTGTGGTAATCTACACCAATGAAAAACATGTACTACAGCTATATTT
 GATTATGTATGGATATATTTGAAATAGTATACATTGTCTTGATGTTTTTTCTGTAATGTAAATAAACTATTTATA
 TCACACAATATAGTTTTTTCTTCCCATGTATTTGTTATATATAATAAATACTCAGTGATGAG

FIGURE 406

MVLWESPRQCSSWTLCEGFCWLLLLPVMLLIVARPVKLAAFPTSLSDCQTPTGWNC SGY
DDRENDLFLCDTNTCKFDGECLRIGDTVTCVCQFKCNNDYVPVCGSNGESYQNECYLRQ
AACKQQSEILVVSEGSCATDAGSGSGDGVHEGSGETSQKETSTCDICQFGAECDEDAED
VWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLGRCQDNTTTTTTK
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSRCRDAGY
TGQHCEKKDYSVLYVVPVPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRQ
KQNTGHYSSDNTTRASTRLI

FIGURE 407

CTCGCAGCCGAGCGCGGCCGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCCTGGCAG
ACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCTGT
GTCCAGACTGAGGCCCCATTTGCATTGTTTAACATACTTAGAAAATGAAGTGTTCATTTTTAA
CATTCCTCCTCCAATTGGTTTAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGTGCTT
GCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGCGCTCTCCCCGTGTCTCTCCACGACT
CGCTCGGCCCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGCCGACGTGCC
CGAGCTCCTCCGGGGGTCCCCGCCGCGAGCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCG
TCTTGAGACATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTCCAA
GCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGT
GTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTTA
ACCAAAATGGCGGGTATTTATGCATTCCCCGACAAAACCTGTGTATCGAGGGCCCTACTCGA
ACCCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAA
ACTATCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATGAAAGCAACC
AATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCACCCAGATCTGCA
TCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCAGT
GCTTAGACATTGATGAATGTGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCTTGAT
CCTATTCTTGATACATGCAACCCTGGTTTTACCTCAATGAGGATGGAAGGTCTTGCCAAGATG
TGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCTGCGTCAACACCTACGGCTCTCTCA
TCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTCATTGCAGTGATATGGACG
AGTGCAGCTTCTCTGAGTTCTCTGCCAACATGAGTGTGTGAACCAGCCCCGGCACATACTTCT
GCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAAT
GTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCA
AATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGT
GTCCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTACCATCTTGTAACCGGGACATGGACG
TGGTGTGAGGACGCTCCGTTCCCGCTGACATCTTCCAAATGCAAGCCACGACCCGCTACCCCTG
GGGCCTATTACATTTTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTTTACATGCGGCAAA
CGGGCCCCATCAGTGCCACCCCTGGTGATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGC
TGGACTTGGAATGATCACTGTCAACACTGTCACTTCAAGGTCAGAGGCAGCTCCGTGATCCGAC
TGCGGATATATGTGTGCGCAGTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCT
CATTGGCACCAAGGGACAGGAGAAGAGAGGAAATAACAGAGAGAATGAGAGCGACACAGACGT
TAGGCATTTCTGCTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCTGACTCTCACCTGTA
CTATTGCAGACCTGTCAACCTGCAGGACTTGCCACCCCCAGTTCCTATGACACAGTTATCAAA
AAGTATTATCATTGCTCCCCGTAGAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATT
TCCACTATTTTCAAAGAAAATAGATTAGGTTTGGCGGGGTCTGAGTCTATGTTCAAAGACTGT
GAACAGCTTGCTGTCACTTCTTCACTCTTCCACTCCTTCTCTCACTGTGTACTGCTTTGCA
AAGACCCGGGAGCTGGCGGGGAACCTGGGAGTAGCTAGTTTGCTTTTTGCGTACACAGAGAA
GGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTAGAGAATGTGTTCAAACCATGC
CTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAAATTTGTATAACGGTTTAATTCT
GTCCTGTTTCAATTTTGAATTTTTTAAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGA
CACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCTCCATTTTAGCCAGTGTTTTCTTT
GAGGACCCCTTAATCTTGCTTTCTTTAGAATTTTACCCTAATTGGATTGGAATGCAGAGGTCT
CCAACTGATTAAATATTTGAAGAGA

FIGURE 408

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSLICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248, 267-273, 310-316

Aspartic acid and asparagine hydroxylation sites.

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

FIGURE 409

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTCA
 GGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTGTT
 TCGCTGGTCCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGTGTT
 TCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCTTACATTGAAGCTGGG
 AAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCAGGACTGAACATGAAGAGT
 TATGCCGGCTTCCTCACCCTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTCTTCCCA
 GCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGGAGGTTCA
 TCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCAACAAGTAACATGACCTTGCGT
 GACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCAGTGGGCACA
 GGCTTCAGTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGTAGCACGGGAT
 TTATACAGTGCACCTAATTCAGTTTTTCCAGATATTTCTGAATATAAAAAATAATGACTTTTAT
 GTCAGTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTCATCCATTCCCTC
 AACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGATGGATATTCTGAT
 CCCGAATCAATTATAGGGGGCTATGCAGAATTCTGTACCAAATTGGCTTGTGATGAGAAG
 CAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATCAGGAAGCAGAACTGG
 TTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAACAAGTGATCCTTCTTAC
 TTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTTTCGGGTGCACGGAACCTGAGGAT
 CAGCTTTACTATGTGAAATTTTTGTCACTCCAGAGGTGAGACAAGCCATCCACGTGGGGAAT
 CAGACTTTTAATGATGGAACATAGTTGAAAAGTACTTGCAGAGAAGATACAGTACAGTCAGTT
 AAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGATCTACAATGGCCAACTGGAC
 ATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGCATGGACTGGAAAGGATCCCAG
 GAATACAAGAAGGCAGAAAAAAAAGTTTGAAGATCTTTAAATCTGACAGTGAAGTGGCTGGT
 TACATCCGGCAAGCGGGTGAATCCATCAGGTAATTATTCGAGGTGGAGGACATATTTTACCC
 TATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGATTCAATTTATGGAAAAGGATGGGAT
 CCTTATGTTGGATAAACTACCTTCCCAAAGAGAACATCAGAGGTTTTTCATTGCTGAAAAGAA
 AATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAATTATCTTTTCATATCTGCAAGATTTT
 TTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGCTTTTGTTTTTTGGGGGGAGATGTTTACT
 ACAAATTAACATGAGTACATGAGTAAGAATTACATTATTTAACTTAAAGGATGAAAGGTATG
 GATGATGTGACACTGAGACAAGATGTATAAATGAAATTTTAGGGTCTTGAATAGGAAGTTTTA
 ATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTGTAACAAACAAAGCTGTAACATCTTTTCTG
 CCAATAACAGAAGTTTGGCATGCCGTGAAGGTGTTTGGAATATTATTTGGATAAGAATAGCTC
 AATTATCCCAAATAAATGGATGAAGCTATAATAGTTTTGGGGAAAAGATTCTCAAATGTATAA
 AGTCTTAGAACAAAAGAATTCTTTGAAATAAAAAATATTATATATAAAAGTAAAAAAAAA

FIGURE 410

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPPKGD SGQPLFLTPYIEAGKIQKGRELSLV
GPFPGGLNMKSYAGFLT VNKT YNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGP
YVVT SNMTLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F F Q I
FPEYKNND FYVTGESYAGKYVPAIAH L I H S L N P V R E V K I N L N G I A I G D G Y S D P E S I I G G Y A E F
L Y Q I G L L D E K Q K K Y F Q K Q C H E C I E H I R K Q N W F E A F E I L D K L L D G D L T S D P S Y F Q N V T G C S N Y Y
N F L R C T E P E D Q L Y Y V K F L S L P E V R Q A I H V G N Q T F N D G T I V E K Y L R E D T V Q S V K P W L T E I M N N Y
K V L I Y N G Q L D I I V A A A L T E R S L M G M D W K G S Q E Y K K A E K K V W K I F K S D S E V A G Y I R Q A G D F H Q V
I I R G G G H I L P Y D Q P L R A F D M I N R F I Y G K G W D P Y V G

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 411

GCAAGCCAAGGCGCTGTTTGTAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CCTGGCCACACTCTTCAAGATCCTGGGCGTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCCGTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC
CAGCATTTGCCAGCTCACGGGCCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT
GGCCTTCCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAACGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGGCGTGACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAGCTCATCGTCCCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCAGCACCT
GCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACAA
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCCTCCCTGCGGACATCGGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG
CAACCGGCTGGAGTGCTGCTGTGGAGCTGGGCGAGTGCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG
GCCGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTTCAGGCCCGAGGGGCAGGCCCTAGCTTCTCCAG
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGGCTGGCCCCCTTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGCTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG
CTGCCACCAGAGGTCTGGGACCCCTCACTTTAGTTCCTTGGTATTTATTTTTTCTCCATCTCCCACCTCCTTCATCC
AGATAACTTATACATTCCCAAGAAAGTTCAGCCCAGATGGAAGGTGTTTCAAGGAAAGGTGGGCTGCCCTTTCCCC
TTGTCTTTATTTAGCGATGCCGCCGGGCATTTAAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCAG
CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCTCCAGCTGGA
AAGGCCAGGCCTGGAGCTTGCTCTTCAGTTTTTGTGGCAGTTTTAGTTTTTTTGTTTTTTTTTTTTAAATCAAA
AAACAATTTTTTTTTTAAAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAAAAGAAAAAAAACCTAAAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAGCCAGACGT
TGAAGTGTGTTTCTTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTTCTTGGGAGGGAGGTTTTTTGTTTTGTTTTTTGGGTTTTTTTTGGTGTCTTGTTTTTCTTCTCTCC
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGGATGAACGGTGTCTCATTCGCACCTCCCCCTCCTCGTGCCTGCCCTGCCTCTCCA
CGCACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTCCCCACCTCCTGCGGCATGGGTGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCCCACCTGGTCTTTCATGAAGAGCAGACACTTA
GAGGCTGGTCCGGAATGGGGAGTTCGCCCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGC
CTGGAGTGCACACAGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCCCTTAGATCAATCACGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACTTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAAAA

FIGURE 412

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYIS
LVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKRF
AVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHLFMLSGIPDTVFDLVELEVLKL
ELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWIYSLK
TLEELHLTGNLSEAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSINNEG
KLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQHLHRLT
CLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLTFLPADIG
LLQNLQNLAITANRIETLPPPELFQCRKLRALHLGNNVLQSLPSRVGELTNLTQIELRGNRLEC
LPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 413

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCATC
TTCATCATTCATATGAGGAAATAAGTGGTAAAATCCTTGGAAATACAATGAGACTCATCAGAA
ACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAGAAG
AAAGGGAACTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTGACCC
CAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTCAACTCCAGAGTTTCAAGATTTT
ATTCTGTCTCCAAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCAACAGCTGGATCTCA
AAACCTTTGAATTCACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTGAAGAGTG
TAACTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTAATGACTTTGACACCA
TGCCTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCCTAGGTTTGAGTGGGGCAA
AAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTCTTCTTAGGAT
TCAGAATCTTCTCATTATGAAGAAGGTAGCCTGCCATCTTAAACACAACAAAATGCACA
TTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGGTGATGGAATCAAGACTTCAAAAA
TATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAAATGCAACGAAATC
TTAGTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGATTTACTCTGGGACG
ACCTTTTCCTTATCTTACAATTTGTTTGGCATAACATCAGTGGAAACACTTTTCAAGATCCGAAATG
TGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTACTCAAATACTGTAATGA
GAACTATAAAATGGAGCATGTACATTTCAAGAGTGTTTTACATTCAACAGGATAAAATCTATT
TGCTTTTGACCAAAATGGACATAGAAAACCTGACAAATATCAAATGCACAAATGCCACACATGC
TTTTCCCGAATTATCCTACGAAATTCGAATATTTAAATTTTGCCAATAATATCTTAACAGACG
AGTTGTTTAAAGAAGTATCCAACCTGCCTCACTTGAAAATCTCATTTTGAATGGCAATAAAC
TGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAACACACCCTTGGAACACTTGGATCTGA
GTCAAAATCTATTACAACATAAAATGATGAAAATTTGCTCATGGCCAGAACTGTGGTCAATA
TGAATCTGTACATAAATAATTTGTCTGATTCTGTCTTCAAGTGCTTGCCCAAAAGTATTCAAA
TACTTTGACCTAAATAATAACCAAAATCCAAACTGTACCTAAAGAGACTATTCATCTGATGGCCT
TACGAGAATAAATATTGCATTTAATTTTCTAACTGATCTCCCTGGATGCAGTCATTTCAAGTA
GACTTTCAGTTCTGAACATTGAAATGAACCTTCACTCTCAGCCCATCTCTGGATTTTGTTCAGA
GCTGCCAGGAAGTTAAAATCTAAATGCGGGAAGAAATCCATTCGGGTGTACCTGTGAATTAA
AAAATTTCACTCAGCTTGAACATATTCAAGGTCATGATGGTTGGATGGTCAGATTCATACA
CCTGTGAATAACCTTTAAACCTAAGGGGAAGTAGGTTAAAAGACGTTCACTCTCCACGAATTAT
CTTGCAACACAGCTCTGTTGATTGTCAACATTGTGGTTATTATGCTAGTTCTGGGGTTGGCTG
TGGCCTTCTGCTGTCTCCACTTTGATCTGCCCTGGTATCTCAGGATGCTAGGTCAATGCACAC
AAACATGGCAGAGGTTAGGAAAACAACCCAAGAACAACCTCAAGAGAAATGTCCGATTCCACG
CATTTATTTTACATACAGTGAACATGATTCTCTGTGGGTGAAGAATGAATTGATCCCCAATCTAG
AGAAGGAAGATGGTTCTATCTTGATTGTGCTTTATGAAAGCTACTTTGACCTTGGCAAAAGCA
TTAGTGAAAATATTGTAAGCTTCACTTGAGAAAAGCTATAAGTCCATCTTTGTCTTCTCCCA
ACTTTGTCCAGAATGAGTGGTGCCATTATGAATTTCTACTTTGCCCACCACAATCTCTTCCATG
AAAATTTCTGATCATATAATTTCTTATCTTACTGGAACCCATTCCATTCTATTGCATTCCACCA
GGTATCATAACTGAAAGCTCTCCTGGAAAAAAGCATACTTGGAATGGCCCAAGGATAGGC
GTAAATGTGGGCTTTTCTGGGCAAACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCA
GAGAAATGTATGAATGCAGACATTCAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCT
CTCTGATGAGAACAGATTGTCTATAAAATCCCACAGTCCTTGGAAGTTGGGGACCACATACA
CTGTTGGGATGTACATTGATACAACCTTTATGATGGCAATTTGACAATATTTATTAATAAAA
AAATGGTTATTCCCTTCATATCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACA
CCTTCACAAGTTTATAAGGGCTTATGGAAAAAGGTGTTTCATCCCAGGATTGTTTATAATCATG
AAAAATGTGGCCAGGTGCAGTGGCTCACTCTTGTAATCCCAGCACTATGGGAGGCCAAGGTGG
GTAGCCACGAGGTCAAGAGATGGAGACCATCTGGCCAAACATGGTGAAACCTGTCTCTACT
AAAAATACAAAATTTAGCTGGGCGTGATGGTGACGCCTGTAGTCCCAGCTACTTGGGAGGCT
GAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTG
CACTCCAGCCTGGTGACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAA
ATGGAAAACATCCTCATGGCCACAAAATAAGGTCTAATTCAATAAATTTATAGTACATTAATGT
AATATAATATTACATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTTGGTATGGAAAAA
CATATTAATATTGTTATAAACTATTAGGTTGGTGCAAAACTAATTGTGGTTTTTGGCCATTGAAA
TGGCATTGAAATAAAAGTGTAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGCTGG
GAGGTTGGATTACAGGGAGCATTTGATTTCTATGTTGTGTATTTCTATAATGTTTGAATTGTT
TAGAATGAATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

FIGURE 414

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQL
QSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSF
NDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLPILN
TTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLLLNV
DLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFIQ
QDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLPHLKTLI
LNGNKLETLSLVSCFANNTPLEHLDLSONLLQHKNDENC SWPETVVNMNLSYNKLSDSVFRCL
PKSIQILDNLNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHF SRLSVLNIE MNFILSPS
LDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLNLRGTRLDV
HLHELSCNTALLIVTIVVIMLVGLAVAFCC LHFDLPWYLRMLGQCTQTWHRVRKTTQEQLKR
NVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI
FVLSPNFVQNEWCHYEFYFAHHNLFHENS DHII LILLEPIPFYCIPTRYHKLKALLEKKAYLE
WPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLMRTDCL

FIGURE 415

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCGGGCCGAGCCACCTCTTCCCCCTCCCCCGC
TTCCCTGTGCGGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT
CGGCAAAGTTTGGCCGAAGAGGAAGTGGTCTCAAACCCCGGAGGTGGCGACCAGGCCAGACCAGGGGCGCTCG
CTGCCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG
AGAAGAGTGGCGGCGGCGACGGAGAAAACAATCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG
CCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG
CACCAGGGAGCCTGGGCGCCCCGGGGCTCCGCGCGCACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTCCG
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG
ACCGGATTATTTTTCCAAATCATGCTTGTGAGGACCCCCAGCAGTGCTCTTAGAAGTGCAGGGCACCTTACAGA
GGCCCCTGGTCCGGGACAGCCGCACCTCCCTGCCAACTGCACCTGGCTCATCTGGGCGAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCCCTACGCTCCCTCTCCAGCCAC
TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCCGGGGCAACGTCACCATCACTTACAGCTATG
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCCTGCTCTCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG
AGTTTCAGTGCCCTGAACACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCTCCCTGCCCTTGCAATG
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCCAACCCCGAGT
CCTGCCATTGGCTGTGAGACCCCATGATGGCCGGCGGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGCTTTG
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCCACTTCA
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGCCAGGCTGTGTGTCTTACCACACAGTTGCTTGGAGCA
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCTTGGGACAGACCCCTGTGGCTTAGGCT
CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACCGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGCTGGCACCT
CTGGTGCCACAGCCTGCTACCTGCCCTGCTGACCGCTGCAACTACCAGACTTCTGTGCTGATGGAGCAGATGAGA
GACGCTGTCCGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCGCAAGGTCATTACAG
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA
TTCCGACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC
CTTCTACGGGCAGCTATTGCCAGGGTGCCATCCACCTGTAGAAGACTTTCTACAGAGAATCCTAATGATA
ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG
CCCCCGTCGTGACGGGGCGCTTGATGCGACGCTGTTACGCCCTCTCCGCCGCTGGGGCTTGCTCCCTCGAA
CCAACACCCCGGCTCGGGCTCTGAGGCCAGATCCAGGTACACCTTCTGCTGCTCCCTTGAGGCCCTAGATG
GTGGCACAGGTCCAGCCCGTGAGGGCGGGGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCACTGCCCATCA
AGGCTCCCTCCCATCTGCTAGCACGTCTCCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
TGCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGACGGCCCTGCCAGGCCGCTGTTGCCAGCCTGGGGCCCC
CAGGACCAACCCGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACC**TGA**GGGGACCTGGGGG
CTCTACTGAGGCCTCTCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCCCTCC
ACCACTTCTTCCCTGTCCCTGGATTTCAGGGACTTGGTGGGCCTCCCGTTGACCCATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT
TCACCACCACTGTCTCCACGCCACCAACCATTTGGGTGGCTGTTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA
GGTCTGGACACTCCATCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGA
CCCTCCAGCCCCCAAGGGAGGATTGGGCAGAACCTGAGGTTTGGCCATCCACAATCCCTCCTACAGGGCCTGG
CTCACAAGAGAGTGAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
GGAATCATACATCTC

FIGURE 416

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit`1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPDRIIFPNHACEDPPAVLLEVQGTLQRPPLVRDSRTSPANCTWLILG
SKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAPMG
QGFLLSYSQDWLMCLQEETFQCLNHRCVSAVQRCGDGDGSDGAGCSDPFPGLTTPRPVPS
LPCNVTLEDFYGVFSSPGYTHLASVSHPOQCHWLLDPHDGRRRLAVRFTALDLGFGDAVHVYDG
PGPPESSRLRLSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGNATYHVRGYCLPWDRPC
GLGSGLGAGEGLGERCYSEAQRCDSWDCADGTDEEDCPGCPPGHFPCGAAGTSGATACYLPA
DRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPDGSDGDEWDCSYVLPKRV
ITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSYGOLIAQGA
IPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGRRLMRRLVRRLRRWGLLP
RTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKAPLPSASTSPA
PTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGPPGPTRSPPGPHTAVLALEDEDDVLL
VPLAEPGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 417

GTCGTTCCCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTGCGAGGAGAGCACCCGGA
 GACGCGGGCTGCAGTCGCGCGGCTTCTCCCCGCCTGGGCGGCTCGCCGCTGGGCAGGTGCTGAGCGCCCTAG
 AGCCTCCCTTGCCGCCTCCCTCCTCTGCCCCGGCCGAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG
 GCCCGGGAGCGCGCGGTGGATGCGGCGCTGGGCAGAACGAGCCGCGGATTCCAGCTGCCCCGCGCGCCCCGGGCG
 CCCCTGCGAGTCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATC
 GCCCGCCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCCCTTAGCACCACCACAGCTCAG
 CCAGAACAGAACGCCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCAGGCGCAGGTGCTAACCTGT
 GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT
 GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG
 ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCAC'TTGCCACCTGGCATGTTCCAGTCTAACGCT
 ACCTGTGCCCCCATACGGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
 TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT
 CTGAGTCAGAACCTGGTGGTGTATCAAGCCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCTTTC
 TCCAGCTCCACCTCACCTTCCCTGGCACAGCCATCTTTCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT
 TCCTCCACTTATGTTCCCAAAGGCATGAATCAACAGAAATCCAACTCTTCTGCCTCTGTTAGACCAAAGGTACTG
 AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGAAGGAAGACGTGAACAAGACCCCTC
 CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG
 GCCACTGGGGGCGAGAAGTCCAGCACGCCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACTACACAAG
 CATTTTGACATCAATGAGCATTGCGCTGGATGATTGTGCTTTTCTGCTGCTGGTGTGTTGTGGTGATTGTGGTG
 TGCAGTATCCGAAAAGCTCGAGGACTTGAAAAGGGGGCCCCGCGCAGGATCCAGTGCCATTGTGAAAAGGCA
 GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGATATCGAT
 ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG
 AGGGAGTTGCTGCTTTCTCAATGGGTACACAGCCGACCACGAGCGGGCCTACGCAGCTCTGCAGCACTGGACC
 ATCCGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG
 AAGATTGCTGGGCTGATGGAAGACACCACCCAGCTGGAACTGACAACTAGCTCTCCCGATGAGCCCCAGCCCCG
 CTTAGCCCCGAGCCCCATCCCCAGCCCCAACCGGAACTTGAGAATTCGCTCTCCTGACGGTGGAGCCTTCCCCA
 CAGGACAAGAACAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC
 TCCGCGCTGAGCAGGAACGGTTCCTTTATTACCAAGAAAAGAAGGACACAGTGTGCGGCAGGTACGCTGGAC
 CCCTGTGACTTGACGCTATCTTTGATGACATGCTCCACTTCTTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG
 ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTGCAAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
 CTCCTGGACTCTGTTTATAGCCATCTTCCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAATTAATCA
 ATTTAGTGGCAGGGTGGTTTTTTTAAATTTCTTCTGTTTCTGATTTTTGTGTTTGGGGTGTGTGTGTGTGTTGT
 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAAGTGTGTGAA
 ATACCCCACTAAAGTTTTTTTAAAGTTCATATTTTCTCCATTTTGCCTTCTTATGTAATTTCAAGATTATTCTG
 TGCATTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC
 TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT
 AAAAAAATAATTATTACTATTTTATATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAGAAAAATTAAGA
 CCCCATTGAGTTACTGTAATGCAATCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTCAATTCATGG
 CTGAACTTGACCACACTATTGCTGATTGTATGGTTTACCTGGACACCGTGTAGAATGCTTGATTGATTGTTGATC
 TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
 GACAACCTGGGCCACCAAAGAACTGAACTTCACTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT
 GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG
 TTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGGTGGGATTCCTTCACCAATT
 ACTTTAATTAATAATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTGCAACTATGCTCCCATTTACAAATG
 TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTGTGG
 GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTGA
 AAAAAAAA

FIGURE 418

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATGQ
VLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMIEKLPAAAL
TDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKCKAY
TDCLSQNLVVIKPGTKETDNVCGTLPSSFSSSTSPSPGTAFPRPEHMETHEVPSSTYVPKGMN
STESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHILKLLPS
MEATGGEKSSTPIKGPGRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRKSSRTLK
KGPRQDPSAIVEKAGLKKSMPTPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNAS
EREVAAFSNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQL
ETDKLALPMSPLSPSPPIPSNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRCDSTSSGS
SALSRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFE
IIGVKSQEASQTLLDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

FIGURE 419

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
 ATCACCGCCTGGCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
 AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
 GCACTGCTTCTGGGCTGCCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCCTTACA
 GAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTAC
 CAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
 CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAACACCAACCTTCAACTCCAGCAGTGAAGCTGAG
 CAGAAGACACAGCGCTTCTACCTATCTTGCTTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGA
 GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG
 GCAGTAGCAGGGACCTACAGGGCCACCCATTCTTACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC
 AATGTTATCCAGGTGGACCAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
 AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
 GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGGCGCGAC
 GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC
 CTGTCTTTCTTGCTGTCAACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
 CAGGTGTGAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
 ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTCTATGGCACTAAGAAG
 TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
 GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG
 GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT
 GATATGATTGGTTTCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
 GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACCTTCTCTGCCAAGGTATGGCTGACCAGCTCCGCAAG
 CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC
 GTCTTCCCCGCTGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACCTTCGGTGGCATC
 GGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGGAGTATGACAAAGAAGGGAACCTG
 CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAGTACAATCAA
 TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG
 GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
 AACCACCAGCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG
 CTGGTGACCGACCCCAACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCTTGCGG
 CACTTCGGCTGCCCTGTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA
 GAAATGGCCAGCTGTCACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTGGGAGGAAGCAA
 ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCACCAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG
 TGCTCTGCTTTGGGGGTGCCCTGCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTACCCCT
 GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

FIGURE 420

MNVALQELGAGSNVGFQKGTQRLGSRQTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHS
TCLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL
KHLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDNFME
VLKAVAGTYRATPFFTUYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVLTAAYLDYM
EELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAPSMDWL
EFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSLDRRFES
AQEKLETLTYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMISEIRTA
EEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLY
NFSKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFYARNHPKALNFGGI
GVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQVNGERLNGRQT
LGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGL
VTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGLCEVW

Type II Transmembrane domain:
amino acids 32-57

FIGURE 421

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGCC
GCCTCTCCGCACGATGTTCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGCAG
GTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGCCTG
CCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGGCCCG
GGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAGCCGCC
CCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGTGCCCTT
CCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCTGAGCAGGAA
GAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAACCGGGCAGC
GCTCATCAACGTGGGCTTCTTGGAGAGCAGCAACAGCACGGACTACATTGCCATGCACGACGT
TGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGCCCTTCCACGT
GGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGCATCCTGCTGCT
CTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGGCTGGGGCCGCGA
GGACGACGAGTTCTACCGGCGCATTAAAGGGAGCTGGGCTCCAGCTTTTCCGCCCCCTCGGGAAT
CACAACTGGGTACAAGACATTTCCGCCACCTGCATGACCCAGCCTGGCGGAAGAGGGACCAGAA
GCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGGAGGCCTGAACACTGT
GAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGCCCCCTGCACTGTCTCAA
CATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTGAGCTGAGCTGGATGGAC
AGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGACAAGGCCTCAGGTCGTGG
GCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCAAGCTACGCAATTGCAGCCA
CCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGGGTGCCTGGGACGCTGCTTGC
CATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCCTGTCCGGGACCCCCCTGCCTTCTGCT
TCACCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGA
CAACCTCTCATCACCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGG
CTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

FIGURE 422

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVRG
QGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKIRH
HIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVASPE
LHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGITTGY
KTFRHLHDPAWRKRDKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVLNIMLD
CDKTATPWCTFS
```

Signal peptide:
amino acids 1-42

Transmembrane domain:
amino acids 29-49 (type II)

N-glycosylation site.
amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 27-31

Tyrosine kinase phosphorylation site.
amino acids 226-233

N-myristoylation site.
amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 423

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGATC
TCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCCTGGATGCT
GCTTTCCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCCCTC
TCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGTTTTT
GTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAACCTGGT
GTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAGTAACAG
CTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATGGAGATGG
ATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCCTCCACCAT
CTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTGGAAGATTA
TAACTGTGATGCAAAGTTACCCCTATGTCTGCAAGTTCAAGGACTTAGGGCAGGTGGGAAGTCAG
CAGCCTCAGCTTGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGACTCACCCCTGGAA
GAGAATATTCTCCCCAAACTGCCCTACCTGACTACCTTGTGTCATGATCCTCCTTCTTTTTCCTT
TTTCTTCACCTTCATTTCAAGGCTTTTCTCTGTCTTCCATGTCTTGAGATCTCAGAGAATAATA
ATAAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 424

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWMD

ADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSSTD

VMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

FIGURE 425

CGGACGCGTGGGCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTGG
CTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGGTC
AACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTGAAT
GTGGCCAGCGAGTGC GGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCGAGAC
CTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGGAGCCT
GACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCCATGTTT
AGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCAGACTTCT
GGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGGTGGTAGGG
GCTTGGGACCCAACCTGTGTGAGTGGAGGAGGTCAGACCCCAGATCACAGCGCTCGTGAGGAAG
CTCATCCTACTGAAGCGAGAAGACTTATATAACCACCGCGTCTCCTCCTCCACCACCTCATCCCG
CCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCCTTCAAAGGGAGAGACCCACTGA
CTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAAAAATTCTAGTAT
TTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAGAGCTCTTGACCAG
TGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAATAGAAGTATATCAA
GCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTACCTCATAGGGCTGTTG
TGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGCCAAATAGGAGGCATTC
AATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAATAAAAACTTGCATCCAAC
ATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTTGTTATTTCTCTGTATTA
TTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCAAACAATACCTCACGATATA
AAATAAAAATGAAAGTATCCTCCTCAAAAA

FIGURE 426

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVVNVASECGFTDQH
YRALQQQLQRDLGPHHFNVLAFCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTGAH
PAFKYLAQTSGKEPTWNFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

FIGURE 427

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGCC
TTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTCTT
CTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGCTTT
GCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCTTCAT
GATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCAAATTT
TTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTTAGGTTT
AAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTATTATCTTCACTA
TTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTTTATCCCTG
GGTGCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAATGTTATTCT
AATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTTAAAAGTTTTG
AGTATATTTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

FIGURE 428

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

FIGURE 429

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCTG
CACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGTGCTGACCATCTTT
GGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGCAAT
GTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGCAGGA
TCATGCTCTTCTACCACAATTTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGCTCTCC
CGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAATCTCCAA
TGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTGGGTCAAG
TACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCACCCATTGAG
AAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACATAATGTCGGT
GCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTGTGCAGACATT
CATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCCTTGGTTTACAC
TCAAAGTCAAATTAAATTCTTTCCCAATGCCCCAACTAATTTTGAGATTCAGTCAGAAAATA
TAAATGCTGTATTTATA

FIGURE 430

```
><ss.DNA57834
><subunit 1 of 1, 176 aa, 1 stop
><MW: 19616, pI: 7.11, NX(S/T): 0
MVLTIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTTIFDYKH
GYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLESLIK
DVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV
```

Important features:

Signal peptide:

Amino acids 1-26

N-myristoylation sites:

Amino acids 48-54;153-159;156-162;167-173

FIGURE 431

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCCA
CAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTATCA
GAGACATTGAGAGGCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTATTT
TGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAATCAT
GACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGATGGAGA
GTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAACTTGATCAAATAAA
GGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGAGTGTGGG
CAGACACTTTTTTGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGGTCACTGTC
CAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGATGGATAGTA
GCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACATCGACCTCAG
AAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 432

MSRSSKVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILTE
QLEAEREKMLLAKGSQKS

FIGURE 433

GAATTCGTGTCTCGGCACTCACTCCCGGCCCGCCGACAGGGAGCTTTTCGCTGGCGCGCTTGGCCGGCGACAGGA
 CAGGTTCCGGACGTCCATCTGTCCATCCGTCCGGAGAGAAATTACAGATCCGCAGCCCCGGGATGGGGCCGGCCC
 CGCTGCCCGCTGCTGGGCCTCTTCCCTCCCGCGCTCTGGCGTAGAGCTATCACTGAGGCAAGGGAAGAAGCCA
 AGCCTTACCCGCTATTCCCGGGACCTTTTCCAGGGAGCCTGCAAACTGACCACACACCGCTGTATCCCTTCCTC
 ACGCCAGTGGGTACCAGCCTGCCTTGATGTTTTTACCACCCAGCCTGGAAGACCACATACAGGAAACGTAGCCATT
 CCCCAGGTGACCTCTGTGCAATCAAAGCCCCCTACCGCCTCTTGCCCTTCAAACACACAGTTGGACACATAACTT
 TCTGAACATAAAGGTGTCAAATTTAATTGCTCAATCAATGTACCTAATATATACCAGGACACCACAATTTCTTGG
 TGGAAAGATGGGAAGGAATTGCTTGGGGGACATCATCGAATTACACAGTTTTATCCAGATGATGAAGTTACAGCA
 ATAATCGCTTCTTACAGATAACCAGTGTGCAGCCTTACAGACAATGGGTCGTATATCTGTAAGATGAAAAATAAC
 AATGAAGAGATCGTGTCTGATCCCATCTACATCGAAGTACAAGGACTTCTCACTTTACTAAGCAGCCTGAGAGC
 ATGAATGTCACCAGAAACACAGCCTTCAACCTCACCTGTGAGGCTGTGGGCCCGCCTGAGCCCCGTCAACATTTTC
 TGGGTTCAAACAGTAGCCGTGTTAACGAACAGCCTGAAAAATCCCCCGCGCTGCTAACTGTTCCAGGCCTGACG
 GAGATGGCGCTCTTCAAGTTGTGAGGCCACAAATGACAAAGGGCTGACCGTGTCCAGGGAGTGCAGATCAACATC
 AAAGCAATTCCTTCCCCACCAACTGAAGTCAGCATCCGTAACAGCACTGCACACAGCATTCTGATCTCCTGGGTT
 CCTGGTTTTGATGGATACTCCCCGTTCAAGGAATTGCAGCATTCAGGTCAAGGAAGCTGATCCGCTGGGTAATGGC
 TCAGTCATGATTTTTTAACACCTCTGCCTTACCACATCTGTACCAATCAAGCAGCTGCAAGCCCTGGCTAATTAC
 AGCATTGGTGTCTTCTGCATGAATGAAATAGGCTGGTCTGCAGTGAGCCCTGGATTCTAGCAAGCAGACTGAA
 GGAGCCCCATCAGTAGCACCTTTAAATGTCACTGTGTTTCTGAATGAATCTAGTGATAATGTGGACATCAGATGG
 ATGAAGCCTCCGACTAAGCAGCAGGATGGAGAACTGGTGGGCTACCGGATATCCCAGTGTGGCAGAGTGCAGGG
 ATTTCCAAAGAGCTCTTGGAGGAAGTTGGCCAGAATGGCAGCCGAGCTCGGATCTCTGTTCAAGTCCACAATGCT
 ACGTGACAGTGAGGATTGCAGCCGTACCAGAGGGGGAGTTGGGCCCTTCAAGTCCACAATGCT
 CCTGCACACGGTTGGGTAGATTATGCCCCCTCTTCAACTCCGGCGCCTGGCAACGCAGATCCTGTGCTCATCATC
 TTTGGCTGCTTTTGTGATTTATTTTGATTGGGTTGATTTTATACATCTCCTTGGCCATCAGAAAAAGAGTCCAG
 GAGACAAAGTTTGGGAATGCATTACAGAGGAGGATCTGAATTAGTGGTGAATTATATAGCAAAGAAATCCTTC
 TGTCCGGCAGCCATTGAACCTTACCTTACATAGCTTGGGAGTCAGTGAGGAACACAAAATAAACTAGAAGATGTT
 GTGATTGACAGGAATCTTCTAATCTTGGAAAAATTCTGGGTGAAGGAGAGTTTGGGTCTGTAATGGGAAGGAAAT
 CTTAAGCAGGAAGATGGGACCTCTCTGAAAGTGGCAGTGAAAGACCATGAAGTTGGACAACCTCTTACATCGGGAG
 ATCGAGGAGTTTTCTCAGTGAGGCAGCGTGCATGAAAGACTTCAGCCACCCAAATGTCATTGCACTTCTAGGTGTG
 TGTATAGAAATGAGCTCTCAAGGCATCCCAAAGCCCATGGTAATTTTACCCTTCATGAAATACGGGGACCTGCAT
 ACTTACTTACTTTATTTCCGATTGGAGACAGGACCAAAGCATATTCTCTGCAGACACTATTGAAGTTTCATGGTG
 GATATTGCCCTGGGAATGGAGTATCTGAGCAACAGGAATTTTCTTCATCGAGATTTAGCTGCTCGAACTGCATG
 TTGCGAGATGACATGACTGTCTGTGTGCGGACTTCGGCCTCTCTAAGAAGATTTACAGTGGCGATTATTACCGC
 CAAGGCCGCATTGCTAAGATGCCTGTTAAATGGATCGCCATAGAAAAGTCTTGCAGACCGAGTCTACACAAGTAAA
 AGTGATGTGTGGGCATTTGGCGTGACCATGTGGGAAATACGTACGCGGGGAATGACTCCCTATCCTGGGGTCCAG
 AACCATGAGATGTATGACTATCTTCTCCATGGCCACAGGTGGAAGCAGCCCCGAAGACTGCCTGGATGAACCTGTAT
 GAAATAATGTACTCTTGTGAGAGACCGATCCCTTAGACCGCCCCACCTTTTTCAGTATTGAGGCTGCAGCTAGAA
 AAATCTTTAGAAAGTTTGCTGACGTTCCGGAACCAAGCAGACGTTATTTACGTCAATACACAGTTGCTGGAGAGC
 TCTGAGGGCCTGGCCCAGGGCCCCACCTTGCTCCACTGGACTTGAACATCGACCCTGACTCTATAATTGCCTCC
 TGCATCCCCCGCTGCCATCAGTGTGGTCACAGCAGAAGTTTCATGACAGCAAACCTCATGAAGGACGGTACATC
 CTGAATGGGGGAGTGAGGAATGGGAAGATCTGACTTCTGCCCCCTCTGCTGCAGTCACAGCTGAAAAGAACAGT
 GTTTTACCGGGGAGAGACTTGTAGGAATGGGGTCTCCTGGTCCCATTCGAGCATGCTGCCCTTGGGAAGCTCA
 TTGCCCGATGAACTTTTGTTTGTGACGACTCCTCAGAAGGCTCAGAAGTCTGATGTGAGGAGAGGTGCGGGGA
 GACATTCCAAAATCAAGCCAATTCTTCTGCTGTAGGAGAATCCAATTGTACCTGATGTTTTTGGTATTTGCTT
 CCTTACCAAGTGAACCTCATGGCCCCAAAGCACCAGATGAATGTTGTTAAGGAAGCTGTCAATAAAATACATAA
 TATATATTTATTTAAAGAGAAAAAATATGTGTATATCATGAAAAAGACAAGGATATTTTAAATAAAACATTACTTA
 TTTCAATTCACCTTATCTTGCATATCTTAAATTAAGCTTCAGCTGCTCCTTGATATTAACCTTTGTACAGAGTTG
 AAGTTGTTTTTTTCAACTTCTTTTCTTTTTCATTACTATTAATGTAAAAATATTTGTAAAATGAAATGCCATATT
 TGACTTGGCTTCTGGTCTTGATGTATTTGATAAGAATGATTAATTTTCTGATATGGCTTCATAATAAAATTGAA
 ATAGGA

FIGURE 434

MGPAPLP LLLGLFLPALWRRRAITEAREEAKPYPLFP GPFP GSLQTDHTPLLSLPHASGYQPALMFSP TQPGRPHT
GNVAIPQVTSVESKPLPPLAFKHTVGHIILSEHKGVKFNCSINVPNIYQDTTISWWKDGKELLGGHHRITQFY PD
DEVTAIIASFSITSVQRSDNGSYICKMKINNEEIVSDPIYIEVQGLPHFTKQPESMNVTRNTAFNLTCQAVGPPE
PVNIFWVQNSSRVNEQPEKSPGVLTVPGLTEMAVFSC EAHNDKGLTVSQGVQINIKAI P SPPT EVSIRNSTAHSI
LISWVPGFDGYSPPFRNCSTQVKEADPLGNGSVMIFNTSALPHLYQIKQLQALANYSIGVSCMNEIGWSAVSPWIL
ASTTEGAPSVAPLNVTVFLNESSDNVDIRWMKPPTKQODGELVGYRISHVWQSAGISKEELLEVGQNGSRARISV
QVHNATCTVRIAAVTRGGVGPFS DPVKIFIPAHGWVDYAPSS TPAPGNADPVLII FGCFCGFILIGLILYISLAI
RKRVQETKFGNAFTEEDSELVVNYIAKKSFCRRAIELTLHSLGVSEELQNKLEDVVIDRNLLILGKILGEGEFGS
VMEGNLKQEDGTSLKVAVKTMKLDNSSHREIEEFLSEAACMKDFSHPNVIRLLGVCIEMSSQGIPKPMVILPFMK
YGD LHTYLLYSRLETGPKHIP LQTLLKFMVDIALGMEYLSNRNFLHRDLAARNCM LRDDMTVCVADFGLSKKIYS
GDYYRQGRIAKMPVKWIAIESLADRVYTSKSDVWAFGVTMWEIRTRGMT PYPGVQNH EMYDYLLHGHRLKQPEDC
LDELYEIMYSCWRTPDLDRPTFSVLRLQLEKLLLES LPDVRNQADVITYVNTQLLESSEGLAQGPTLAPLDLNI DPD
SIIASCTPRAAISVVTAEVHDSKPHEGRYILNGGSEEWEDLTSAPSAAVTAEKNSVLPGERLVRNGVSWSHSSML
PLGSSLPDELLFADDSSEGSEVLM

Signal sequence:	Amino acids 1-18
Transmembrane domain:	Amino acids 501-520
N-glycosylation sites:	Amino acids 114-118;170-174;207-211; 215-219;234-238;294-298;316-320;329-333; 336-340;354-358;389-393;395-399;442-446; 454-458;625-629
Tyrosine kinase phosphorylation sites:	Amino acids 675-683;865-873;923-930
N-myristoylation sites:	Amino acids 41-47;110-116;171-177; 269-275;275-281;440-446;507-513;535-541; 966-972
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 351-362
Tyrosine protein kinases specific active-site signature:	Amino acids 719-732

FIGURE 435

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTAGCACCAGTACTGGATG
TGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCCGATTCTGATTCGGCAAGGAT
CCAAGCATGGAAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTCCTG
CTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTGGGGC
CCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCTACTCTCTGAGGCGCTGCCTG
AGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGACTGCCCA
CCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCACCATGGC
CAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCAAGTGCCAA
GCCAAAGGAACAACCCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACGCGTTGCTAT
ACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGATCACCAGCTG
GGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCACCTGCCGGCTG
GTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAATCGGATGATACTGTGGTTGCACCTT
CCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTTATATCTGGAAACC
AAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAACCTTTCCTTGTGGAC
AATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGAATGGCTGGACCACTC
ACAGCAGATTTTATTGTCAAGATTTCGTAACCTCGGGCTCCGCTGACAGTACAGTCCAGTTCATC
TTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTCCTTGCTCAGCAACCTGT
GGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGGAGCAACCGTGTGGTTGCT
GACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACCAAGCTTCAGGAGTGCAAC
TTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGCCTTATGACCTCTACCATCCC
CTTCCTCGGTGGGAGGCCACCCCATGGACCGGTGCTCCTCCTCGTGTGGGGGGGGCATCCAG
AGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCATGTCACTTCAGTGGAAGAGTGG
AAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTTTGACTGCCCTAAA
TGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTCAGATACCGTGTG
GTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCCAAAACAAAGCCCCAC
ATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAACCCAAAGAGAACTTCCAGTCGAG
GCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTAGAAGAAGGAGCTGCTGTGTGAGAGGAG
CCCTCGTAAGTTGTAAAAGCACAGACTGTTCTATATTTGAAACTGTTTTGTTTAAAGAAAGCA
GTGTCTCACTGGTTGTAGCTTTTATGGGTTCTGAACTAAGTGTAATCATCTCACCAAAGCTTT
TTGGCTCTCAAATTAAAGATTGATTAGTTTCAAAAAAAAAA

FIGURE 436

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCCLSS
KSCCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPNCSLKCQAK
GTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCRLVR
GQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDLHLYLETKTLQGTKGENSLSSSTGTFLVDNS
SVDFQKFDPKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFPFCSATCGG
GYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYDLYHPLP
RWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWL
AQEWSPCTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPKKLPVEAK
LPWFKQAQELEBEGA AVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

FIGURE 437

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTGT
CTTTATGTCTTTCTCCTCTTCCTATTCTGTCACTCTCCCTCACTTAAGTCTCAGGCCTGTCAGC
AGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATGTTA
TGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGTGATC
TCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATGAGATG
GCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCCTGCCCTATTCCCTCCTCCCAAGTCTGT
TCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAGCAATCTG
TGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGTAGCCACCT
CCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTACAGGACATTTCGC
CCCTGTGTGCCACCAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCTCTCCTGGTAC
CCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACTATGGCGATGGC
CATGATGTTACAATCCCCTTGCCTGAATAATCAAGTGGGAAGGGGAAGCAGAGGGAAATGGG
GCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAAGGGGAAGCAACAGG
AACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGCTGTTGAAGGGGCAC
AAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAAATAGAACAGTCTGCT
GGGAGTCAGACCTGGAATTCTGATTCCAAACTCTTTATTACTTTGGGAAGTCACTCAGCCTCC
CCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACA
ATGTAGGTTACTAGTGAATACCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATA
AAACAAAATTCTCTAACACTGAAA

FIGURE 438

MWLPLGLLSLCLSPILSSPSLKSQLQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGMEH
RNHLCFCDLYDRATSPPLKCSLL

FIGURE 439

GTTTCTCATAGTTGGCGTCTTCTAAAGGAAAAAACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT
GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTGTCTGAGGGGCTGG
GGCAAAGGTGAAAGAGTTTTCAGAACAAAGCTTCTGGAACCCATGACCCATGAAGTCTTGTGCGACATTTATACCGT
CTGAGGGTAGCAGCTCGAAACTAGAAGAAGTGGAGTGTGGCCAGGGACGGCAGTATCTCTTTGTGTGACCCCTGGC
GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCTGGAGAGGAAATG
AGGCCTGAGGTACACTGGCTTGCTCCTCCTAGCCACAGCAGGCTGCTTTGTGACTTGAACGAGGTCCCTCAG
GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTGGCGTGGCTGGTGGAACTCCA
AGGATGAATGTAACTGGCGCTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCACC
CACGGGACCCTCGTCATCCTGCCCCTTAACAACCACTGTGCGGACGGTACCAAGTGTGTGGCCCCGGATGCCTGCG
GGGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCACGTG
ATTGAAGTGGATGAGGGAAACACAGCAGTCAATGCGCTGCCACCTGCCTGAGAGCCACCCCAAAGCCAGGTCCGG
TACAGCGTCAACAAGAGTGGCTGGAGGCCTCCAGAGGTAACCTGATCATGCCCTCAGGGAACCTCCAGATT
GTGAATGCCAGCCAGGAGGACGAGGGCATGCAAGCTGTGCGGACCAATGGGGTGTGGCCAGGAGGAAATG
TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCAGAGGCC
CAAACCATCATCGTCAACAAAGGCCAGAGTCTCATTCTGGAGTGTGTGGCCAGTGGAAATCCACCCCCACGGGTC
ACCTGGGCCAAGGATGGGTCCAGTGTACCGGCTACAACAAGACGCGCTTCTGCTGAGCAACCTCCTCATCGAC
ACCACAGCCAGGAGGACTCAGGCACCTACCGCTACCAAGCTGTGCGGACCAATGGGGTGTGGCCAGGAGGAAATG
ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTCAACCATGGAGCTATCCAGCTGGTTCATCCCTGGGGC
CAGAGTGCCAAAGCTTACCTGTGAGGTGCGTGGGAACCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCCC
CTCATCTCCAGCCAGCGCCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGTCTCAGCATGGGGCTGAGGACGAAGGC
GTCTACCAATGTCACTGGCCGAGAACGAGGTTGGGACGCCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC
ATAACCCCAAGGCTATGCGAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATCACCTCCAAACTCGGCAAC
CCTGAGCAGATGCTGAGGGGCAACCGGCGCTCCCCAGACCCCAACGTCAGTGGGGCTGCTTCCCCGAAGTGT
CCAGGAGAGAAGGGGAGGGGGCTCCCGCGGAGGCTCCCATCATCTCAGCTCGCCCCGACCTCCAAGACAGAC
TCATATGAATGGTGTGGCGGCTCCGCGATGAGGGCAGTGGCCGGGCGCAATCCTCTACTATGTGGTGAACAC
CGCAAGCAGGTCAAAAATTCCTCTGACGATGGACCATCTCTGGCATTCCAGCCAACAGCAGCCGCTGCCAATC
ACCAGACTTGACCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACGTGTGCGGGAGAGGGCCAGACAGCC
ATGCTCACCTTCCGAAGTGGACGGCGGCCCAAACCCGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC
GACCTTGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGACCAGCGCCCTCTCCCCCAGAAAGCTCCCCAGAGG
CCCGTGGCAGGTCAAAAATTCCTCTGACGATGGACCATCTCTGGCATTCCAGCCAACAGCAGCCGCTGCCAATC
CAGTCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCAGCGCCATCCCCCA
TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCCTACAAGTTTCGAGTCCGGGCTCTGAACATG
CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGGGGCTACAGCGGTGCGGTGTACGAGAGG
CCCGTGGCAGGTCAAAAATTCCTCTGACGATGGACCATCTCTGGCATTCCAGCCAACAGCAGCCGCTGCCAATC
ATAGAGCGGCCGTTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGTCTGTC
CTGGGCTCCATCGTTCTCATCATCGTCACTTCTATCCCTTCTGCTTGTGGAGGGCTGGTCTAAGCAAAAACAT
ACAACAGACCTGGGTTTTCTCGAAGTGCCCTTCCACCCTCCTGCCCGTATACTATGGTGCCATTGGGAGGACTC
CCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCCGGGCTGAAGCCCCAGCAGCACTGCCAGGCGAGCTTCAG
CAGCAGAGTGACACCAGCAGCCTGCTGAGGCAGACCCATCTTGGCAATGGATATGACCCCCAAAGTCACAGATC
ACGAGGGGTCCTCAAGTCTAGCCCGGACGAGGGGCTCTTCTTATACACACTGCCCGACGACTCCACTACCAGCTG
CTGCAGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCTGCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCC
CCCGACAGTCTCTGCTGGAAGCAGTGTGGGACCTCCATTTCAGCTCAGGGCCCCATGCTGCTTGGGCTTGTG
CCAGTTGAAGAGGTGGACAGTCTGACTCTGCAAGTGAAGTGGAGGAGACTGGTGTCCCAGCACCCCGTAGGG
GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCCGGGGCCACTGGTGCCTGTGTCTTTTGAACACCACCT
CTCACAATTAGGAGCAGAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAAAGAAGAAAA
AGAGACAGAGAAAAATTGGTATTTATTTTCTATTATAGCCATATTTATATATTTATGCACTGTAAATAAATGTA
TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTTACCCGTTGAGGTTGGAGAGGGAAAAATAAAGAAGCTGCCA
CCTAACAGGAGTCACCCAGGAAAGCACCGCACAGGCTGGCGCGGGACAGACTCCTAACCTGGGGCTCTGCAGTG
GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTTCATCACGAGCA
TGAGGGAACAGCAAGGGGCACGGTATCACAGCTGGAGACACCCACACAGATGGCTGGATCCGGTGCTACGGGAA
ACATTTTCTAAGATGCCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAACCACTTCCAGAAT
CAATAATCCGTGGCAACATATCTCTGTAAAAACAACACTGTAACCTCTAAATAAATGTTTAGTCTTCCCTGTAAAA

FIGURE 440

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPPR
MNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLAN
LQDFKLDVQHVIIEVDEGNTAVIACHLPESHHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQIVN
ASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARI IYPPEAQTIIVTKGQSLILEC
VASGI PPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA AVILY
NVQVFEPPEVTMELS QLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLSRRALRV
LSMGPEDEGVYQCAENEVGSAAHVVQLRTSRPSITPRLWQDAELATGTPPVSPSKLGNPEQM
LRGQPALPRPPTSVGPASPKCPGKQGAPAEAPIILSSPRTSKTDSYELVWRPRHEGSGRAP
ILYYVVKHRKQVTNSSDDWTISGIPANQHRLLTLRLDPGSLYEVEMAAYNCAGEGQTAMVTFR
TGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASETSVYVTWIPR
GNGGFPIQSF RVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRVRALNMLGESEP
SAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMI PASNNNTPIHGFYIYYRPT
DSDNDS DYKKDMVEGD KYWHSISHLQ PETS YDIKMQCFNEGGESEFSNVMICETKARKSSGQP
GRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVLIIVTFIPFCLWRAW
SKQKHTTDLGFPR SALPPSCPYTMVPLGGLPGHQASGPYLSGISGRACANGIHMNRGCPSAA
VGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPKSSPDEGSFLYTL PDDS
THQLLQPHHDC CQRQEQPA AVGQSGVRRAPDSPVLEAVWDPPFHS GPPCCLGLVPVEEVDSPD
SCQVSGGDWCPQHFPVGAYVGQEPGMQLSPGPLVRVVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 441

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGC
TCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCTGG
GCCTGGCCCAGCCAGCCTCTGCCCCGCCGAAGCTGCTGGTGTCTCTGCTGGATGGTTTTTCGCT
CAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTTCAAAGAGATTGTGAGCAGGG
GAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTATACCC
TAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACCTACATGTGGGACCCACCA
CCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGGAATGGAT
CAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTACTGGCCAG
GCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAAAATGTCCCAA
CGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGTGGCCGGGCCG
ACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGGGCCTGCATCTC
CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGACCAAGTGGATCC
AGGAGCGGGGCCTGCAGGACCGCCTGAACGTCATTATTTTCTCGGATCACGGAATGACCGACA
TTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAATGACCTGCAGCAAG
TGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAACACTCTGAGATATATA
ACAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGCAGGTTCT
ATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGATGAAGGCTGGTTCATAA
CTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCAGGCGGGAAGGTTGGCAGC
GTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGCATCTTCCTGGCCTTCGGAC
CTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTCGGTGGACGTCTACAATGTCATGT
GCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCTGGTCCAGGGTGATGTGCATGC
TGAAGGGCCGCGCCGGCACTGCCCCGCTGTCTGGCCCAGCCACTGTGCCCTGGCACTGATTC
TTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAG
TGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCA
AGACCATGCACATTGTAAATACATTATTCTTGGATAATTCTATACATAAAAGTTCCTACTTGT
TAAA

FIGURE 442

MAVKLGTTTTLLALALGLAQPASARRKLLVFLLDGFRSDYISDEALESPLPGFKEIVSRGVKVDYL
TPDFPSLSYPNYYTTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSLMLPLWWNGSEPLWVT
LTKAKRKVYMYYPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAAIYH
ERIDVEGHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLNVIIIFSDHGMTDIFWMDKV
IELNKYISLNDLQQVKDRGPVVSLLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYKKGKF
VSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGPDFKSNF
RAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALILLFLLA

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

FIGURE 443

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAGC
ACCAGTGTGTGAGGGGAGCAGGCAGCGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACCCA
GCCCCCGGCACAGAGCTGCTCCACAGGCACCAATGAGGATCATGCTGCTATTCACAGCCATCCT
GGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGGTTCC
TGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTCAAAAG
CCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAAGGAATC
AACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGAGGAGCGT
CCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCCCCTTCATCC
CAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACCTTTATAAGA
CTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTATCCCCGAG
AGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTCTTCCCTGTCC
CAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGTAACATTCTTGTG
CTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACTGCATAGTGAATATCCC
CAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGTCTACATTAATAAT
ATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTTGCATATGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 444

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKA
LSQASTDPKESTSPKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSS
LGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 445

TGGACTTCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCAGTCCACCATGATCCATCTGGGTCACAT
CCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTA
CCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGA
TGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGG
CAAAGTCTACATCAACATGCCAGGCAGGGGGCTTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATC
CTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCAACTTTTGGATTGTAATAAAACAATTGAAACACCA

FIGURE 446

MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGLSLPLLAGLVAADAVASLLIVGAVFLCARPR
RSPAQDGKVIINMPGRG

Signal peptide:	Amino acids 1-18
transmembrane domain:	Amino acids 51-70
Glycosaminoglycan attachment site:	Amino acids 40-44
N-myristoylation sites:	Amino acids 34-40;37-43;52-58
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 29-40

FIGURE 447

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCC
CGGCCTCCTGTTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGG
GCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCTCGGCCAGGC
CCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTC
CAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCC
GGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGGAG
ATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCTGTG
CAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCT
CCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACC
TGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGGCTGCACCTGCGTGCTGCC
CCGTTCAGTGTTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG
CACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACTACCCTTGGGGTC
TGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGT
TGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGG
CTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGC
CCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAG
TGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

FIGURE 448

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALP
VALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDYPQKLAF
AECLCRGCIDARTGRETAALNSVRLQLSLVLRRRRPCRDSGLPTPGAFAFHTEFIHVPVGC
TCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

FIGURE 449

TGCAGAGCTTGTGGAGGCC**ATG**GGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGTT
 GTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGATAA
 AATCGCGATTATTTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAAATT
 TGGGAAAGATGTGAAGATAGACCTGTTTGAAAAGAGAAGAGGTCGGGGGCGCCTGGCTACCAT
 GATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTTCATCCATCCTTTAAATCTGCACAT
 GAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAAGCCTCTGGTGGCCTACTGGGGAT
 ATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGATTAAATT
 AGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTGTTAGACAA
 GTTCATGAGGATCTACCGCTACCACTCTCATGACTATGCCTTCAGTAGTGTGAAAAATTACT
 TCATGCTCTAGGAGGAGATGACTTCCTTGGAATGCTTAATCGAACACTTCTTGAAACCTTGCA
 AAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATGAGGGTCAATTA
 TGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCACTGTCTGTTCTGATTCTGG
 CCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGCAGGCATCCAAAAG
 CAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACCAAGTACACAGGAAA
 TCCAACAAAGATGTATGAAGTGGTCTACCAAATTTGGAAGTGAAGTCTGTTTCTCACTTCTATGA
 CATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTACTTTTCTCACTTTGA
 TCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACAACCTTTAGTTAAGGGGGA
 ATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAAATTTGGCCTTAATACAGTTTAAAC
 CACTGATAATTCAGATTTGTTTATTAAACAGTATTTGGGATTGTGCCCTCTGTGAGAGAAAAGGA
 AGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAGATCTTTTCCCAAGAACTCTTAC
 TAAAGCACAAATTTTAAAGCTCTTTCTGTCTTATGATTATGCTGTGAAGAAGCCATGGCTTGC
 ATATCCTCACTATAAGCCCCCGAGAGAAATGCCCTCTATCATTCTCCATGATCGACTTTATTA
 CCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATGAGTGCCATTGCAGCCCACAACGC
 TGCACCTCCTTGCCATACACGCTGGAACGGGCACACAGACATGATTGATCAGGATGGCTTATA
 TGAGAACTTAAACTGAAC**TGA**AGTGACACACTCCTTTTTCCCCTCCTAGTTCCAAATGA
 CTATCAGTGGCAAAAAAGAACAAATCTGAGCAGAGATGATTTTGAACCAGATATTTTGCCAT
 TATCATTGTTTAAATAAAAGTAATCCCTGCTGGTCATAGGAAAAAAAAAAAAA

FIGURE 450

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880
<subunit 1 of 1, 505 aa, 1 stop
<MW: 56640, pI: 6.10, NX(S/T): 4
MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPDKIAIIGAGIGGTSAAYYLRQKFGKDVKI
DLFEREEVGGRLATMMVQGOEYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGLLGIYNGETL
VFEESENWFIINVIKLVWRYGFQSLRMHMMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHALGGD
DFLGMLNRTLLETLOKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLWAVEG
GNKLVCSGLLQASKSNLISGSVMYIEEKTCTKYTGNTKMYEVVYQIGTETRSDFYDIVLVAT
PLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGLNTVLTDDNSDL
FINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTQAQILKLFLSYDYAVKKPWLAYPHYKP
PEKCPSTIILHDLRYLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDGLYEKLKTEL
```

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23, 232-243

FIGURE 451

[illegible]

FIGURE 452

MASYLYGVLFVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLET
PSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVPSK
DLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGVVD
IIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAFGVDT
ELNCFVLQMDYKGDVAFFVLPSKGMQRQLEQALSARTLIKWSHSLQKRWIEVFIPRFSISAS
YNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTTKFIVRS
KDGPSYFTVSNRFTLMMITNKATDGILFLGKVENPTKS

Signal peptide:
amino acids 1-20

FIGURE 453

CTCCGGGTCCCCAGGGGCTGCGCCGGGCGGCGCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
CCCCGGGGGGGCGATGACCGTGCGCTGACCCTGACTCACTCCAGGTCCGGAGGCGGGGGCCCCGGGGCGACTCG
GGGGCGGACCGCGGGGCGGAGCTGCCGCCCGTGAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGGACACCGTC
GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCCCTGAGGAGCTGGCTCGCCGCCCCATGGGGCGCGCTGCCG
CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGACGCCCGCCCTCCGACCTGGGCGCTCAGC
CCCCGGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCTCTCAGATTGAAAGCTGAAACATCTCCAACCTAC
ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCCTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC
AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCAGACGCAGAGAAGAAACAGCAGTGC
AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAACCTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC
CTGTTACCTGTGGCAGCAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAACTTCACCTTGGCAAGG
GACGAGAAGGGGAATGTCTCTGGAAGATGGAGGCCCTGTGCTCCTTCGACCCGAATTTCAAGTCCAGTGGC
CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCTCAGCCTAC
ATTCTGAGAGCCTGGGCAGCTTGCAAGGCGATGATGACAAGATCTACTTTTTCTTCAGCGAGACTGGCCAGGAA
TTTGAGTTCTTTGAGAACACCATTGTGTCCCGCATTCGCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG
CTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCACGGCCCCGACGATGGCTTCCCCTTCAAC
GTGCTGCAGGATGTCTTCACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCTTTTCTATGGGGTCTTCACT
TCCCAGTGGCAGGGGAACTACAGAAGGCTCTGCCGTCTGTGCTTTCACAATGAAGGATGTGCAGAGAGTCTTC
AGCGGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG
CCTGGAGCGTGATCACCAACAGTGCCCGGGAAGGAAGATCAACTCATCCCTGCAGCTCCAGACCGCGTGCTG
AACTTCTCAAGGACCACTTCTGATGGACGGGCGAGTCCGAAGCCGCATGCTGCTGCTGCAGCCCCAGGCTCGC
TACCAGCGCGTGGCTGTACACCGCGTCCCTGGCCTGCACCACACCTACGATGTCTCTTCTGGGCACTGGTGAC
GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCCGGGTGACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA
CAGCCCGTGCGAATCTGCTCCTGGACACCCACAGGGGCTGCTGTATGCGGCCTCACACTCGGGCGTAGTCCAG
GTGCCCATGGCCAAGTGCAGCCTGTACCGGAGCTGTGGGACTGCCTCCTCGCCCGGACCCCTACTGTGCTTG
AGCGGCTCCAGCTGCAAGCACGTCAGCCTCTACCAGCCTCAGCTGGCCACCAGGCGTGGATCCAGGACATCGAG
GGAGCCAGCGCCAAGGACCTTTGCAGCGCTCTTCGGTTGTGTCCCCGTCTTTTGTACCAACAGGGGAGAAGCCA
TGTGAGCAAGTCCAGTTCAGCCCCAACACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA
CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCTCGGCCTCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG
GTGGGCACCCAAACAGCTGGGGGAGTTCCAGTGCTGGTCACTAGAGGAGGGCTTCAGCAGCTGGTAGCCAGCTAC
TGCCCCAGAGGTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCAATTATCAGCACA
TCGCGTGTGAGTGACACAGCTGGTGGCAAGGCCAGCTGGGGTGCAGACAGGTCTACTGGAAGGAGTTCTGGTG
ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTTATTCTTGCTCTACCGGCACCGGAACAGCATGAAA
GTCTTCTGAAGCAGGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGCTGCCCCCTGAGACCCGC
CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG
GGGGCCCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG
TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTTCTGGGAAC
ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
TACCACCCAGACACCCAAACAGCCGTGGCCCCAGAGGTCTGGCCAAATATGGGGGCCTGCCTAGGTGGTGGA
CAGTGCTCCTTATGTAACTGAGCCCTTTGTTTAAAAAACAATTCCAAATGTGAACTAGAAATGAGAGGGAAGAG
ATAGCATGGCATGCAGCACACCGGCTGCTCCAGTTTCATGGCCTCCAGGGGTGCTGGGGATGCATCCAAAGTGG
TTGTCTGAGACAGAGTTGGAAACCCCTACCAACTGGCCTCTTCACCTTCCACATTATCCCGCTGCCACCGGCTGC
CCTGTCTCACTGCAGATTGAGACAGCTTGGGCTGCGTGCGTTCTGCCTTGCCAGTCAGCCGAGGATGTAGTTG
TTGCTGCCGTGCTCCACCACTCAGGGACAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCTCTGGGCTC
GGACCCAACCTTGGACCTTTCCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGGAGCTCAGGAGAGA
TTTCGTGACAATGTACGCCCTTCCCTCAGAATTCAGGGAAGAGACTGTGCGCTGCCCTTCTCCGTGTTGCGTGA
GAACCCGTGTGCCCTTCCACCATATCCACCCCTGCTCCATCTTTGAACTCAAACACGAGGAACCTAAGTGCACC
CTGGTCTCTCCCCAGTCCCCAGTTACCCCTCCATCCCTCACCTTCTCCACTTAAGGGATATCAACACTGCCC
AGCACAGGGGCCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACTTTATGTCAATTTTTAATAAA
GTCTGAAGAACTACTGTTTAAAAAATAA

FIGURE 454

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRFE
AEHISNYTALLLSRDGRTLTVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKGKD
PQRDCQNYIKILLPLSGSHLFTCGTAAFSMCTYINMENFTLARDEKGNVLLEDGKGRCFPDP
NFKSTALVVDGELYTGTVSSFQNDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGS
LQGDDDKIYFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLCSRDD
GFPFNVLQDVFTLSPSPQDWRDTLFGYGVFTSQWHRGTTEGSAVCVFTMKDVQRFVSGLYKEVN
RETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFMDGQVRSRMLLLQ
PQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIEELQIFSSGQPVQNLLLD
THRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQPQLATRPWIQ
DIEGASAKDLCSASSVSPSFVPTGEKPCEQVQFQPNVTNLTACPLLSNLATRLWLRNGAPVN
ASASCHVLPTGDLVLVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQTEGGSVPVII
STSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAVS
HPKTCPVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKRPLSIQDSFVEVSP
VCPRPRVRLGSEIRDSV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 455

TAAGATGAGGGCATCCCTCACGTTTACACCCCCTGGTGGCATCTGCCAGCCCTGTTCTGGGGAC
AAGGCGGGCTTTCGTGGGAGCCATGCTCAGCCTGCCAGGAAGCCAAGCCCTACAGTGCAGAGG
AAACAGAATTTCAACGGGAAGCTGGTTTGCCTTCATACCATTGGGATCTGCTGGTAAAGCTGTT
ATTTGGGTTTtagggactgatcccttgcagtttacttctggatcaccatgaatggccaagatgg
TGGCAGAACACGCTGTGGACCCTGAGTTAGAGACAATGCAAATGTTGGATTGGGTGTAATTCT
TTTTGAATCCCAGATCCAGTCTGTACTTGAATATGAGCAGAAGATCTACAAGAATGCTGACAG
GGAACCGTGTTAAGACCCAGCACCCCTATTCCCAGGAGCTTCTGGCCTGACCATCTGCAGCCA
AAGCACTAACAGGGACAGATATGGGAATGTCCACCTTTGATCCGCATCCTGCACAATAGTGGT
CCCACCATGGCTGCCACTTTTTTATACTATTTGGAGAAAAGACCTTGTATAAATTCGAGGCC
GAGTGACTAACGTCTCTGTACACGGAAATGGGTACTTGGTGGCATAGAGAAACACAATTAGC
CACTTTTTTCAGCTACACTTCTCACTCAGCTGCACCCTACACTTCTCACTCAGGTGCACCCCT
TCTGCTGTCCTTCCCCAACGTACTGGGTCCCGAGCGTGGTGGGTATTTGCCACACTGGGTGC
CAGCTCAGCAGCCCCCACCTCTCTTTATTCTCTCAAAGCTGGTCTTTCTGACTATCATTGT
GGTAGGGGGAGGACAGATGCTAAAGGTGGAAGCTGACCTGGAGAAAGAGACACACGGGGTGAC
TGTGGCAAAGGACAGCTGGAAAAGAACTCTATCACTTCTTCATTGGCAACCACAAGGCACCC
GAGGCCATGGCACTCCCAGAGGCTGTGCGCAGAGCCAAGCCTCTCAACCTCTTCTGGCCCTGC
GTCCTGCAGCGAAGTCTCTGCTGTAAGACAGTAGACTCCTTCGATGAGGTGCTCAAAAATGCT
ACCCGGGGTGGTGGTGTCTGGCTTGCAGTCTGGCCCAGTTCAGAGAAAGTTGCAGAGATCAGGG
GCCAAGGATGTCATAGCCCCAGGTTGTCTCAGGGTCCCAATCCTAGGGCAGGGTGTGCATGG
AAGCAAGAACTATGGAAACCTAGCTCCAGTCTGCAGGCTCTGAGCCCCTAGTTCCTCACTCCA
GCGGGGCTCCCTCACTGCACAGAACCCACCCCTTCTGTGTGGGCACTGCTGACCACACAGATG
ACCCAGACCCAAAGAGCCTGGCAGAAGCTCTGTGGTTGGAGCTGGGCTCCGTCTCAGGTCTG
GTTCAGGGGGATCAGGAAGGCTCTTTTCCACCTGTGGCTTCACTGGCCCTTTGAGATTTCTTA
TCTCACCGTTACTTCAGTTACCCTTGCAGGGGGCCAGGGAGTCAAGAATATACCGTGTTCTC
CAGGGTTTAAGCCGGCCATGCCTTCCCCGAGAGCATAACCAACTTGACAGGGGTGCCCAGTTAC
CCCACAACTGAAGGAAGGAGATCCTTCCCCCGTCCCCAGGAGTGCTCTCAACCAGCCTCAGA
AAGCTTGAGAAGATGGACCCTTTGCCCACCAGGGTTAATTCCTGGTGGGGCAGCTCGGCTGTG
ATCAGGGCAACCAAACCTATAGGAAGCCTTCCAGTGTGAGCTGGAATTAGACTGAACATGTGC
TTGGGCCTGCCTCTCCCTAGACGCAGTTGCGGGGCACTCCAGGGAATGAACCAGCTCAAGTGT
GTCCCTAACAGCAGCCTGGAGCTACCCCCAATCCCTCACAGCCTGACCCTCCTCATTCCATCA
GATCTCGTGCCG

FIGURE 456

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA69555
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16214, pI: 10.22, NX(S/T): 0

MGTWWHRETQLATFSATLLTQLHPTLLTQVHPLLLSFPQRTGSRWWVFATLGASSAAPH
LSLFSPKLVFLTIIVVGGGQMLKVEADLEKETHGVTVAKDSWKRNSITSSLATTRHPRPW
HSQRLCAEPSLSTSSGPASCSEVSAVRQ

Important features of the protein:

Signal peptide:

Amino acids 1-28

Transmembrane domain:

Amino acids 64-78

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 103-107

N-myristoylation sites:

Amino acids 53-59;94-100

FIGURE 457

CCCGCGCGCCCCTGGCACTCAATCCCCGCCATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTC
 GCGCCGGCCGTCGGCCCGGCTCTGGGGGCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCC
 GGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCGGCACAGCCGCCGGCG
 GAGACAGCTAACGGGACCTCAGAACAGCATGTCCGGATTCGAGTCATCAAGAAGAAAAAGGTC
 ATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGGCCC
 CTTGTGACCCCCACTCCAGCAGGGACCCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCTT
 CCTTTGGGTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCC
 TTTGGTCTTGGAACACACCGAGGACGGCTCAACATTTCATTAGGCCTGGAGGACGGCGATCTA
 TATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGG
 CACCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACCTCTGTCTGGAGGTATGACTGG
 GTCACATCATAAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACCAC
 AGCAGTGGGATGGACGCAGTATTTCTGCCAATTCAGACCCAGAACTCCAGTGCTGAACCTC
 CTGCCGGAGCCCCAGGTGGCCCGCTTCATTGCGCTGCTGCCCCAGACCTGGCTCCAGGGAGGC
 GCGCCTTGCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCAATGACCTATTCCTT
 GAGGCCCCCTGCGTCGGGATCCTCTGACCTCTAGACTTTCAGCATCACAAATTACAAGGCCATG
 AGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCAACATCACCCGCATCTACAGCATTTGGG
 AAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCGGACAAGCCTGGGGAGCATGAG
 CTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAG
 TTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACC
 CGGCTGCTCTCTGAGATGCGCATTCACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATC
 GCCTACCACCGGGGTTTCAAGCTGGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATC
 GATCTTAACCATAATTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAG
 GTGCCCCACATCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCC
 ACCGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGT
 GCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTTACCCATTCGACATGACTCGCACCCCGTGG
 GCTGCCCGCGAGCTCACGCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTAT
 GCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCC
 GTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTC
 AGCTACCTACACACCAACTGCTTTGAGGTCACCTGTGGAGCTGTCTGTGACAAGTTCCTCAC
 GAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGCCCTCCTCACCTACCTGGAGCAG
 GTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGACGCT
 GTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTATTGGCGT
 CTGCTGACCCAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTCAGTGACACGG
 AACTGTCGGGTACCTTTGAAGAGGGCCCCCTTCCCCTGCAATTTCTGTGCTACCAAGACTCCC
 AAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGC
 CTGGAGCGGCTAAGGGGACAGAAGGATTGATACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGG
 ACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTGCTCAT
 TAAAGCTACCGGGCACCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 458

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71162
><subunit 1 of 1, 734 aa, 1 stop
><MW: 81677, pI: 6.60, NX(S/T): 6
MWGLLLALAAFAVAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
ESLRVSDSRLEASSSQSFGLGPHRGRLNIHSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVS DPNDLFLEAPASGSSDPLDFQHH
NYKAMRKLMKQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGEHHELGEPEVRYVAGMH
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIA YHRGSELVG
WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETR
AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
NELPQEWENNKDALLTYLEQVRMG IAGVV RDKDTELGIADAVIAVDGINHDVTTAWGGDY
WRLLT PGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
DLRRRLERLRGQKD
```

FIGURE 459

TAAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAA
AGAACTGACTGAAACGTTTGAGATGAAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGT
GGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAGCGA
TGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCACCAAT
TCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCTATTCCAATACCTGAATCTGCCCC
TACAAC'TCCCC'TCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGGTCACCT
GAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAATTCCTGT'TAATAAAAGAAAAACAAAT
GTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTAATAAACAT
GAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

FIGURE 460

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYFPRPLPPIPFPRFPW
FRRNFPIPIPIESAPTTPLPSEK
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

Important features of the protein:

Signal peptide:

Amino acids 1-20

N-glycosylation sites:

Amino acids 57-61;210-214;220-224;318-322;428-432;472-476

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 80-84

N-myristoylation sites:

Amino acids 3-9;20-29;39-48;152-161;161-170;262-271;358-364;
538-544;560-566;637-643

Zinc carboxypeptidases, zinc-binding region 2 signature:

Amino acids 498-509

Zinc carboxypeptidases:

Amino acids 391-411

FIGURE 461

AGCAGGAGCAGGAGAGGGACAATGGGAAGCTGCCCCGTCCAGGTTTCATGTTCCCTCTTATTTCTC
CTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTGGT
GCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCCACT
GAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCATAGC
ATGGTGCAAAAATTCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGACACAC
TACAACATCACTGGGAACACCATCTGCCTCTTTTCGCCTGGTAGACAATGAACAACCTGAATTTA
GAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGATCAACAGC
CTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCGTAATTCAG
ATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATGCACAGATAC
CAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAGTGGTATGAAA
GAAAATGGGAAGGTGATATCATTTTTCAAACCTAAAGGAGTCTCAACTGCCAGCTTTGGCAATT
TACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAAGTTTCCGTAGAGCATGTG
CAAACTTTTGTGATGGATTCCCTAAGTGGAAAATTGTTGAAAAGAAAATCGTGAATCAGAAGGA
AAGACTCCAAAGGTGGAACCTCTGACTTCTCCTTGGAACCTACATATGGCCAAGTATCTACTTTA
TGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAGGATCACTAGGCCTGC
CAACCACACACACACGCACGTGCACACACGCACGCACGCGTGCACACACACACGCACACAC
ACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTCTTCTTCCTTCTTTTAAA
TTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATTCTACTCTGTAAGCCCAT
CTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATGCCTCTATGAAAGAGAGGCA
TTCCTAGAGAAAGATTGTTCCAATTTGTCAATTAATATCAAGTTTGTATACTGCACATGACTT
ACACACAACATAGTTCTCTGCTCTTTTAAGGTTACCTAAGGGTTGAACTCTACCTTCTTTTCAT
AAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGGATGGTTTTTAACACCTTTGTGA
AATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTCCCTGAACTCAGCAGAAATAGACC
ATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCCCTATGTAAATCAACAACCTGCATAA
TAAATAAAAGGCAATCATGTTATA

FIGURE 462

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLLFLLTCELAAEVAAEVEKSSDGPGAAQEPTWLTDVPAAMEFIAATEVAVIGF
FQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRLVDNEQLNLEDEDIES
IDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAAKLF
QGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNFCDGF
LSGKLLKENRESEGKTPKVEL
```

Signal peptide:
amino acids 1-20

Transmembrane domain:
amino acids 143-162

FIGURE 463

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAGG
GTGCCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGGCC
ATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGC
CCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCTGCGG
GTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAACTTGGAGACTCCTGGGACGTG
AACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCTGCAGCCAGGCGAATACATCACA
AAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAAGGACCGC
TATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAGAGGGGCAG
GTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGAATGG
AATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGCAAACCTCA
CCCGTGGGTCGCTTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGTGTGGTGGTGGC
TGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATAAAATAAAGCTTCT
GCAGAAAA

FIGURE 464

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVVKL
GDSWDVKLGALGGNTQEVTLPGEYITKVVFVAFQAFLRGMVMTSKDRYFYFGKLDGQISSAY
PSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:
amino acids 1-22

FIGURE 465

CGGACGCGTGGGTCCGGCGGCTTGAGGCTGCACCGGGACGGGTTCGGCCGCAATCCAGCCTGGGCGGAGCCGGAG
TTGCGAGCCGCTGCCTAGAGGCCGAGGAGCTCAAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGACCCCGT
TGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGTGCTTCAAGGACATATCCCTGGGC
AGCCAGTCAACCCGCACTGGGTCTGGATGGACAACCCCTGGCGCACCGTCAAGCTGGAGGAGCCGGTCTCGAAGC
CAGACATGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAGAACCAACAGGCTGC
TGGCCCCAGGATACATAGAAACCCACTACGGCCAGATGGGCAAGCTGGTGTGGTGGCCCCAACCAACAGGATC
ATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCTCTGCACCTGCTCTGGGATGAGTG
GCCTGATCACCCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAA
CCACAGAGATCTTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAG
CGGCGATGACCAGGCTTCTCTGGTGGTCCCCAGAGCAGGGGCGAGGCGAGAAGCGCGCAGGACCCGGAGTACCTGG
AAGTGTACATTGTGGCAGACCACCTGTTCTTGACTCGGCACCGAAACTTGAACCACCAAAACAGCGTCTCC
TGGAAGTCGCCAACTACGTGGACCAGCTTCTCAGGACTCTGGACATTAGGTGGCGCTGACCGGCTGGAGGTGT
GGACCGAGCGGGACCGCAGCCGCGTCAAGCAGGACGCCAACGCCACGCTCTGGGCCCTTCTGCAGTGGCGCCGGG
GGCTGTGGGCGCAGCGGCCACGACTCCGCGCAGCTGCTACGGGCGCGCCTTCCAGGGCGCCAAGTGGGCC
TGGGACCCGCTCGAGGGGCTGTGCCGCGCCGAGGCTCGGGAGCGGTGAGCAGCGACCACTCGGAGCTCCCCATGG
GCGCGCAGCCACCATGGCCATGAGATGGGCCACAGCTCAGGCTCAGCCACGACCCCGACGCGTGTGCGTGG
AGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCTTCCGCGCGCTGTTTCAAGCGCT
GCAGCCGCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGCGCTTGCCTCTCCAATGCCCGGACCCCGGAC
TCCCGGTGCGCGCCGGCGCTCTGCGGGAACGGCTTCTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGG
AGTGCCGCGACCTCTGCTGCTTTGCTCAAACTGCTGCTGCGCGCCCGGGGCCAGTGCGGCCACGGGGAGCTGCT
GCGTGCCTGCTGCTGCTGAGCCGGCTGGAGCGCTGTCGCGCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTT
GCAGGGGACCTCTCTCCACTGTCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGAGTGGCT
ACTGCTGGGATGGCGCATGTCCACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCTGGCTCCACCCAGCTC
CCGAGGCTGTTTCCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACT
TCCTGCCCTGTGTCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGGCCAGCTGCTCGCAC
CGCATATGGTGCCAGTGGACTCTACCGTTACCTAGATGGCCAGGAAGTGAAGTTGTGCGGGAGCCTTGGCATCC
CCAGTGCCAGCTGGACCTGCTTGGCCTGGGCTGGTATGAGCCAGGACCCAGTGTGGCTGGAATGAGTGTGCC
AGAGCAGGCGCTGCAGGAAGAATGCCCTCCAGGAGCTTACGCGCTGCTGACTGCTGCCACAGCCACGGGGTTT
GCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCA
GCATGGACAGCTGGGCCCTGTGCAGGCTGAAACCATGACACCTTCTGCTGGCCATGCTCTCTCAGCGTCTGCTGC
CTCTGCTCCGAGGGGCGGCTGGCTGGCTTGTGCTACCGACTCCAGGAGCCCATCTCGAGCGATGCTGAGCTGGG
GCTGCAGAAGGGACCTTGCCTGAGTGGGCCCCAAGATGGCCACACAGGGACCAACCCCTGGGCGGCGTTTACC
CCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGGCCCTGGACCCTGAGAACTCTCATGAGCCAGCAGCC
ACCTGAGAAGCCTCTGCCAGCAGTCTGCGCTGACCCCCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCT
GGTGAAGGAGGTAGCTCTTAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTGAACTG
CAGGGGCGAGGACCTGAATCACCGGACCTCCAGCAGCTCGAGGAGCTTGAAGTTTCTTCCCCGAGTGGAGCT
TCGACCCACCCACTGGAACCCAGAGCCACATTAGAAGTTCTGAGGGCTGGAGAACACTGCTTGGGCAACACT
CTCCAGCTCAATAAACCATCAGTCCAGAGCAAAAGGTACACAGCCCCCTGACCTCCCTCACAGGATGGAGGCTGG
GTAGTGCTGGCCATCCCAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCTACATGCAATTTCCACGGACCCA
GCTCTGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTGACTGAGTCCACACTCC
CCTGCAGCCTGGCTGGCCTCTGCAAAACAAACATAATTTTGGGGAGCTTCTCTCTGTTTCTTCCCACCTGTCTT
CTCCCTAGGTGGTTCTGAGCCCCACCCCAATCCAGTGCTACCTGAGTTCTGAGCTCAGAATCTGAC
AGCCTCTCCCCATTCTGTGTGTGTCCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAA
AAGAAAAGACATGTTGGCTATAGGCGTGGTGGCTCATGCCATATAATCCAGCACCTTTGGGAAGCCGGGGTAGGAGG
ATCACCAGAGGCCAGCAGGTCCACACCAGCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTTAAAA
TTAGTGGGCGCTGGTGGTGTGTATCTGTAGGCTTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTG
AGTTCAACACTGCTGAGTCACTGTTGGCCACCACTGCACTCCAGGCTGGGTGACAGAGCAAGACCCCTGTCTCTAA
AATAAAATTTTAAAGGACTTAAAAAAGGCTTAAAAAAGGCTTAAAAAAGGCTTAAAAAAGGCTTAAAAAAGGCTT

FIGURE 466

></usr/segdb2/sst/DNA/Dnaseqs.min/ss.DNA76788
><subunit 1 of 1, 813 aa, 1 stop
><MW: 87739, pI: 6.94, NX(S/T): 5

MGWRPRRRARGTPLL LLLLLLLLLLWVPVPGAGVLQGHIPGQPVTPHWVLDGQPWRTVSLEEPVSKPDMGLVALEAEGQ
ELLLELEKNHRL LAPGYIETHYGPDGQPVVLAPNHTDHCYQGRVGRGFPDSWVVLCTCSGMSGLITLSRNASYL
RPWPPRGSKDFSTHEIFRMEQLLTWKGTGHRDPGNKAGMTSLPGGPQSRGRREARRTRKYLELYIVADHTLFLT
RHRNLNHTKQRLLEVANYVDQLLR TLDIQVALTGLEVWTERDRSRVTQDANATLWAFLOWRRGLWAQRPHDSAQL
LTGRAFQGATVGLAPVEGMCRAESSGGVSTDHSELPIGAAATMAHEIGHSLGLSHDPDGCCVEAAAESGGCVMAA
ATGHPFPRVFSACSRRLRAFFRKGGGACLSNAPDPGLPVPPALCGNGFVEAGEECDGPGQECRDLCCFAHNCS
LRPGAQCAHGDCCVRCLLKPAGALCRQAMGDCDLPEFCTGTSSHCPPDVYLLDGSPCARGSGYCWGACPTLEQQ
CQQLWGP GSHPAPEACFQVVNSAGDAHGNCGQDSEGHFLPCAGRDALCGKLQCQGGKPSLLAPHMVPVDSTVHLD
GQEVTCRGALALPSAQLDLLGLGLVEPGTQC GPRMVCQSRRCRKNAFQELQRCLTACHSHGVCNSNHNCHCAPGW
APPFCDKPGFGGSMDSGPVQAENHDTFLLAMLLSVLLPLLPAGAGLAWCCYRLPGAHLQRCSWGCRRDPACSGPKD
GPHRDHPLGGVHPMELGPTATGQPWPLDPENSHEPSSHPEKPLPAVSPDPQADQVQMPSCLW

Important features of the protein:

Signal peptide:

Amino acids 1-27

Transmembrane domain:

Amino acids 702-720

N-glycosylation sites:

Amino acids 109-113;145-149;231-235;276-280;448-452

Tyrosine kinase phosphorylation site:

Amino acids 236-244

N-myristoylation sites:

Amino acids 29-35;185-191;195-201;308-314;318-324;326-332;338-344;370-376;
400-406;402-408;454-460;504-510;510-516;517-523;580-586;
601-607;661-667;687-693;717-723;719-725

Amidation site:

Amino acids 200-204

Neutral zinc metallopeptidases, zinc-binding region signature:

Amino acids 342-352

FIGURE 467

[illegible]

FIGURE 468

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10160, pI: 6.56, NX(S/T): 0
MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLPL
VTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD
```

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

FIGURE 469

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAGT
TTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAACC
TAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCTGGA
AAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAGACAG
AAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACTTCAGCGTGTGGC
TTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCCAAGCAAGGAAGTAGAATCTTTTGC
AAGAAAAAACTACGGAGTAACTTTCCCCTCTTCCACAAGATTAAGATTCTAGGATCTGAAGG
AGAACCTGCATTTAGATTTCTTGTGATTCTTCAAAGAAGGAACCAAGGTGGAATTTTGGAA
GTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCCCATTGAAGT
CATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAGAGGATCTATG
AGAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTGGTCTCATTTTA
AACATTTTTTTTTTGGAGACAGTGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTAGTGCGTT
CTCAGCTCATTGCAACCTCTGCCTTTTTAAACATGCTATTAAATGTGGCAATGAAGGATTTTT
TTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCCAGGATGAGGATGTTACCCAAAG
CAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAATACTACTTCCTCTGACCATACT
AAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTGTTCAACTTGACATTTT
CTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTTGGATTCAAGAGCACTGT
GTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATGGAATAAAACACAAATGTT
GAAAAATGTAAATATATATACATAGATTCAAATCCTTATATATGTATGCTTGTTTTGTGTAC
AGGATTTTGTTTTTTCTTTTTAAGTACAGGTTCTAGTGTTTTACTATAACTGTCACTATGTA
TGTAAGTACATATATAAATAGTCATTTATAAATGACCGTATTATAACATTTGAAAAAGTCTT
CATCAAAAAAAAAAAAAA

FIGURE 470

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136

><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTFLQLKFLKPKINSFYAFEVKDAKGRTVSLE
KYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFPCNQFGESEPRPSKEVESFA
RKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEPIEV
IRPDIAALVRQVVIKKKEDL

Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

FIGURE 471

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCATTCCCTCCGGCTGCGAGAAAGGACGCGCGCCCTGCG
 TCGGGCGAAGAAAAGAAGCAAACTTGTGCGGAGGGTTTCGTCAATCAACCTCCTTCCCGCAAACCTAAACCTCCT
 GCCGGGGCCATCCCTAGACAGAGGAAAGTTCTGCGAGAGCCGACAGCCCTAGTGGATCTGGGGCAGGCAGCGGC
 GCTGGCTGTGGAATTAGATCTGTTTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTACCGTCCGCGGGC
 ACCGGGTTGGCGCTGCCCGAGTGGAAACCGACAGTTTGCAGGCCTCGGCTGCAAGTGGCTCTCCTCCCCGCGGTT
 GTTGTTCAGTGTGCGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGGTCCGAAGAGCGCTGCG
 CTCTACTCGCGTTTCGCTTCTTCTCTCTCGGTTCCCTACTGTGAAATCGCAGCGACATTTACAAAGGCCTCCG
 GGTCTACCGAGACCGATCCGCGAGCGTTTGGCCCGGTCTGCTTATTGCATCGGGAGCCCCGAGCACCGGCGAA
 GACTGGCGGGTGGGGTAGGGAGGTGGCGGCGCGGCATGGCGAGGTTCCCGAAGGCCGACCTGGCCGCTGCAGG
 AGTTATGTTACTTTGCCACTTCTTCACGGACAGTTTCAGTTCGCGGATGGGAAACCCGGAGACCAAATCCTTGA
 TTGGCAGTATGGAGTTACTCAGGCCTTCCCTCACACAGAGGAGGAGGTGGAAGTTGATTCACACGCGTACAGCCA
 CAGGTGGAAAAGAACTTGGACTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGA
 GCCCAGAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGATACAGACCA
 CAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTTATGGGTGAACATAGACCAAAT
 GGAAAAGATAAAGTGAAGATTTCATGGAATATTGTCCAATACTCATCGGCAAGCTGCAAGAGTGAATCTGTCTT
 CGATTTTCCATTTTATGGCCACTTCCCTACGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGT
 CGTACATCGAATGCTAACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCAGTGTATCCAGAAA
 TTCAACTGTCAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTCCAGGATAATTA
 TAACCTGGGAAGCTTCACATTCCAGGCAACCCCTGCTCATGGATGGACGAATCATCTTTGGATACAAAGAAATTC
 TGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAGTGAAAGTCGGACTGTCCGATGCATTTGTCTGTGTTCCA
 CAGGATCCAACAAATTTCCAATGTTTGAAGAAGAACATTTATGAATACCACCGAGTAGAGCTACAAATGTCAA
 AATTACCAACATTTTCGGCTGTGGAGATGACCCCATACCCACATGCCTCCAGTTTACAGATGTGGCCCCCTGTGT
 ATCTTCTCAGATTTGGCTTCACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGATTTGATCGTCATCG
 GCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAGAGAGATGTGTGAGAATACAGAACCAGTGGAAAC
 TTCTTCTCGAACCACCACAACCGTAGGAGCGACAACCCAGTTTCAGGGTCTTAACCTACCACCAGAAGAGCAGT
 GACTTCTCAGTTTCCCACCAGCCTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGC
 TTCTACAGATGACAGTGCAGCTGAGAAGAAAGGGGGAACCCCTCCACGCTGGCCTCATCATTGGAATCCTCATCCT
 GGTCTCATTTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCACATCAGCAGCCAGCATCTT
 CTTTATTGAGAGACGCCCCAAGCAGATGGCCTGCGATGAAGTTTAGAAGAGGCTCTGGACATCCTGCCTATGCTGA
 AGTTGAACCAGTTGGAGAGAAAGAAGGCTTTATTGTATCAGAGCAGTGCTAAAATTTCTAGGACAGAACAAACACC
 AGTACTGGTTTACAGGTGTTAAGACTAAAATTTTGCTATACCTTTAAGACAAACAAACACACACACAAAC
 AAGCTCTAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCAGGAAACAAAGGGTAAACAA
 AAACTAAAACCTTATACAAGATACCATTTTACTGAACATAGAATTCCTAGTGGAAATGTCATCTATAGTTCACT
 CGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTATAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAG
 GGATCAGAAAAAAAATCATAATAAAGCTTTAGTTTCATGAGGG

FIGURE 472

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVVTQAFPHTEEEVEVD SHAYSH
RWKRNLDFLKAVD TNRASVGQDSPEPRSF TDLLLDGQDNNTQIEEDTDHNYYSRIYGPSDS
ASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVV
HRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQATLLMD
GRIIFGYKEIPVLVTQISSSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKIT
NISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCPEESKEK
MCENTEPVETSSRTTTT TGATTTQFRVLT TTTT RRAVTSQFPTSLPTEDDTKIALHLKDNGASTD
DSAAEKKGGT LHAGLIIGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPAMKFRR
GSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:

Transmembrane domain:

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.

amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

FIGURE 473

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCCG
CGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCCTGAGCCTCGGGCTCCGGCCCGGACCT
GCAGCCTCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGC
TTTAAAAGTGCTACTAGAACAAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTT
GTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGG
AAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGC
TATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTC
CAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCA
GCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTG
GGCTTTCAGACATGGAGTGTGTGCCCTTGTGGAGACCCTCCTCCTCCTTACGAACCGCACTGT
GCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCCTCCAGCCCACGGGACACGGCGCTG
GCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCCTGCTGGCCCTGCTCATCCTCTGTGTCATC
TATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTTCGAGGACATTTCAG
TACAACGGCTCTGAGCTGTGCTGTTTTGACAGACCTCAGCTCCACGAATATGCCACAGAGCC
TGCTGCCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCGGTGCCTTGCTCCCATCCATG
TGCTGTGAGGAGGCTGCAGCCCCAACCCGGCGACTCTTGGTGTGGGGTGCATTCTGCAGCC
AGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGGAGATGGTGCCGACTTCTTCGGATCCCTC
ACGCAGTCCATCTGTGGCGAGTTTTTCAGATGCCTGGCCTCTGATGCAGAATCCCATGGGTGGT
GACAACATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCACTCTCAAT
CCAGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCT
GTTCCAGTCCAGTCTCATTCTGAAAACCTTTACAGCAGCTACTGATTTATCTAGATATAACAAC
ACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAG
AGTGGCGCTGTCATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAGAACCTGCTTC
TTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTTAGGCTTATGGACTGA
GCAGTCTGGACCTTGTCATGGCTTCTGGGGCAAAAATAAATCTGAACCAAACCTGACGGCATTTG
AAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTCAATGAATAACA
AGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCCTACATGAGAAGCTTCTCTGCCAC
AAAAGTGACTTCAAAGACTGATGGGTTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAA
GAAACAGAAATGCCCTCATGCTTATTTTCATGGTGATTGTGGTTTTTACAAGACTGAAGACCCA
GAGTATACTTTTTCTTTCAGAAATAATTTTATACCGCCTATGAAATATCAGATAAATTACCT
TAGCTTTTTATGTAGAATGGGTTCAAAAGTGAGTGTTTCTATTTGAGAAGGACACTTTTTTCATC
ATCTAAACTGATTTCGCATAGGTGGTTAGAATGGCCCTCATATTGCCTGCCTAAATCTTGGGTT
TATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTTCAGAAATCC
ACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTA
GGGAATGTGGTCGAGAAAGGGCAGCCCATTTGCCCAGAATTAACACATATTGTAGAGACTTGTA
TGCAAAGGTTGGCATATTTATATGAAAATTAGTTGCTATAGAAACATTGTGTCATCTGTCCC
TCTGCCCTGAGCTTAGAAGGTTATAGAAAAGGGTATTTATAAACATAAATGACCTTTTACTTG
CATTGTATCTTATACTAAAGGCTTTAGAAATTACAACATATCAGGTTCCCCTACTACTGAAGT
AGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTT
GGATGAAGCAGCTGTAACCTAGTGAGTTTGACCAGGACATTGTGCTGCTCCTTCCAAT
TGTGTAAGATTAGTTAGCACATCATCTCTACTTTAGCCATCCGGTGTGGATTTAAGAGGAC
GGTGCTTCTTTCTATTAAAGTGCTCCATCCCCTACCATCTACACATTAGCATTGTCTCTAGAG
CTAAGACAGAAATTAACCCCGTTAGTCACAAAGCAGGGAATGGTTCACTTACTCTTAATCTT
TATGCCCTGGAGAAGACCTACTTGAACAGGGCATATTTTTTTAGACTTCTGAACATCAGTATGT
TCGAGGGTACTATGATATTTTGGTTTGAATTGCCCTGCCCAAGTCACTGTCTTTTAACTTTT
AAACTGAATATTAAATGTATCTGTCTTTCCT

FIGURE 474

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVCRLHRFKEDWGFQKCKPCLDCAVVNRFOKANCSATSDAICGDCLPG
FYRKTKLVGFQDMECVPCGDP PPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILCVIYCKRQFMKKPSWSLSRQDIQYNGSELSCFDRPQLHEYAHRACCQCRD
SVQTCGPVRLLPSCCEEACSPNPATLGC GVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA
```

Important features of the protein:

Signal peptide:

Amino acids 1-25

Transmembrane domain:

Amino acids 169-192

N-glycosylation sites:

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids 207-214

N-myristoylation sites:

Amino acids 55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids 89-96

FIGURE 475

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCAATG
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCCAA
GCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTTGACCTCAGGGCCATGAAG
CTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGGGTAT
CGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGACGCAA
TCGAACCCGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAAGTACAAATGC
AACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCCGCCGACG
CTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTATCGGCAGG
TCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGCAGAATGACA
GTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTGCACCACCGAG
GGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGC
AACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTA
CAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGCATAGACCGCCCCT
CCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGCCCCTATCACATAGC
TCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 476

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSLD
TGYRAPVTILVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQAPD
PPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSPVYIIRTCHRPSC
TTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 477

CCCACGCGTCCGGGACAGATGAACTTAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGGGAAAGGACAAAA
AGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCTACTGCTGTTCTTTTATGCTGGGAGCTGTGGCTGTAAC
CAACTAGGAAATAACGTATGCAGCAGCTATGGCTGTGAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCTGTT
TCTTTTTCTTTTGGGGAGTGTCTTGGCAGGTTCTGGGTTTGGACGTTATTCGGTGACTGAGGAAACAGAGAA
AGGATCCTTTGTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCCAGGGT
GGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCACAAATGAGAACTGGA
CCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTCCAAATTTTAATGGATGATCCCTTTCAGAT
TTACCGGGCTGAGCTGAGAGTCAGGGATATAAATGATCACGCGCCAGTATTTTCCAGGACAAAGAAACAGTCTTAAA
AATATCAGAAAAATACAGCTGAAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGG
TATCCAAAACCTACACGATCAGCCCCAACTCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCATGATATA
TCCAGAGCTAGTGTGACAAAGCACTGGAGAGGAGCAGGAGAGCTCAGCTTAACCTCAGAGCGCTGGA
TGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATCGTTGTCTTGGACGTCAATGACAAATGCCCCACA
GTTTGGCCAGGCTCTGTATGAGACCCAGGCTCCAGAAAACAGCCCCATTGGGTTCTTATTGTTAAGGTATGGGC
AGAAGATGTAGACTCTGGAGTCAACGCGGAAGTATCCTATTCTTTTTTGTATGCTCAGAAAATATTGCAACGAC
CTTTCAAATCAATCCTTTTTCTGGGAAATCTTCTCAGAGAAATGCTTGATTATGAGTTAGTAAATCTTACAA
AATAAATATACAGGCAATGGACGGTGGAGGCCCTTCTGCAAGATGTAGGGTTTTAGTGGAAAGTATTGGACACCAA
TGACAATCCCCCTGAACCTGATCGTATCATTTTTCCAACCTCTGTTGCTGAGAATCTCCTGAGACGCCGCTGGC
TGTTTAAAGATTAATGACAGAGACTCTGGAGAAAATGGAAGATGGTTTGTACATTCAAGAGAATCTGCCATT
CCTACTAAAACCTTCTGTGGAGAATTTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGA
GTACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAAACCGAGCACAAACATAACGGTCTGGT
CTCCGACGTCAATGACAACGCCCCCGCCTTCAACCAAACCTCCTACACCTGTTCTGTCGCGAGAACAAACAGCCC
CGCCCTGCACATCGGCAGCGTCAAGCGCCACAGACAGAGACTCGGGCACCAACGCCAGGTCACCTACTCGCTGCT
GCCGCCCAAGACCCGCACCTGCCCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCCGCCCT
CAGGTGCTGGACTACGAGGCCCTGCAGGCTTTCGAGTTCGCGTGGGCGCCACAGACCGCGGCTCCCCCGCGCT
GAGCAGAGAGCGCTGGTGCGCGTGTGCTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACCCGCTGCA
GAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCGGGCGGCGAGCCGGGCTACCTGGTGACCAAGGTGGTGCG
GGTGGACGGCGACTCGGGCCAGAACGCTGGTGTGCTACAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTTCGG
TGTGTGGGCGCACAAATGGGGAGGTGCGCACCGCCAGGCTGCTGAGCGAGCGGACGCGAGCCAAGCACAGGCTCGT
GGTGCTTGTCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACCTTGCTCCTGGTGGACGGCTT
CTCCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCCGGCCCCAGGCCAGGCCGAGGCCGACTTGCTCACCCTCTA
CCTGGTGGTGGCGTTGGCCTCGGTGCTCTTCGCTCTTCCCTCCTCTCGGTGCTCCTGTTCTGTTGGCGGTGCGGCTGTG
CAGGAGGAGCAGGGCGGCTCGGTGGGTGCTGCTCGGTGCCGAGGGTCTTTTCCAGGGCATCTGGTGGACGT
GAGGGGCGCTGAGACCTGTCCAGAGCTACCAGTATGAGGTGTGCTGACGGGAGGCCCGGGGACCAAGGTGAGTT
CAAGTTCTTGAACCAAGTTATTTCCGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAATTCCACCTT
CCGAAATAGCTTTGGATTTAATATTAGTAAAGTCTGTTTTTAGTTTCATATACTTTTGGTGTGTTACATAGCCA
TGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTATTATGCAACTTCAAGCATTATTTTCAAGTAGTATA
CCCCTGTGGTTTTACAATGTTTTCATTTTTTTTTGCAATTAATAACAACTGGGTTTAATTTAATGAGTATTTTTT
CTAAATGATAGTGTAAAGTTTTAATTCTTCCAACCTGCCAAGGAATTAATTACTATTATCTCATTACAGAA
ATCTGAGGTTTTGATTCATTTTCAAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTGTACTTGTCTA
TTTAAGAAGGCATATCTACATTTCCAAACTCATTTCAACATTTCTATATATTCGTGTTTGAAGAACCATGTCAATTA
TTTCTACATCATGTATTTAAAAAGAAATATTTCTCTACTACTATGCTCATGACAAAATGAAACAAAGCATATTGT
GAGCAATACTGAACATCAATAATACCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTT
GGCCAATATTTTCTTATGTTAACTTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATAA
TCTGCCTGAAATGAATAAAAAATAAAACATTTTGAAATGTGAAAAAATAAAAAAAAAAAAAA

FIGURE 478

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976
><subunit 1 of 1, 800 aa, 1 stop
><MW: 87621, pI: 4.77, NX(S/T): 7
MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGGRYSVTEETEKGSFVVNLAKDLGLAEGELAARG
TRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVVDI
NDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGLNGIQNYTISPNSFFHINISGGDEGM
IYPELVLDKALDREEQGELSLTLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYETQAP
ENSPIGFLIVKVWAEDVD SGVNAEVSYSFFDASENIRTTTFQINPFSGEIFLRELLDYELVNSY
KINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKINDRDSGEN
GKMVCYIQENLPFLKPSVENFYILITEGALDREIRAENITITVTDLGTPRLKTEHNITVLV
SDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDPHLPLASLV
SINADNGHLFALRSLDYEALQAFEFVRGATDRGSPALSREALVRVLVLDANDNSPFVLYPLQN
GSAPCTELVPRAAEPGYLVTKVVAVDGDSQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLL
SERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDFGSQPYLPLPEAAPAQAEADLLTVYLV
VALASVSSILFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGHLVDVRGAETLSQSYQYEV
LTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ
```

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

FIGURE 479

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCCC
GAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTC**AT**GGGACCTGTGCGGTGG
GAATATTGCTTTTTCCTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGGAGG
ACGATGACACAGAACGCTTGCCCAGCAAATGCCAAGTGTGTAAGCTGCTGAGCACAGAGCTAC
AGGCGGAAGTGAAGTGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTGGATA
CAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGGCCTTAG
AGAATTTATGTGAGCGGATCCTGGACTATAGTGTTTCACGCTGAGCGCAAGGGCTCACTGAGAT
ATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCCTAGTGCAGAAGGGGGTGAAGG
TGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACATACCTCAAGA
AGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTACTTCCACCATC
AGGAGCAGCCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCAGCTGCTGAACTGCAT
GTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAAACAGAAGGGGAGG
AAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAG
GAAGCCACCCCAAACCTTGACCGAGAAGATCTT**TGA**CCCTTGCCTTTGAGCCCCCAGGAGGGGA
AGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAGCTTTCAGGGTGTGTT
TATGAGTGAATCCACCAAGCTTGTAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGG
TGAAACAGCATGACATGGCTTCTGGGGTGGAGGTTGGGGGTGGAGGTCCTGCTCCTAGAGATG
AACTCTATCCAGCCCCTTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCCTCTTT
AACTGATCCACCCCAACCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGAAGTC
ACTTAGCTCCTTAAGGTCTGTTTTTAGACCTTCCAAGGAAGAGGCCAGAACGGACATTCTCT
GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAATGG
GACACTGGGTCATGGCCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCTACTTAA
GCTCAATGTAACCCAGAGCCCACCATATAGTTTATAGGTGCTCAACTTCTATATCGCTATT
AACTTTTTTCTTTTTTTCTA

FIGURE 480

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVL
LGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMATLKGL
VQKGVKVDLGIPLELWDEPSVEVITYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEGHVL
PAAETACLQETWTGKEITDGEKTEGEEEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

FIGURE 481

GGCGTGTGCAAGGCGGGGTCCGGCCCCGCGCAGGTCGGGTAAGCGCGTCTAGGGCGCTGCGCGG
CGCAGCGAAAAATGGCGGCTTCCAGGTGGGCGCGCAAGGCCGTGGTCTGCTTTGTGCCTCTGA
CCTGCTGCTGCTGCTGCTACTGCTACCACCGCTGGGTCTGCGCGGCCGAAGGCTCGCCCGG
GACGCCCCGACGAGTCTACCCACCTCCCCGGAAGAAGAAGAAGGATATTGCGGATTACAATGA
TGCAGACATGGCGCGTCTTCTGGAGCAATGGGAGAAAGATGATGACATTGAAGAAGGAGATCT
TCCAGAGCACAAGAGACCTTCCAGCACCTGTGCACTTCTCAAAGATAGACCCAAGCAAGCCTGA
AAGCATATTGAAAATGACGAAAAAAGGGAAGACTCTCATGATGTTTGTCACTGTATCAGGAAG
CCCTACTGAGAAGGAGACAGAGGAAATTACGAGCCTCTGGCAGGGCAGCCTTTTCAATGCCAA
CTATGACGTCCAGAGGTTTATTGTGGGATCAGACCGTGCTATCTTCATGCTTCGCGATGGGAG
CTACGCCTGGGAGATCAAGGACTTTTTTGGTCCGTCAAGACAGGTGTGCTGATGTAACCTTGGA
GGGCCAGGTGTACCCCGGCAAAGGAGGAGGAAGCAAAGAGAAAAATAAAACAAAGCAAGACAA
GGGCAAAAAAAGAAGGAAGGAGATCTGAAATCTCGGTCTTCCAAGGAAGAAAATCGAGCTGG
GAATAAAAGAGAAGACCTGTGATGGGGCAGCAGTGACGCGCTGTGGGGGGACAGGTGGACGTG
GAGAGCTCTTTGCCCAGCTCCTGGGGTGGGAGTGGTCTCAGGCAACTGCACACCGGATGACAT
TCTAGTGTCTTCTAGAAAGGTCTGCCACATGACCAGTTTGTGGTCAAAGAATTACTGCTTAA
TAGGCTTCAAGTAAGAAGACAGATGTTTTCTAATTAATACTGGACACTGACAAATTCATGTTT
ACTATAAAATCTCCTTACATGGAAATGTGACTGTGTTGCTTTTTCCCATTTTACACTTGGTGAG
TCATCAACTCTACTGAGATTCCACTCCCCTCCAAGCACCTGCTGTGATTGGGTGGCCTGCTCT
GATCAGATAGCAAATTCATGATCAGAGAAGACTTTAAAACTCTTGACTTAATTGAGTAAACTCT
TCATGCCATATACATCATTTTTCATTATGTTAAAGGTAAATATGCTTTGTGAACTCAGATGTC
TGTAGCCAGGAAGCCAGGGTGTGTAATCCAAAATCTATGCAGGAAATGCGGAGAATAGAAAA
TATGTCACCTTGAAATCCTAAGTAGTTTTGAATTTCTTTGACTTGAATCTTACTCATCAGTAAG
AGAACTCTTGGTGTCTGTCAGGTTTTATGTGGTCTGTAAAGTTAGGGGTTCTGTTTTGTTTTCC
TTATTTAGGAAAGAGTACTGCTGGTGTGCGAGGGGTATATGTTCCATTTAATGTGACAGTTTT
AAAGGATTTAAGTAGGGAATCAGAGTCCTTTGCAGAGTGTGACAGACGACTCAATAACCTCAT
TTGTTTCTAAACATTTTTCTTTGATAAAGTGCCTAAATCTGTGCTTTTCGTATAGAGTAACATG
ATGTGCTACTGTTGATGTCTGATTTTGCCGTTTCATGTTAGAGCCTACTGTGAATAAGAGTTAG
AACATTTATATACAGATGTCATTTCTAAGAACTAAAATTTCTTTGGGAAAAACCTCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 482

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92289
><subunit 1 of 1, 234 aa, 1 stop
><MW: 26077, pI: 8.13, NX(S/T): 1
MAASRWARKAVVLLCASDLLLLLLLLLLPPPGSCAAEGSPGTPDESTPPPPRKKKKDIRDYND
ADMARLLEQWEKDDDDIEEGDLPEHKRPSAPVDFSKIDPSKPESILKMTKKGKTLMMFVTV
SGSPTEKETEEITSLWQGSLEFNANYDVQRFIVGSDRAIFMLRDGSYAWWEIKDFLVGQDRC
ADVTLEGQVYPGKGGGSKEKNKTKQDKGKKKKEGDLKSRSSKEENRAGNKREDL
```

Important features of the protein:

Signal peptide:

Amino acids 1-32

N-glycosylation site:

Amino acids 201-205

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 85-89

Tyrosine kinase phosphorylation site:

Amino acids 50-59

N-myristoylation sites:

Amino acids 30-36;138-144;153-159;176-182

Amidation site:

Amino acids 207-211

FIGURE 483

[illegible]

FIGURE 484

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGT
PRLAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNV
QFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLD
AQNPWL TNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLPRENM
SLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIYRVSSV
SSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

FIGURE 485

AGAGTTCCTTTTTCTAGGTCGATTAGGTTATACATTGTTGAAGTATAGTTTCGAGTTAGAATT
GGTCATTTTATTTTCAGTGTTTCACAGAAATCGAAGAAGACAGAAATGCGCGCTTCTGTGGTGG
ATATCTACAGTAGCAATACTGTTGTTTACTTCGACGATTTTGGGAACATACGTTGAAGCTGGT
GCCGCTAAGTCTAACGAAGAAGAGATTGTGAACAAAAGCGAATTGGAAGATTCCACGAGGG
TCGAGAAAGGATGCATCGGGGTGCCACAAGCCGGGCTACCCTGTACCCCTCATTCTCGCTGC
CCTCCACCTCCCATGTGCAGCGTCCTCGTCCTATTCTGCATGCTTAGTCTAACACCATCAGG
CTCGTTTATCTTTTCTGTCATTGATCTCACCAGGAGCAAATCACTAGTGCGTGCTTCTGATT
ACGTAACGTAGTATGTAAATAAATGTCAGTGATATTATGAATTGGTAAAACATTTCTGTTATC
TAAATAAACAGTGAAGTTTGTGTTGACTAAAAAA

FIGURE 486

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96855
><subunit 1 of 1, 84 aa, 1 stop
><MW: 9274, pI: 9.70, NX(S/T): 1
MALLWWISTVAILLFTSTILGTYVEAGAAKSNEEEIVNKSEFGRFPRGSRKDASGCHKPG
YPVPPHSRCPPPPHVQRPRPILHA
```

Signal peptide:

Amino acids 1-21

N-glycosylation site:

Amino acids 38-42

N-myristoylation site:

Amino acids 27-33

FIGURE 487

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCCGGGGCGATGTGGAGCGCG
GGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGGGC
GGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTCAAT
ACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCAGCAA
TCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGGCTCG
GAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACGCATGTG
CTTACGGGCAAGAACCCTGCACACGCACCACTTCCCCTCGCCGCTGTCCAACAACCAGGAGGTG
AGTGCCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCTGCTCTGGA
CAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTGTTCTGTCA
GTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGGCATGCCAGT
GCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTAGTGTGGAGCCC
TCTGCAGGTCACGATGAACTCTGAGTGTGTGGATGGATGGGTGGATGGAGGGTGGCAGGTGGG
GCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCTCAAGTGCCCTTTGTG
ATTAAAGAATGTTGGTCTATGAAA

FIGURE 488

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857
><subunit 1 of 1, 221 aa, 1 stop
><MW: 23598, pI: 6.96, NX(S/T): 0
MWSAGRGGAAPVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGSG
SGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSN
NQEVSAGFEDGEGEDDLDLWTVRCGQHWEREAARFQHVGTSVFLSVTGEQYGSPIRGQHEVH
GMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196

Endoplasmic reticulum targeting sequence.

amino acids 218-223

FIGURE 489

CAGCAGCCGAGACAGCAGCTGAGACGGCAGCGCAGCTTCTCAGGGCCGGAGCCAGTTCTTGGAGGAGACTCTGC
ACAGGGCATGATCACTGTGGTGCCCTTTTCTGTGCTGTGCCTTCTGACTTTGCAGAAATGCAACAACAGAGAC
ATGGGAAGAACTCCTGAGCTACATGGAGAATATGCAGGTGTCCAGGGGCCGGAGCTCAGTTTTTCTCTCGTCA
ACTCCACCAGCTGGAGCAGATGCTACTGAACACCAGCTTCCCAGGCTACAACCTGACCTTGCAGACACCCACCAT
CCAGTCTCTGGCCTTCAAGCTGAGCTGTGACTTCTCTGGCCTCTCGCTGACCAGTGCCACTCTGAAGCGGGTGCC
CCAGGCAGGAGGTGAGCATGCCCCGGGTGAGCAGCCATGCAGTTCCCCGCCGAGCTGACCCGGGACGCCTGCAA
GACCCGCCCCAGGGAGCTGCGGCTCATCTGTATCTACTTCTCCAACACCCACTTTTTCAAGGATGAAAACAACCT
ATCTCTGCTGAATAACTACGTCCTGGGGGCCAGCTGAGTCATGGGCACGTGAACAACCTCAGGGATCCTGTGAA
CATCAGCTTCTGGCACAACCAAGCCTGGAAGGCTACACCCTGACCTGTGTCTTCTGGAAGGAGGGAGCCAGGAA
ACAGCCCTGGGGGGGCTGGAGCCCTGAGGGCTGTCTGACAGAGCAGCCCTCCCACTCTCAGGTGCTCTGCCGCTG
CAACCACCTCACCTACTTTGCTGTCTCATGCAACTCTCCCCAGCCCTGGTCCCTGCAGAGTTGCTGGCACCTCT
TACGTACATCTCCCTCGTGGGCTGCAGCATCTCCATCGTGGCCTCGCTGATCACAGTCTCTGCTGCACITCCATTT
CAGGAAGCAGAGTGACTCCTTAACACGTATCCACATGAACCTGCATGCCTCCGTGCTGCTCCTGAACATCGCCTT
CCTGCTGAGCCCCGATTCGCAATGTCTCCTGTGCCCCGGGTGAGCATGCACGGCTCTGGCCGCTGCCCTGCACTA
CGCGCTGCTCAGCTGCCCTCACTGGATGGCCATCGAGGGCTTCAACCTCTACCTCCTCCTCGGGCGTGTCTACAA
CATCTACATCCGCAGATATGTGTTCAGCTTGGTGTGCTAGGCTGGGGGGCCCCAGCCCTCCTGGTGCTGCTTTT
CCTCTCTGTCAAGAGCTCGGTATACGGACCCCTGCACAATCCCCGTCTTCGACAGCTGGGAGAATGGCACAGGCTT
CCAGAACATGTCCATATGCTGGGTGCGGAGCCCCGTGGTGACAGTGCTCCTGGTTCATGGGCTACGGCGGCCTCAC
GTCCCTCTTCAACCTGGTGGTGCTGGCCTGGGCGCTGTGGACCTGCGCAGGCTGCGGGAGCGGGCGGATGCACC
AAGTGTGAGGGCCTGCCATGACACTGTCACTGTGCTGGGCCTCACCGTGCTGCTGGGAACCACTGGGCCTTGGC
CTTCTTTTCTTTTGGCGTCTTCTGCTGCCCAGCTGTTCTCTTCAACATCTTAACTCGCTGTACGGTTTCTT
CCTTTTCTGCTGCTTCTGCTCCCAGCGGTGCCGCTCAGAAGCAGAGGCCAAGGCACAGATAGAGGCCCTTCAGCTC
CTCCCAAACAACACAGTAGTCCGGGCCTCCTGGCCTGGAATCCTCAGCCTCTCTGGCCGCCAGTAGCCTGAGGCT
ACGGCTCCTGCTAGAGAGGGTGGCAGGCCTGCTGCTGGACCCAGAGGCCACTGTGACCGCCAAGGGGCCTTTTC
CACTTCCACGGCCTCTCCAGGCACTGAGGGGAAGGCATTGCTCTACCTCTCCCTGACATTTTGCTCCGGGGCAGA
TCCAACCTTACCTGGGGCAGCAAACTTTGTCTGTTACCTGGGCCAGCTCGCCAGGGATGTGGGCAGAGCACCA
GCCTGGGCATCAGGAAGCCAAGTTTCAAGGACTGTCTTTGAGTCTGTCTGTATGACCTTGGGCCTGCCACTTCTC
ACAGACCCTAGGTATCCACAGCTGTGACATGGGGGCAAGCAGCTTTGTTTCAGCCTAACCCAGGAGCTTAGTAAA
AATTGCATAAGACCAGGGGGAAGAGTGTGAGCGTGGGGTGGGAATTCCCGCGGCCTCCACCTGCTTGTAGGGGC
AGGATCTCATTAGGCTGCCCTGGAAGCACCTGCTTGGCCCTGCCACCTTCTCCAGGGGAGGGCCAGATGGCAT
CCTGGCTTGGGGCGGGTGGGACCTACCCAGGCTCTGAGACTTTACTGGCCTATGCCTGAGGCCTCTTTTCTTTTA
ACTCCCTAAATTATGATGACTCCAAGTCCAAGCCCACCTTCCCAAAGATTGGGAGGTTCCGCCGTTCACAGAGG
CTCCTCCTGCGGTGCTCCCAAGACTTCCATAGACCATCTGGACCAGTAGCCCATCCCGCAGTTTTCTTGGGGGCA
GAGGAAAAACGCTTCTTTCTCTCCAGCTGAATCAGCTGGATCCAGTGCTCCTGGCTGTTTGGTGATTGGGCAAGA
TTGAATTTGCCAGGTAGGCGTGAGAGTGTGGGTTTAAATTGGAAGCTCAGGCCATAGTTTTCAGAGAATCACCC
TTACCCACAGACCTTATGAGACAGTGCTCATGAAGCCAGTGCGTTTTCCAGAACGAACACTAGGCGGCACCGTTG
GTCCACACTCAGAGGCCCTTGGCGCCAAGACTGCATCTAGAATCGCTCAAACACCTGTTTGCAGACCCCATGCAC
CAGCTGGAGGGGCCGTAAGTGCAGGACTGCGCCTACTGAGTGACCCATTTCTCCAGGAGGAAAGGCAAGACACG
CTTACACGGCCATTTGTCTCTTTTCCCAATGCGGCGGTGCACTTTCGCTCTTGGGGGCTGCACCCAGACATAGC
TGGCACCAGAGCAGGGTGTCTCAGGTGGTGGGTGCTCAGGGCCCTGCCCCAGGCCACTGGGCGGTTTTGATGACCT
CAAAGGTACAGGCAGAAAATAGGAGCAGGATTTCCCTGGGGAAAAGTTATCCTGGGACATCTTCTGCTCTTCT
GTACATTTCTAGATGCAATAACTCCTTACCAGGCAGTGAGTGGCGTAGGCTCTGGAGCCAGGCTGCCTGGGCT
CCAATGCCAGCTCTGCCACTTGTAGCTGTGAGACTGTGGACAAACCACTCAGCCTCTGTGTGCCTCAGTTTTCC
TATTTGTAAATAGAGACCATAGTGGTACCTATTTTGAAGACTAAGTAAAAGAATTCAAATAAAGAGACTTGGCA
CAGAGTAAGTGCTCAGTAAAAA

FIGURE 490

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96860
><subunit 1 of 1, 528 aa, 1 stop
><MW: 59000, pI: 8.73, NX(S/T): 9
MDHCGALFLCLCLLTQLQATTETWEELLSYMENMQVSRGRSSVFSSRQLHQLEQMLLNTS
FPGYNLTQLQTPTIQSLAFKLSCDFSGLSLTSLTLKRVLPQAGGQHARGQHMQFPALTRD
ACKTRPRELRLICIYFSNTHFFKDENNSSLLNNYVLGAQLSHGHVNNLRDPVNISFWHNQ
SLEGYTLTCVFWKEGARKQPWGGWSPEGCRTEQPSHSQVLCRCNHLTYFAVLMQLSPALV
PAELLAPLTYISLVGCSISIVASLITVLLHFHFRKQSDSLTRIHMNLHASVLLLNIAFLL
SPAFAMSPVPGSACTALAAALHYALLSCLTWMAIEGFNLYLLLGRVYNIYIRRYVFKLGV
LGWGAPALLVLLSLSVKSSVYGPCTIPVFDSENGTGFQNMSCWVRSPVHSLVMGYG
GLTSLFNLVVLAWALWTLRRLRERADAPSVRCHDTVTVLGLTVLLGTTWALAFFSFGVF
LLPQLFLFTILNSLYGFFLFLWFCSQRCRSEAEAKAQIEAFSSSQTTQ
```

Important features of the protein:

Signal peptide:

Amino acids 1-21

Transmembrane domains:

Amino acids 244-264;290-309;316-344;358-376;411-431;468-491

N-glycosylation sites:

Amino acids 18-22;58-62;65-69;146-150;147-151;173-177;
179-183;394-398;400-404

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 274-278

N-myristoylation sites:

86 GLSLTS
101 GGQHAR
157 GAQLSH
255 GCSISI
311 GSACTA
420 GGLTSL
467 GTTWAL

Prokaryotic membrane lipoprotein lipid attachment sites:

Amino acids 246-257;318-329

Eukaryotic thiol (cysteine) proteases histidine active site:

Amino acids 410-421

G-protein coupled receptors family 2 proteins:

Amino acids 273-302;314-343

FIGURE 491

CTTGGCTGCCCCGACAACAAGCTCGCCACCTGCGCTGGGCGCATCCACCATCCAAGGCCAGCT
GAGGGGCACCAGACAGAGGATGAGGAGAGAGAGTGCACACGGGCTGCCCTGAGAGACATTTC
CATGGACATCCTCATGCTGCTTCTGCTTTTGTGTGTAATATATGGGAGATTTCCCAAGATGA
ATACTCCCTCAATCAAGCTATCCGGAAAGAATTTACAAGAAATGCCAGAACTGCTTGGGTGG
CCTGAGAAACATCGCTGACTGGTGGGACTGGAGTCTGACCACACTTCTGGATGGCCTGTACCC
GGGAGGCACCCGTCAGCCCGTGTGCCGGGGGCTCAGCCTGGAGCTCTTGGAGGAAAATGCTA
CCTAATAGGCAGTTCCGTAATTAGGCAGCTAAAAGTTTTTCTAGGCATTTATGCAAGCCTCC
CAGGCCATTTTCAGCACTCATCGAAGACTCTATTCTACATGTAGTCCCGAAGTTGGAGGCC
TGAGAACCCCTACCTGATAGACCCAGAGAACCAAAACGTGACCCTGAATGGTCTTGGGGGCTG
TGGGACAAGGGAGGACTGTGTGCTCAGCCTGGGCAGAACAAAGGACTGAAGCCCACACAGCCCT
GTCCCGACTCAGGGCCAGCATGTGGATTGACCGCAGCACCAGGGCTGTGTCTGTGCACTTCAC
TCTCTATAACCCCTCCAACCCAACTCTTCACCAGCGTGTCCCTGAGAGTGGAGATCCTCCCTAC
GGGGAGTCTCGTCCCTCATCCCTGGTGGAGTCATTCAGCATCTTCCGCAGCGACTCAGCCCT
GCAGTACCACCTCATGCTTCCCCAGCTGGTCTTCTGCACTCAGCCTGATCCACCTCTGTGT
TCAACTCTACCGTATGATGGACAAGGGCGTCTCAGCTACTGGCGAAAGCCAAGGAAGTGGCT
GGAGGTAGCCTCTCTTGTGTCATTTTCTTTTGAAAAATACAATAAACTGTTTATATCTTGAA
AAAAATAATTTAAATAAGAAATTGATTATGCACTAGCTACTGCCAACATTATTGCAGTTTTCTC
CCTCTGTAGTGTTAATCTCAAAACAGCATTTGAGATCAGGTATCATTTAGTGTTGTACAGTT
ACCGTCATGTACCACACGAATTTAGCCAAGGTGGTGGTCCCATAGATCATATGGTGCTAAG
AAATTTCTGTACCTAATGACATCTTGATTCTGACCTTGTATGTAGGCCTAGGCTAAATATGT
CTGTTTGTATCTTAGCTTTTAATAAAGAAGTTAAAAATAAAAAA

FIGURE 492

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96861
><subunit 1 of 1, 300 aa, 1 stop
><MW: 33649, pI: 9.26, NX(S/T): 1
MRRESRTRAALRDISMDILMLLLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGLRN
IADWWDWSLTTLLDGLYPGGTPSARVPGAQPGALGGKCYLIGSSVIRQLKVFPRHLCKPP
RPFSAIEDSIPTCSPEVGGPENPYLIDPENQNVTLNGPGGCGTREDCVLSLGRTRTEAH
TALSRLRASMWIDRSTRAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIF
RSDSALQYHMLPQLVFLALSLIHLVCVQLYRMMDKGVLSYWRKPRNWLEVASLVSFSEK
```

Important features of the protein:

Signal peptide:

Amino acids 1-30

Transmembrane domain:

Amino acids 250-267

N-glycosylation site:

Amino acids 153-157

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 2-6

N-myristoylation sites:

Amino acids 56-62;75-81;79-85;80-86;88-94;92-98;160-166

FIGURE 493

TCTCAGGGCTTCATACAGGAAATCTATTGCTGTGTCAAGTTCCAGAGAAAAGCTTCTGTTCGT
 CCAAGTTACTAACCAGGCTAAACCACATAGACGTGAAGGAAGGGGCTAGAAGGAAGGGAGTGC
 CCCACTGTTGATGGGGTAAGAGGATCCTGTACTGAGAAGTTGACCAGAGAGGGTCTCACCATG
 CGCACAGTTCCTTCTGTACCTGTGTGGAGGAAAAGTACTGAGTGAAGGGCAGAAAAAGAGAAA
 ACAGAAATGCTCTGCCCTTGGAGAACTGCTAACCTAGGGCTACTGTTGATTTTACTATCTTC
 TTAGTGGCCGAAGCGGAGGGTGTCTCAACCAAACAACCTCATTAAATGCTGCAAACTAGCAAG
 GAGAATCATGCTTTAGCTTCAAGCAGTTTATGTATGGATGAAAAACAGATTACACAGAACTAC
 TCGAAAGTACTCGCAGAAGTTAACACTTCATGGCCTGTAAAGATGGCTACAAATGCTGTGCTT
 GTTGGCCCTCCTATCGCATTAAAGAAATTTGATCATAATAACATGGGAAATAATCCTGAGAGGC
 CAGCCTTCCTGCACAAAAGCCTACAGGAAAGAAACAAATGAGACCAAGGAAACCAACTGTACT
 GATGAGAGAATAACCTGGGTCTCCAGACCTGATCAGAATTCGGACCTTCAGATTTCGTCCAGTG
 GCCATCACTCATGACGGGTATTACAGATGCATAATGGTAACACCTGATGGGAATTTCCATCGT
 GGATATCACCTCCAAGTGTTAGTTACACCTGAACTGACCCTGTTTCAAAACAGGAATAGAACT
 GCAGTATGCAAGGCAGTTGCAGGGAAGCCAGCTGCGCAGATCTCCTGGATCCCAGAGGGCGAT
 TGTGCCACTAAGCAAGAATACTGGAGCAATGGCACAGTGAAGTGTAAAGAGTACATGCCACTGG
 GAGGTCCACAATGTGTCTACCGTGACCTGCCACGTCTCCCATTTGACTGGCAACAAGAGTCTG
 TACATAGAGCTACTTCTGTTCAGGTGCCAAAAAATCAGCAAAATTATATATTTCCATATATC
 ATCCTTACTATTATTATTTTGACCATCGTGGGATTCATTTGGTTGTTGAAAGTCAATGGCTGC
 AGAAAATATAAATTGAATAAAACAGAATCTACTCCAGTTGTTGAGGAGGATGAAATGCAGCCC
 TATGCCAGCTACACAGAGAAGAACAATCCTCTCTATGATACTACAAACAAGGTGAAGGCATCT
 CAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATAAGTTGTTGGACTCTAGTAC
 CAAGAAACAACAACAACGAGATACATTATAATTACTGTCTGATTTTCTTACAGTTCTAGAAT
 GAAGACTTATATTGAAATTAGGTTTTCCAAGGTTCTTAGAAGACATTTTAATGGATTCTCATT
 CATACCCTTGTTATAATTGGAATTTTTGATTCTTAGCTGCTACCAGCTAGTTCTCTGAAGAACT
 GATGTTATTACAAAGAAAATACATGCCCATGACCAAATATTCAAATTGTGCAGGACAGTAAAT
 AATGAAAACCAAATTTCTCAAGAAATAACTGAAGAAGGAGCAAGTGTGAACAGTTTCTTGTG
 TATCCTTTCAGAATATTTTAATGTACATATGACATGTGTATATGCCTATGGTATATGTGTCAA
 TTTATGTGTCCCCTTACATATACATGCACATATCTTGTCAAGGCACCAGTGGGAACAATACA
 CTGCATTACTGTTCTATACATATGAAAACCTAATAATATAAGTCTTAGAGATCATTTTATATC
 ATGACAAGTAGAGCTACCTCATTCTTTTAAATGGTTATATAAAATTCATTGTATAGTTATAT
 CATTATTTAATTAAAAACAACCCTAATGATGGATATTTAGATTCTTTTAAGTTTGTGTTATTT
 CTTTAAAGTTTTGTTTGTGGTATAAACAATACCACATAGAATGTTTCTTGTTCATATATCTCT
 TTGTTTTTGAGTATATCTGTAGGATAACTTTCTTGAGTGGAATTGTCAGGTCAAAGGGTTTGT
 GCATTTTACTATTGATATATATGTTAAATTGTGTCAAATATATATGTCAAATTCCTCCAACA
 TTGTTTAAATGTGCCTTTCCCTAAATTTCTATTTTAAATACTGTACTATTCCTGCTTCTACAG
 TTGCCACTTTCTCTTTTAAATCAACCAGATTAAATATGATGTGAGATTATAATAAGAATTATA
 CTATTTAATAAAAAATGGATTTATA

FIGURE 494

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96866
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39069, pI: 8.13, NX(S/T): 10
MLCPWRTANLGLLLILTIFLVAEAEAGAAQPNNSLMLQTSKENHALASSSLCMDEKQITQN
YSKVLAEVNTSWPVKMATNAVLCCPPIALRNLIITWEIILRGQPSC TKAYRKETNETKE
TNCTDERITWVSRPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLVTPELTL
FQNRNRTAVCKAVAGKPAAQISWIPEGDCATKQEYWSNGTVTVKSTCHWEVHNVSTVTCH
VSHLTGNKSLYIELLPVPGAKKSAKLYIPYIILTIILTIIVGFIWLLKVNGCRKYKLNKT
ESTPVVEEDEMOPYASYTEKNNPLYDTTNKVKASQALQSEVD TDLHTL
```

Important features of the protein:

Signal peptide:

Amino acids 1-24

Transmembrane domains:

Amino acids 78-98;267-286

N-glycosylation sites:

Amino acids 31-35;60-64;69-73;116-120;122-126;185-189;
218-222;233-237;247-251;298-302

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 112-116

N-myristoylation sites:

Amino acids 103-109;259-265

FIGURE 495

CCAGGTGCACAGCGCATCGCCCCGAGGCTGTACCGCCCTGCCCCGCCCACCCCAGCTGTCCTG
GACCCAGGGGCGAGGAGAGGCTGGACGCCAGGTGCGCGGACACAGAAGCGTCTAAGCACAGCT
TCCTCCTTGCCGCTCCGGGAAGTGGGCAGCCAGCCAGGAACCAGTACCACCTGCACCAATGGG
GCTGTCCCGGAAGGAGCAGGTCTTCTTGCCCTGCTGGGGGCTCGGGGGTCTCAGGCCTCAC
GGCACTCATTCTCCTCCTGGTGGAGGCCACCAGCGTGCTCCTGCCCACAGACATCAAGTTTG
GATCGTGTGTTGATGCGGGCTCCTCCACACGTCCCTCTTCTGTATCAGTGGCCGGCGAAACAA
GGAGAATGGCACGGGTGTGGTCAGCCAGGCCCTGGCCTGCCAGGTGGAAGGGCCTGGAATCTC
CTCCTACACTTCTAATGCTGCACAGGCTGGTGAGAGCCTGCAGGGCTGCTTGAGGAGGCGCT
GGTGTGATCCCAGAGGCCAGCATCGGAAAACACCCACGTTCTGGGGGCCACGGCTGGCAT
GAGGTTGCTCAGCCGGAAGAACAGCTCTCAGGCCAGGGACATCTTTCAGCAGTCACCCAGGT
CCTGGGCCGTCTCCCGTGGACTTTTGGGGTGCCGAGCTCCTGGCCGGGCAGGCCGAAGGTGC
CTTTGGTTGGATCACTGTCAACTACGGCTTGCGGACGCTGGTCAAGTACTCCTTCACTGGAGA
ATGGATCCAGCCTCCGGAGGAGATGCTGGTGGGTGCCCTGGACATGGGAGGGGCCCTCCACCCA
GATCACGTTTCGTGCCTGGGGGCCCCATCTTGACAAGAGCACCCAGGCCGATTTTCGCCTCTA
CGGCTCCGACTACAGCGTCTACACTCACAGCTACCTGTGCTTTGGACGGGACCAGATGCTGAG
CAGGCTCCTCGTGGGGCTGGTGCAGAGCCGCCCGCTGCCCTGCTCCGTACCCGTGTACCT
CAGCGGCTACCAGACCACACTGGCCCTGGGCCCGCTGTATGAGTACCCTGTGTCCACGCCAC
GCCCCCGCTGAGCCTCCCCAGAACCTCACAGTTGAAGGGACAGGCAACCCTGGAGCCTGCGT
CTCAGCCATCCGGGAACTTTTCAACTTCTCCAGCTGCCAGGGCCAGGAGGACTGCGCCTTTGA
CGGGGTCTACCAGCCCCCGCTGCGGGGCCAGTTCTATGTGGAGGCCAGCTACCCTGGGCAGGA
CCGCTGGCTGCGGGACTACTGTGCCTCAGGCCTGTACATCCTCACCTCCTGCACGAGGGCTAC
GGGTTACAGCAGGAGACCTGGCCCAGCCTCGAGTTCCGAAAGCAGGCGGGCGGTGTGGACATT
GGCTGGACACTGGGCTACATGCTGAACCTGACCGGGATGATCCCGGCCGATGCGCCGGCTCAG
TGGCGGGCAGAGAGCTACGGCGTCTGGGTGGCCAAAGTGGTGTTCATGGTGTGTCCTGGTG
GCGGTGGTGGGGCTGCCCTTGGTCCAGCTCTTCTGGTTGCAGGACTAGTGGGAAGGCGGAGGT
GGGCCCCACAGAGCCCACAGGCAGCTGCGTCCCGGATGCTGGAGGCTTCTGAGCCCTGAGC
GCCGTGGGGCCTTGCTCTGTGGCTCTGCCCACGGTCAGGTGACAGCCACCTCCAGGGCACCGT
CAGGGTGGTGTGTCGCCACAGAGGCTGCATGACCTCCCCTCCCGCGTCCCTCCCCAACCTCC
TTCCGCAACTGGGCTTCCAGGGCCGTAGGTGCCTTTCTGCACACAGGCCGCCAGGACTCGTGG
TGTCTCCAGGCTGTGTGACTGCAGGGCCACATGCTGCCTGCAAACAGGGCAAGACCACGGAGG
CACAGGGGTCTGCTCCTGATGGGGCCTCAGGAGGGGCGGAGAGGGGTGGAAGGGAGGGAGCT
GCCCCACCTGGACCCCCGCTCTCCCTGCTGTTGTCTGAGCAGATGGATGGAGTCCAGGCCTGG
GGGCTTCTGCTGGGCCAGCCCGGCTCCACACCCACTTGGAGGGTGAGACTGCAGTGGGGT
TGTTTTTATTAAAAGCATCATGGACACAGCAAAAAAAAAAAAAA

FIGURE 496

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96870
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49377, pI: 4.98, NX(S/T): 5
MGLSRKEQVFLALLGASGVSGLTALILLVLEATSVLLPTDIKFGIVFDAGSSHTSLFLYQ
WPANKENG TGVSQALACQVEGPGISSYTSNAAQAGESLQGCLEEALVLIPEAQHRKTPT
FLGATAGMRLLSRKNSSQARDIFAAVTQVLGRSPVDFWGAELLAGQAEAGFGWITVNYGL
GTLVKYSFTGEWIQPPEEMLVGALDMGGASTQITFVPGGPILDKSTQADFRLYGSDYSVY
THSYLCFGRDQMLSRLLVGLVQSRPAALLRHPCYLSGYQTTLALGPLYESPCVHATPPLS
LPQNLTVEGTGNPGACVSAIRELFNFSSCQGQEDCAFDGVYQPPLRGQFYVEASYPGQDR
WLRDYCASGLYILTLLHEGYGFSEETWPSLEFRKQAGGVDIGWTLGYMLNLTGMIPADAP
AQWRAESYGVVAKVVMVLALVAVVGAALVQLFWLQD
```

Important features of the protein:

Signal peptide:

Amino acids 1-21

Transmembrane domain:

Amino acids 428-449

N-glycosylation sites:

Amino acids 67-71;135-139;304-308;325-329;410-414

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 133-137

N-myristoylation sites:

Amino acids 50-56;123-127;165-171;207-213;234-240;
 259-265;311-317;314-320;331-337;398-404;
 413-419;429-435

GDA1/CD39 family of nucleoside phosphatases proteins:

Amino acids 43-59;202-215

FIGURE 497

GCCTTATAAAGTAGCCTCTGCATCTGCCTGCCTCGGGCAGAGGAGGGCTACCCCTGGGGCTGAG
 AGTTCACCTGTCTCAGGAACCACCTGAGCCACAGATCCTGTGGGCAGCGGCCAGGGCAGCCA
TGGCTTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCCGTGGTCGGTGCCTCCA
 CGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTGAAATTGGGAAAG
 CCCCTCTCCAGCGGGCCCTGCAGGTCACTGTCCCTCATTTCTGGACTGGAGTGGAGAGGCGC
 TTCAGCCCCACCAGGATCCGGATTCTGAATGTCCATGTGCCCCGCCCTCCACCTGAAATTCATTG
 CTGGTTTCGGAGTGC GCCTGCTGGCAGCAGCTAATTTTACTTTCAAGGTCTTTCGCGCCCCAG
 AGCCCCTGGAGCTGACGCTGCCTGTGGAAGTCTGGCTGACACCCGCGTGACCCAGAGCTCCA
 TCAGGACCCCTGTGGTCAGCATCTCTGCCTGCTCTTTATTCTCGGGCCACGCCAACGAGTTTG
 ATGGCAGTAACAGCACCTCCACGCGCTGCTGGTCCCTGGTGCAGAAGCACATTAAAGCTGTCT
 TGAGTAACAAGCTGTGCCTGAGCATCTCCAACCTGGTGCAGGGTGTCAATGTCCACCTGGGCA
 CCTTAATTGGCCTCAACCCCGTGGGTCTGAGTCCAGATCCGCTATTCCATGGTCAGTGTGCT
 CCACTGTCAACAGTGA CTACATTTCCCTGGAAGTCCAATGCTGTTCTCTTCTGCTGGGCAACC
 CCATCATCCTGCCCACGGATGCCACCCCTTTTGTGTTGCCAAGGCATGTGGGTACCGAGGGCT
 CCATGGCCACCGTGGGCCTCTCCCAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGG
 CCGGTGCCCTCAACCTGGACATCACAGGGCAGCTGAGGTCCGATGACAACCTGCTGAACACCT
 CTGCTCTGGGCCGGCTCATCCCGAGGTGGCCCGCCAGTTTCCCGAGCCCATGCCTGTGGTGC
 TCAAGGTGCGGCTGGGTGCCACACCTGTGGCCATGCTCCACACAAACAACGCCACCCCTGCGGC
 TGCAGCCCTTCGTGGAGGTCTGGCCACAGCCTCCAACCTCGGCTTTCAGTCCCTCTTCTCCC
 TGGATGTGGTAGTGAACCTTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA
 CGTCTGTGCTGGGGGATGTCCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATACAGAT
 CAGGTGCGCACACTGATGGGCACCGTTTTTTGAGAAGCCCCCTGCTGGACCATCTCAATGCTCTC
 TTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCCCCTGAGATCTTT
 GTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAGAGCTGAGGCAAGACCACT
 GGGAGGCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCATTTCAAGCCACTGGGGA
 AACTGAGGCAAAACCATACTTAGTCATCACCAACAAGCTGGACTGCTTAGCTGGGCTGTTTTTA
 TCTTCCCTGAGTGCCTGGGTCTCCCTCCCTCACTTCTGCCCCTTTCCCTTCCTCCTCTTCT
 CCTCCCTCTTCCCTCATCTCCCCCTCCTTCCTCTGCCCCACCCAGGGGGGAGCAGACTGCT
 CCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTAAACAACCTTCTCTTGAGCTGC

FIGURE 498

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96872
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49158, pI: 8.72, NX(S/T): 4
MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTVPHFLDWS
GEALQPTRIRILNVHVPRLHLKFIAGFGVRLLAANFTFKVFRAPPELELTLPVELLADT
RVTQSSIRTPVVSISACSLFSGHANEFDGSNSTSHALLVLVQKHIKAVLSNKLCLISISNL
VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVTSDYISLEVNAVLFLLGNPIILPTDAT
PFVLPRHVGTEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDDNLLNTSALGRL
IPEVARQFPEPMPVVLKVR LGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV
VVNLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGFIDTDQVRTLMGTVFEKPLLDHLNA
LLAMGIALPGVVNLHYVAPEIFVYEGYVVISSGLFYQS
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

Transmembrane domain:

Amino acids 217-236

N-glycosylation sites:

Amino acids 96-100;151-155;293-297;332-336

N-myristoylation sites:

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

LBP / BPI / CETP family proteins:

Amino acids 22-50; 251-287

FIGURE 499

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCCATGAAGC
CCTTATGCTGCTCACCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTGCTGTCACTC
CTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGGACA
GCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCTGTGG
CACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTGACATA
TAACACCACCTGCTGCAACAAGGACAACTGCAACAGCGCAGGACCCCGGCCCACTCCAGCCCT
GGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACTGAACTCATT
CCATTGGCTGCCCCCTCCTCCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCTCTGTATCC
CCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTGTTCCGAGTG
GTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGTCCCTTCCAC
TTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCTATACTCTGCTG
TCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTGTTGTCCCCAGTG
AAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCC
ATATGTACCCCATCCCCATACTCACCTCTTTCCATTTTGAGTAATAAATGTCTGAGTCTGGA
AAAAAAAAAAAAAAAAAAAA

FIGURE 500

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSNL
RCGTPEEPCQEAFNQTNRKLGLTYNITTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH
```

Important features of the protein:

Signal peptide:

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

FIGURE 501

GGAGCCTCCTAATGCAGTCTTCTGCACAGTCCTGGGGACTGACTGACTGAATCACACCTCTGG
GGCTGGGGGCTGCTGACATGTGTGCCTTTCCTTGGCTGCTTCTTCTCCTGCTGCTCCAGGAGG
GCAGCCAAAGGAGACTCTGGAGATGGTGTGGATCCGAGGAAGTGGTTGCGGTCCTTCAGGAGT
CCATCAGCCTCCCCCTGGAAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCAC
AAAAGTCTTGCCACTGTGGTGCCAGGGAAAGAGGGACATCCAGCTACCATCATGGTGACCAAT
CCACACTACCAGGGCCAAGTGAGCTTCTGGACCCAGCTATTCCCTGCATATCAGCAATCTG
AGCTGGGAGGATTCAGGGCTTTACCAAGCTCAAGTCAACCTGAGAACATCCCAGATCTCTACC
ATGCAGCAGTACAATCTATGTGTCTACCATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCC
TTCTGCCTCCTGGCCAAGGGATTGCTCATCTTCTTGCTCTTGGTAATTCTGGCCATGGGACTC
TGGGTCATCCGAGTCCAGAAAAGACACAAAATGCCAAGGATGAAGAAACTCATGAGAAACAGA
ATGAAATTGAGGAAGGAGGCAAAGCCTGGCTCCAGCCCTGCCTTGACTGCTCCTTGGGAACCCC
AGTCCTGAGCTTGGTTTCTTCCAGCACCCAGAGAATCCTTCCTCAGCTCTTCTTTCCAGG
GGAAGGAGGTGCTCAGGGGTGGGTATCCAGAGAGCCATACTTCTGAGGGAAGACTGGCTGGCA
ATAAAGTCAAATTAAGTGACCACA

FIGURE 502

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96879
><subunit 1 of 1, 198 aa, 1 stop
><MW: 22584, pI: 9.40, NX(S/T): 1
MCAFPWLLLLLLLLQEGSQRRLLWRWCGSEEVVAVLQESISLPLEIPPDEEVENIIWSSHKS
LATVVPGKEGHPATIMVTNPHYQGQVSFLDPSYSLHISNLSWEDSGLYQAQVNLRTSQIS
TMQQYNLCVYHPNYASEKPSTAFCLLAKGLLI FLLLVILAMGLWVIRVQKRHKMPRMKKL
MRNRMKLRKEAKPGSSPA
```

Important features of the protein:

Signal peptide:

Amino acids 1-18

Transmembrane domain:

Amino acids 144-165

N-glycosylation site:

Amino acids 99-103

N-myristoylation site:

Amino acids 106-112

FIGURE 503

ACGGGCCGCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCAG
 TCGGGCCGTTCCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCTAC
 CGCACCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCCATGGC
 CGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTCTGCT
 GACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTAAAAGC
 TCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCACAGTTGAA
 ATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTGAGAACA
 AGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCATACAAATT
 TGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGTACTAAGAGG
 TTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAACTGAAGGAGTC
 TGGAAAGCAGCACGGCTTTGCCTCTTTCTCTGATTATTATTATAAGTGGTCTCGGCGGATTCT
 CTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTTTGTAGTCTATAA
 GCTGTTCTTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCA
 CCGTTACCAGAGATTACCAACTCAGCAGGACCTCCTCCCCAGGCTTTAAGTCTGAGTTCAC
 AGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGCTTTTACAGGACAACA
 AGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTGGTGGAATACTAGGATA
 TTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGGTACTACCCGTCCTATCC
 TCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCATGGAGGCTCGGGCAGCTA
 TTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAGGATATGGTGGTACCAGGAG
 ACGATAAAAGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAATTTTGGATTTTTCATCACTTT
 CTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAGGGGATATTCAAAGTTCTGTG
 GTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAGGCTAAAAGTTGATGTGTGACAA
 AATACTTATGTGTTGTATGTCAGTGTAAATGCAGATGTATATTGCAGTTTTTGAAAGTGATC
 ATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAACCTGTGATGCCCTAAGAAGCATTA
 GAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTCAAGTTTATAGGTGGTTGTAGC
 TGATGAGTTATTACCTCATAGAGACTATAATATTCTATTTGGTATTATATTATTTGATGTTTG
 CTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAATTATGCTAATTTGTGAGTTCTGATCAC
 TTTTGAGCTCTGAAGCTTTGAATCATTCAAGTGGTGGAGATGGCCTTCTGGTAACTGAATATTA
 CCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTAGAAGGTTGTTGTGAATGACTCTGTGCTGG
 CAAAAATGCTTGAAACCTCTATATTTCTTTCGTTTCATAAGAGGTAAAGGTCAAATTTTCAAC
 AAAAGTCTTTTAATAACAAAAGCATGCAGTTCTCTGTGAAATCTCAAATATTGTTGTAATAGT
 CTGTTTCAATCTTAAAAAGAATCA

FIGURE 504

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIQ
LKCVGGTAGCDSYTPKVIQCQNKGWGDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQYVL
RGSCGLEYNLDYTELGQLKESGKQHGFAFSFYKWSADSCNMSGITIVVLLGIAFVV
YKLFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGSAFTG
QQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPLHGGS
SYSVCSNSDTKTRTASGYGGTRRR

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318

FIGURE 505

GCAAAAGGAAGGGAGGGAAGCACTCCATCATCTCACTGGGAAGAACGGCACGGGCATACCTGC
AGCTACTGGGGTTCCACTGGGCTTGAGGGTCGATTTTTCACCTTTTGAAGGACAAGATGCATT
GGAAGATGTTGCTGCTTCTGCTGTTGTATTACAATGCTGAGGCTTCTATGTGCCACAGGTGGA
GCAGGGCTGTGCTCTTCCCTGCCGCCACCGGCCAAAGAGGTCTCATCACTGCCATTGAACC
CAGTCCTGCAGACCTCCCTGGAGGAGGTGGAGCTGCTCTACGAGTTCCTGCTGGCCGAACCTG
AGATCAGCCCTGACCTGCAGATCTCCATCAAGGACGAGGAGCTGGCCTCCTTGCGGAAGGCCT
CAGACTTCCGCACCGTCTGCAACAACGTCAATCCCAAGAGCATCCAGACATCCGCCGGCTCA
GCGCCAGCCTCTCCAGCCACCCCTGGCATCCTCAAGAAAGAAGACTTTGAAAGGACAGTGCTGA
CCCTGGCCTACACAGCCTACCGCACAGCCCTGTCCACGGCCATCAGAAGGACATCTGGGCGC
AGTCCCTCGTTAGCCTCTTCCAGGCCCTGAGGCACGACTTGATGCGCTCCTCACAGCCGGGAG
TACCTCCCCTGAGAGACTGGCCACACCAGGACCTCAGAGCAGGGACCAGCACAGTAATCCAGA
AAGTCTTTCATTCTCTACTCCATTTACAGAGACCAGCAACAAAACACTTACCGCTGACACAGAG
CAGCAGAGATCAAACAGTAACCCCGATGCTCTTTTCTCCTTGATGTTTCTGGAAGACACATC
TGATTCATGCCATCATGTGACCTGGGCTGGAAGAAAGGGCTGGAATGGTCATTCAAGACGCCT
CCATGGGCAGAATGGTTTGCCTATGGCAGGCAGAATTCTGATATGCTTCAACCCAGAGCAGTG
GCCACACACTCAAGAGTGAGAACAGGCGTGAGCCACCGTGCCTGGCCCAGGATCTAAAACTT
TCTAAGTTTCTCCATCGTTGGCATCCTCACAGCTATCTCCAATGTCACTCAAGAGACATCAA
CAGACATTTAACTGCTGCAGACTTCATTGCTCTGTACCTCACCTTGAATCTAACAAATCAAA
GTATTTCTGCAGGTCCAATGGTCTAAAATCAAAATGCTTGTTAAATGACTTTTACAACACCCCTT
ACTTTCCTAATCCATTTCAATCTTATTTTTTTTATTGTGGTAAAAAACACATCACGTAAAAATG
TACCATCTTAACCATTTTAAAGCATATGGTACAGCAGTGTTAACTCCATGCATGTTGTGAAAC
AGACCCCCGGAACTTTCTCATCTTGTAATTCTGAAGTTCTATACCCACCGAACAACTCCTCTT
TTCCCCTTCCCCCTGCCTGCCCCAGCTCTTGGCACCATTATTCTGCTTTCTGTTTTTGAGAGT
CTGACTACTTAAGATACCTCATACAAGCGGGATCTGGCTTACATTTCTTGAGCATTGTATTCT
GGAAAAGTGTTTCCTTCTCTGAAAAATGGGTAGAGTTCTGAAGGAGAACTACTGGTCTTATT
GTACACTTGCTGTACCTATTTTTATTTAAACAAATATTCATCTATGGTATAATAAAGATGTCAT
GGTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 506

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96893
><subunit 1 of 1, 173 aa, 1 stop
><MW: 19733, pI: 8.78, NX(S/T): 0
MHWKMLLLLLLYYNAEASMCCHRWSRAVLFPAAHRPKRSSSLPLNPVLQTSLEEVELLYEF
LLAELEISPDQLISIKDEELASLRKASDFRTVCNNVIPKSIPDIRRLSASLSSHPGILKK
EDFERTVLTLAYTAYRTALSHGHQKDIWAQSLVSLFQALRHDLMRSSQPGVPP
```

Important features of the protein:

Signal peptide:

Amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 36-40;84-88;105-109

FIGURE 507

GGCGGCGGGCTGCGCGGAGCGGCGTCCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGC
CGGCCGAGCAATGCCAAGTGAGTACACCTATGTGAACTGAGAAGTGATTGCTCGAGGCCTTC
CCTGCAATGGTACACCCGAGCTCAAAGCAAGATGAGAAGGCCAGCTTGTTATTTAAAGACAT
CCTCAAATGTACATTGCTTGTGTTTGGAGTGTGGATCCTTTATATCCTCAAGTTAAATTATAC
TACTGAAGAATGTGACATGAAAAAATGCATTATGTGGACCCTGACCATGTAAAGAGAGCTCA
GAAATATGCTCAGCAAGTCTTGCAAGGAATGTCGTCCAAGTTTGCCAAGACATCAATGGC
GCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCAGAAGGCCCCCAAAGA
CAGTGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCGGAAGTTCTCCAGTAAAGTCCA
GACCCTCTTGGAACCTCTTGCCAGAGCACGACCTCCCTGAACACTTGAAAGCCAAGACCTGTGC
GCGCTGTGTGGTTATTGGAAGCGGAGGAATACTGCACGGATTAGAACTGGGCCACACCCTGAA
CCAGTTCGATGTTGTGATAAGGTTAAACAGTGCACCAGTTGAGGGATATTGAGAACATGTTGG
AAATAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCCTGTCTGACCTTGAATATTAT
TCCAATGACTTATTTGTTGCTGTTTTATTTAAGAGTGTGATTTCAACTGGCTTCAAGCAATG
GTAAAAAAGGAAACCTGCCATTCTGGGTACGACTCTTCTTTTGAAGCAGGTGGCAGAAAAA
ATCCCACTGCAGCCAAACATTTTCAGATTTTGAATCCAGTTATCATCAAAGAGACTGCCTTT
GACATCCTTCAGTACTCAGAGCCTCAGTCAAGGTTCTGGGGCCGAGATAAGAACGTCCCCACA
ATCGGTGTCATTGCCGTGTCTTAGCCACACATCTGTGCGATGAAGTCAGTTTGGCGGGTTTT
GGATATGACCTCAATCAACCCAGAACACCTTTGCACTACTTCGACAGTCAATGCATGGCTGCT
ATGAACTTTTCAGACCATGCATAATGTGACAACGGAAACCAAGTTCCTCTTAAAGCTGGTCAA
GAGGGAGTGGTGAAAGATCTCAGTGGAGGCATTGATCGTGAATTTTGAACACAGAAAACCTCA
GTTGAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGACAGCCTTCTTGATGTATTTCTCCAT
CCTGCAGATACTTTGAAGTGCAGCTCATGTTTTTAACCTTTTAATTTAAAAACACAAAAAAAT
TTTAGCTCTTCCCCTTTTTTTTTTCTATTTATTTGAGGTCAGTGTGTTTTTGCACACCAT
TTTGTAATGAACTTAAGAATTGAATTGGAAGACTTCTCAAAGAGAATTGTATGTAACGAT
GTTGTATTGATTTTTTAAGAAAGTAATTTAATTTGTAAACTTCTGCTCGTTTACACTGCACAT
TGAATACAGGTAACATAATTGGAAGGAGAGGGGAGGTCACTCTTTTGATGGTGGCCCTGAACCT
CATTCTGGTTCCCTGCTGCGCTGCTTGGTGTGACCCACGGAGGATCCACTCCAGGATGACGT
GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGGCGTGAGGCCTGGGCTGGTTG
GAGAAGGTCAACCCCTTCTCTGTTGGTCTGCCTTCTGCTGAAAGACTCGAGAACCAACCAGG
GAAGCTGTCCTGGAGGTCCCTGGTGGGAGAGGGACATAGAATCTGTGACCTCTGACAACCTGTG
AAGCCACCCTGGGCTACAGAAACCACAGTCTTCCCAGCAATTATTACAATTCTTGAATTCCTT
GGGGATTTTTTACTGCCCTTTCAAAGCACTTAAGTGTAGATCTAACGTGTTCCAGTGTCTGT
CTGAGGTGACTTAAAAAATCAGAACAAAACCTTCTATTATCCAGAGTCATGGGAGAGTACACCC
TTTCCAGGAATAATGTTTTGGGAAACACTGAAATGAAATCTTCCCAGTATTATAAATTGTGTA
TTTAA

FIGURE 508

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897
><subunit 1 of 1, 362 aa, 1 stop
><MW: 41736, pI: 8.80, NX(S/T): 3
MRRPSLLLKDILKCTLLVFGVWILYILKLNYYTTEECMDMKMHYVDPDHVKRAQKYAQQVL
QKECRPKFAKTSMAALLFEHRYSDLLPFVQKAPKDSEAESKYDPPFGFRKFSSKVQTLLE
LLPEHDLPEHLKAKTCRRCVVIGSGGILHGLELGHNTLNQFDVVIRLNSAPVEGYSEHVG
KTTIRMTYPEGAPLSDLEYYSNDLFVAVLFKSVDFNWLQAMVKKETLPFWVRLFFWKQVA
EKIPLQPKHFRILNPVLIKETAFDILQYSEPQSRFWGRDKNVPTIGVIAVVLATHLCDEV
SLAGFGYDLNQPRTPPLHYFDSQCMAAMNFQTMHNVTTETKFLCLKLVKEGVVKDLSGGIDR
EF
```

Important features of the protein:

Transmembrane domains:

Amino acids 11-27;281-297

N-glycosylation sites:

Amino acids 30-34;180-184;334-338

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 2-6;109-113;223-227

N-myristoylation sites:

Amino acids 146-152;150-156;179-185;191-197

FIGURE 509

GGGCGGACGCAGTGCAGTAAGAGCAGATGGGCGGACCCAAATTTCTTCGGCTTCACGATTTTG
CCGAGGTCTAGCCCTGCATCCAGCCTTGAAACAGGGTGGGGAGGAGGCAGAAAGGGGAGGGAC
TGCACTCCCTCTGAGCGTGCTAGCTCCGACTGCCTGACGGATCACCTTCCGCTCCAACATGG
CTAGTTCTCAACGCCGTGACTCAAGCCTGTTGTGCCAGGCAGGGCGCACTCAGCAGCGCAGC
CCCACAGGTGGCGAAGGCTCCGCGAGAGGGTTCCCGCCAGGCTAGACAGTGGAGTGCCGCACA
GCGCGCCTTCCAGCCTCGCAGCCGCCACCCTAGCGGTTCCGACCCGGCGCCAGCAGGCCTGCT
TGGTCGATCTTCGAGCCAAAGATGCGGCGAGGCTGGAAGATGGCTCTGTCTGGGGGGCTGCGG
TGCTGCCGCCGGGTACTGTCCTGGGTGCCAGTGCTCGTTATTGTCCTCGTCGTGCTCTGGTCC
TACTATGCCTACGTCTTTGAACTCTGCCTGGTTATTTACCTCATACTCTACCATGCCATCTTT
GTGTTCTTTACCTGGACCTACTGGAAGTCTATCTTTACACTCCACAGCAGCCAAACCAGAAG
TTCCACTTGTCCTACACAGACAAGGAGCGCTATGAAAATGAAGAAAGACCTGAGGTCCAGAAG
CAGATGCTTGTTGATATGGCCAAAAAGCTACCGGTTTACACAAGAACTGGAAGTGGAGGTCAG
TTCATCCAAAGGCAGCTAGAGAGGCAGCTCAGCAAGTATCTCAGAAAGGCTAAGTCATATATG
TTCTCAAACTAGCCCTTTTTTTTTCTCCCATCTTCTGAAAACCACTATGGAGATTTTTCTCCA
CATTTTATTTCTAAAAAATTTTAAACACATATCAAAGCTGGAAGAATTGTATAGTAAACAAAC
TGTATACCCCAAACCTGGATTCTTCTGCTAACATTTTTCTGTGTTGCTATATCACATATCTATC
CACATATGCATACCTCTATTTATCTTTTCGTCAAGCCATCTTATGTTTCTGATGCATTTCAAAG
TAAATAGCTGACATCAGTAAGACATCTACCTAAATATTTTATTCTGTTTTGTAAATTTACA
TACAAAAACATGCATAATCTTAAGGGTACCATTCCATGTATTTTGAAAAGTGTAACATCTGT
GTAACATAACCCCAATAAAATTGCCATCACCTCAG

FIGURE 510

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98564
><subunit 1 of 1, 143 aa, 1 stop
><MW: 17255, pI: 9.99, NX(S/T): 0
MRRGWKMALSGGLRCCRRVLSWVPVLVIVLVVLWSYYAYVFELCLVIYLLILYHAIFVFFT
WTYWKSIFTLPQQPNQKFHLSYTDKERYENEERPEVQKQMLVDMAKKLPVYTRTGSGGQF
IQRQLERQLSKYLRKAKSYMFSN
```

Important features of the protein:

Transmembrane domain:

Amino acids 24-45

N-myristoylation sites:

Amino acids 11-17;12-18

FIGURE 511

CAGCCGGGGCGATGGCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCG
CGGCGAGTGCCCTTTCCCTGGCCGGCGCCAGTCTGGTCCTGAGCCTGCTGCAGAGGGTGGCGA
GCTACGCGCGGAAATGGCAGCAGATGCGGCCCATCCCCACGGTGGCCCGCGCCTACCCACTGGTG
GGCCACGCGCTGCTGATGAAGCCGGACGGGCGAGGTAAGGGCCGGCGCTCCTCCTGGAGCGCA
ACGGGGTCCGAGCCCCGTTCACCCCTCCGATCAGCCAGGAACCCGCTGCTTGTGGCGCTGG
CCGAGGAGAGAGGAGCCTGTACCCCTGTGGAGAATGCACTCCAGTTCTAGTCGTTGCCCT
TGGCACCCGCCGACACTGCTAGTGCCCCATCCCAAAGTGAGCATTTTCTTTGTGTGTAGCACA
GGATGCGGTATTTCCAAACCCCTGCCCTCGGTCTTTTCCACCTCACCGCTGCTCAGCTCTCA
AAGCCCTGCCGTTTCTCCTGCCCTTGGCTTGGGAAGCCTTAGGAACAGAAGCTCCCTGGGAGC
ACAGAGCGGTTTTAACTGGCCAACACCTTAACGCCAGAGCCGCCCTCCTCTCGCTGCCACT
TTGGAAAATAAGAGACTAGAGATTCACTGGACGCTTCTCCCGGCATCACAAGACTTGACTGC
TGCTTCAGTTCCCGCTTGACCTTCATACTTTAGCCCTTTAAAGGATGTTACATAATAACAATT
AAGAGACGGCAGGGCCTTCAGGCAGACTTCTTTGGAGGGTGTCAAACGCCTTGTTTATTAAAG
AGTGAATTTTAAATTAAATCATGTTTAAACAGAGATGGACATTTTATTGATGGAAAAA
ATCACGTTAAGTTAGAAAGCTCTCAAAGTACCTGGTATTTACAACCTCCCTGTCAGGGAGGGC
GAATCGATCTCAGAGTTTATTTTTCATCAGGGATTACGTTGAGGTACCCAGAAATGAGAAGA
TTTGCCCAAAATGGCATATTTTAAATTTGGCCAGACCAGAACCCAGTTTCTCTGGGATTAT
TTGTTAGTAAATCGTTTTTACAGGCTGAGCATTAACCTCAACTCCAAAGCTTGAAGGACTTTTTCTC
ATTTTCACTTGTTTTCTCTAATAAAATAATGCTGTAATTTCAACTTCACAAGATGAGGCCTC
ATGGAAGAGTGTTTACCAAAATATTAATAATACTTTGACAGAAAAAATCAAGCGAACTCTTT
GCCAACCAAAATATCATCATGACTGATGTAACAAGTAATCCAACACAGATATGAAAATCACTGG
TAAAAATCATCTCAGTTAATTCTAAAAGCAGAGCTAACCACCCCTTTTGTCTAAGGCTTTAT
GGTATTAATAAAATAAACTGTACAAAAATATAGATTTTCCCCTATCCCCTACCCCTGGAAAGTA
ATATACTGAAGTCTCATCATACTGTTTTGGGGATTCCAGTAATTAATAATCTCTAGTGAACAAA
GACCTGTTTCAAAACAACCTGTGAGCTGACTGGACTATTTAAAGTAATTCTCCTTGTAAGTAC
TTTCAGAGTGAAGACAATGACGAATACTGTCTTTTACAAAGGGACTTTTTATTCCACCAACAA
ATTCTGGATTTTGGCATCAGGAAAACCACTGTTCAATTTCCAACACTATATCCAAGTTGTTTG
AGAAATTATTTAAACTCTTTAACTTAGAGGGTTTTCTTTCTCCTTTACTTGTTAAAGTGA
ATATTACAGAGTCACTTTAAGGATTAAATTTATTGCATGCAAAGTTTCTAGATCACTGTCTAG
AAGTCAGTTAGAGTAAGTTCTTTAGTTGTCAATCAAGCATTTAGTAAGGCCCTGCTTTGTGCC
CAGTGTGACCTCAACAAAGTTGGGGATATCAGAATATTCTAAGATACAGTCGTTGTTCCCAA
GAATCTTGCTTTTACATACAAGAGGTGTTGCGTTTCATTTTGGCGCTAATGTCCAAACGCTG
GCCTCAGCCATTTACCTTGAAGATTGCAGTTGGCTTCCAAGTGGCTCTAACTCTAATCTA
GCATTTTCCAGTCCATTGTGACAAAGTCTGCCTTCCCAGCTACTCCAGCTGTTGGACCTGC
TGCCTTAGAACCACAGATTGGTACCTCGTGCC

FIGURE 512

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA107443
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19353, pI: 10.97, NX(S/T): 0
MAGLWLGLVWQKLLLWGAASALSLAGASLVLSLLQRVASYARKWQQMRPIPTVARAYPLV
GHALLMKPDGRGKGRRSSWSATGSAAPFPPSDQPGTRCLWRWPQERGACHPVENALPVLV
VAPWHPPTLLVPHPKVSIFVCSTGCGISKPLPSVFSHLTAAQLSKPCRFLLPWLGKP
```

Important features of the protein:

Signal peptide:

Amino acids 1-25

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 75-79

N-myristoylation sites:

Amino acids 3-9;17-23;145-151

Amidation site:

Amino acids 73-77

Leucine zipper pattern:

Amino acids 8-30

FIGURE 513

GGCGGCTGGACGAGGACGCTCAGAGCCCAGCTCTCGAGAGTTCAAGCAACCGACGGTTCC
 CCACTGCTCCCAGGAGCGGTTACCTGGGCACTCTGTGCCCCCTCCTTCTGTTCGGGCCCA
 GGCCGAGGACCTGCCAGTAGGGCTCAGTTGCCTGGAGCCCGTTCAGCCCATCCCCAGTT
 CACTTTGCTTGTGGGATCTCCCCGTTGCTCCTGCCCGTGGACTGAGTGGCAGGCCATCCT
 ACAAGCACCCGGACACTTGACATCAGTGGTGTCAAGACAACCTCTAAGAAGGTTTTCCGTG
 ATCCTGCAAGCCCTGCCCTTCTTCTGCGGATCCTGCCCTTCAATTTGATTGCACAGGTACC
 ACAGCAAGCCAGTGCTGTGTGCTCCGAGTTCCAGGGCGTCTCCAGCTCAGCCACTGCAC
 TGAGAACATGGAAGTCTCTGTGGGGCCCAGGAGCCGGGAGTCAACCCCTTTGGGGTCCACAA
 CACCCGGCTGTCCCCAGACTTGTGTCCAGGGAAGATAGTGTGAGGGCCCTCAAGGAGAG
 CGGGGCAGGGATGCCTGAGCAGGACAAGGACCCTAGAGTCCAAGAGAATCCTGGTGATCA
 GAGAAGGGTCCCCGAGGTCAACGGGGATGCACGGTCTGCATTTTCGGCCCCCTGCGGGACAA
 TGGAGGCCTCTCTCCCTTTGTGCCCCGGCCCCGGGCTCTGCAGACAGACCTCCATGCCCA
 GAGGTCAGAAATCAGATATAACCAGACATCCCAGACCTCCTGGACGAGCTCCTGCACCAA
 CCGAAATGCCATCTCCAGCTCCTACAGCTCCACGGGAGGCTTGCTGGGGCTAAAGCGGAG
 GAGGGGGCCAGCCTCATCCCACTGCCAGCTGACCCTCAGTTCTCAAAGACAGTGAGTGA
 GGACAGGCCTCAGGCTGTCTCTTTCAGGTACACCCAGTGTGAAAAGGCAGCAGATATAGC
 ACCAGGGCAGACACTCACCTCAGGAATGACTCCTCCACATCCGAGGCCTCTAGGCCCAG
 TACACACAAGTTTTCCCTGTGTCACGCAGGCGAGGGGAGCCTTTGATGCTGCCACCTCC
 CTTAGAGCTGGGGTACCGGGTCACTGTTGAAGACCTGGACCGGGAGAAGGAGGCGGCCTT
 CCAGCGCATCAACAGTGCACTGCAGGTTGAGGACAAGGCCATCTCGGACTGCAGACCCTC
 ACGGCCTTCCCACACTTTGTCTCACTTGCAACAGGGGCTTCTGGTCTGCCTGCCGTTTC
 TAAAGCACCCAGTATGGATGCACAGCAGGAGACACACAAGTCCAAGACTGCCTGGGCCT
 ACTGGACCCCTTAGCATCTGCTGCAGGGGTCCCCTCTACAGCTCCCATGTCTGGGAAGAA
 GCACAGACCACCAGGCCCCCTGTTCTCCTCCTCAGATCCCCTTCTGCCACCTCTTCTGA
 TTCCCAGGACTCAGCCCAGGTACCTCGCTGATTCCTGCCCCCTTCCCAGCTGCAAGCAT
 GGATGCGGGCATGAGAAGAACAAGGCATGGCACTTCTGCTCCTGCAGCTGCCGCAGCAGC
 CCTCCCCGCTCCACATTGAACCCACGTTGGGGTCACTACTGGAGTGGATGGAGGCCCT
 TCACATTTCTGGGCCTCAGCCACAGCTGCAGCAGGTGCCCAGAGGTGAGAACCAGAGATC
 CCAGACCTCCTGGACCAGCTCGTGCCCCAAATGAATGCCATCTCGAGCCCCCTACAGCTC
 TACGGGAGGCCTCCCGGAACAAAAGCGGAAGAGGGGCCAGCCTCATCCCCTGCCAGCTG
 ACCCTCAGTTCTCAAACACAGTGAGTGAGGACGGACCTCAGGCTGTCTCTTCGGGTCAC
 ACCCAGTGTGAAAAGACGGCAGATACAGCACCCAGGGCAGACACTCGCCTCCAGGGGTGGC
 TCCCCCAGATCCCAGGCCTTAGGCCCCGTATATGCAAGTTTCCCCTGCTGCCACGCAGG
 CGAGGGGAGCCTTTGATGCTGCCACCTCCCTTAGAGATGGGGTACCGGGTCACTGCTGAA
 GACCTGGACCGGGAGAAGGAGGAGGCATTCAGCGCATCAACAGTGCACTGCAGGTTGAG
 GACCAGGCCATCTAGGACTGCAGACCCTCACGGCCTTCCCACACTTTGTCTCACTTGCA
 ACAGGGGCTTCTGGTCTGCCTGCCGTTTCTAAAGCACCCAGTATGGATGCACAGCAGGAG
 ACACACAAGTCCAAGACTGCCTGGGCCTAGTGGCCCCCTGCATCTGCTGCACAGGCCT
 GTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACGGCATAAACCCGGGAGGCAGAGC
 TTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGT
 CTC

FIGURE 514

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA107786
><subunit 1 of 1, 428 aa, 1 stop
><MW: 45450, pI: 9.28, NX(S/T): 3
MDSLWGPAGSHPGFVHNTRLSPDLCPGKIVLRALKESGAGMPEQDKDPRVQENPGDQRR
VPEVTGDARSAFRPLRDNGGLSPFVPGPGPLQTDLHAQRSEIRYNQTSQTSWTSSCTNRN
AISSSYSSTGGLLGLKRRRGPASSHCQLTLSSSKTVSEDRPQAVSSGHTQCEKAADIAPG
QTLTLRNDSSSTSEASRPSTHKFPLLPRRRGEPLMLPPPPELGYRVTVEDLDREKEAAFQR
INSALQVEDKAISDCRPSRPSHTLSSLATGASGLPAVSKAPSMDAQQETHKSQDCLGLLD
PLASAAGVPSTAPMSGKKHRPPGPLFSSSDPLPATSSSDSQAQVTS LI PAPFPAASMDA
GMRTRRHGTSAPAAAAAAPPRSTLNPTLGSLLEWMEALHISGPQPQLQQVPRGQNQRSQT
SWTSSCPK
```

Important features of the protein:

N-glycosylation sites:

Amino acids 105-109;187-191

Glycosaminoglycan attachment site:

Amino acids 38-42

N-myristoylation sites:

Amino acids 15-21;130-136;180-186;307-313;361-367

Amidation site:

Amino acids 315-319

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 106-117

FIGURE 515

GTCAGGGCCAGGGTGAGCGCCCGACTCCGAGCTGTCCCCGCTCCCGGCGCGGCGCTCCGCTCT
 CAGCCACCTCACGGCTGCCAGGAGTGCGCGGGAGTTTGTCCCGGAGCGCGGGGAAGTTTCCTC
 CGAAGCTGCGCTCCTGGAACAGCAGCACCTGCAAGCGCCCGGCAGCGGCCCCGCGAGGTTACTT
 TATGGAATTGGGCTCTTAGAGAACAAGAAAAGACTGAAGTTTACGGGAAAACAAATCATGTG
 GTCTTCAGATTCTGAAATAAGGAGAAATGCAGCCATCTGAAATGGTCATGAACCCCAAAACAAG
 TCTTCCTCTCTGTGCTGATATTTGGAGTAGCTGGGCTACTCCTCTTCATGTATTTGCAAGTCTGG
 ATTGAAGAACAACATACAGGGAGAGTGGAGAAGAGAAGAGAACAAAAAGTAACCTTCAGGATGG
 GGACCAGTGAAGTACTTGC CGCCTGTACCCAGAATCATGAGTACAGAAAAAATCCAGGAACAT
 ATCACCACCAGAACCCCAAGTTTCACATGCCTGAGGATGTACGAGAAAAAAGGAAAAATCTT
 CTACTCAATTCTGAGAGATCTACTAGGCTCTTAACAAAGACCAGTCATTCACAAGGAGGGGAT
 CAAGCTTTAAGTAAGTCCACAGGGTCACCAACAGAGAAGTTGATTGAAAAACGTCAAGGAGCT
 AAGACTGTTTTTAACAAGTTCAGCAACATGAATTGGCCAGTGGACATTACCCCTTTAAACAAA
 AGTTTAGTCAAAGATAATAAATGGAAGAAAACCTGAGGAGACCCAAGAGAAACGAAGGTCTTTC
 CTTCAGGAGTTTTTGCAAGAAATACGGTGGGGTGAGTCATCATCAGTCACATCTTTTTTCATACA
 GTATCCAGAATCTATGTAGAAGATAAACACAAAATCTTATATTGTGAGGTACCTAAGGCTGGC
 TGTTCCAATTGGAAAAGAATTCTGATGGTACTAAATGGATTGGCTTCCTCTGCATACAACATC
 TCCCACAATGCTGTCCACTACGGGAAGCATTGAAGAAGCTAGATAGCTTTGACCTAAAAGGG
 ATATATACCCGCTTAAATACTTACACCAAAGCTGTGTTTGTTCGTGATCCCATGGAAAGATTA
 GTATCAGCCTTTAGGGACAAAATTTGAACACCCCAATAGTTATTACCATCCAGTATTTCGGAAAG
 GCAATTATCAAGAAATATCGACCAAATGCCTGTGAAGAAGCATTAAATTAATGGATCTGGAGTC
 AAGTTCAAAGAGTTTATCCACTACTTGCTGGATTCCCACCGTCCAGTAGGAATGGACATTCAC
 TGGGAAAAGGTCAGCAAACCTCTGCTATCCGTGTTTGATCAACTATGATTTTGTAGGGAAATTT
 GAGACTTTGGAAGAAGATGCCAATTACTTTTTACAGATGATCGGTGCTCCAAAGGAGCTGAAA
 TTTCCCAACTTTAAGGATAGGCACCTCTCCGATGAAAGAACCAATGCTCAAGTCGTGAGACAG
 TATTTAAAGGATCTGACTAGAACTGAGAGACAATTAATCTATGACTTTTATTACTTGGACTAT
 TTAATGTTTAATTATACAACCTCCACTTTTGTAGTTTGCATTCATTTTCTAAAACCCTGTATAT
 ACTTAATGATGATAAGTTCAAATCAGCTGTAATTTTTCTATAATTCTCTGTATGACAGAAAT
 TAACCAAGTGCAGTTGTCTTGATTTAATGTAGATTTTTTACCAAATAGTATGACACCAATTGGC
 ACAAAGTTATAGGAAAATCACCTACAGGAGATGTAAACAACCTGAGTTGCTCTAAAATGTTTG
 GAAAAGAGCTGCTTTTGCATTATGAATTATATTGTTGAAGCAATAACCTAGCCAGCTGTTGCA
 TTAGCTAAAGCAGCCTCTTGCAATGGTAGGAAAAAAGGATCTCAAATAGCATGAGTGTATGTC
 TATATCCTGAAATTTATTGTCTAAAATGCATGAATATATTTTTTAGCAGTCTGTGGCATATTAA
 TCAAACCTGTTGAATTGTTTTCTTACACCCTGGAAATCTTTCTATCAACTATAATGATAAATCC
 ATTTTGAAGTGATATTTTGGACTTAGGCATTTTACTTTAGATTGGAAGGCATTATGTGATTTACA
 ATATGAGAATATAGCAGAAAAACCA

FIGURE 516

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108682
><subunit 1 of 1, 443 aa, 1 stop
><MW: 52021, pI: 9.63, NX(S/T): 4
MQPSEMVMNPKQVFLSVLIFGVAGLLLFMYLQVWIEEQHTGRVEKRREQKVTSGWGPVKY
LRPVPRIMSTEKIQEHITNQNPKEFHMPEDEVREKKENLLLNSERSTRLLTKTSHSQGGDQA
LSKSTGSPTEKLEIKRQGAKTVFENKFSNMNWPVDIHPLNKSLVKDNKWKKTEETQEKRRS
FLQEFCKKYGGVSHHQSHLFHTVSRITYVEDKHKILYCEVPKAGCSNWKRILMVLNGLASS
AYNISHNAVHYGKHLKKLDSFDLKGITYTRLNTYTKAVFVRDPMERLVSAPFRDKFEHPNSY
YHPVFGKAIKKYRPNACEEALINGSGVKFKEFIHYLLDSHRPVGMDIHWEKVSKLCYPC
LINYDFVGKFETLEEDANYFLQMIGAPKELKFPNFKDRHSSDERTNAQVVRQYLKDLTRT
ERQLIYDFYYLDYLMFNYTTPLL
```

Important features of the protein:

Signal peptide:

Amino acids 1-24

N-glycosylation sites:

Amino acids 159-163;243-247;324-328;437-441

Glycosaminoglycan attachment site:

Amino acids 53-57

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 177-181

Tyrosine kinase phosphorylation site:

Amino acids 329-337

N-myristoylation sites:

Amino acids 116-122;236-242

FIGURE 517

GGAACTTCCCAGGCACCCCTGTGTGGCCGCACTGCTCCCTCTGGCCCAACC**ATG**CCTCTGTCCAGCCACCTGCTGC
CCGCTTGGTCTCTGTTCTTGGCAGGGTCCTCAGGCTGGGCCTGGGTCCCCAACCCTGCAGGAGCCCTGGCCAGG
CCGTGTGCAACTTCGTGTGTGACTGCAGGCACTGCTCAGATGAGGCCCACTGTGGTTACACGCGGCCCTCGCCCA
CCCTGGGCGCCCCCTTCGCCTGTGACTTCGAGCAGGACCCCTGCGGCTGGCGGGACATTAGTACCTCAGGCTACA
GCTGGCTCCGAGACAGGGCAGGGGCCGCACTGGAGGGTCCCTGGGCCCTCACTCAGACCACACACTGGGCACCGACT
TGGGCTGGTACATGGCCGTTGGAACCCACCGAGGGAAAGAGGCATCCACCGCAGCCCTGCGCTCGCCAACCCCTGC
GAGAGGCAGCCTCCTCTTGCAAGCTGAGGCTCTGGTACCACGCGGCCCTCTGGAGATGTGGCTGAACTGCGGGTGG
AGCTGACCCATGGCGCAGAGACCCCTGACCCCTGTGGCAGAGCACAGGGCCCTGGGGCCCTGGCTGGCAGGAGTTGG
CAGTGACCACAGGCCGATCCGGGGTGACTTCCGAGTGACCTTCTCTGCCACCCGAAATGCCACCCACAGGGGCG
CTGTGGCTCTAGATGACCTAGAGTTCTGGGACTGTGGTCTGCCCACCCCCAGGCCAACTGTCCCCCGGGACACC
ACCACTGCCAGAACAAAGGTCTGCGTGGAGCCCCAGCAGCTGTGCGACGGGGAAGACAACCTGCGGGGACCTGTCTG
ATGAGAACCCACTCACCTGTGGCCGCCACATAGCCACCGACTTTGAGACAGGCCTGGGCCCATGGAACCGCTCGG
AAGGCTGGTCCCGAACACCCGTGCTGGTGGTCTGAGCGCCCCCTCTGGCCACGCCGTGACCACAGCCGGAACA
GTGCACAGGGCTCCTTCTGGTCTCCGTGGCCGAGCCTGGCACCCCTGCTATACTCTCCAGCCCCGAATTCGAAG
CCTCAGGCACCTCCAACCTGCTCGTGGTCTTCTATCAGTACCTGAGTGGGTCTGAGGCTGGCTGCCTCCAGCTGT
TCCTGCAGACTCTGGGGCCCCGGCGCCCCCGGGCCCCCGTCTGCTGCGGAGGCGCCGAGGGGAGCTGGGGACCG
CCTGGGCTCCGAGACCGTGTGACATCCAGAGCGCCTACCCCTTCCAGATCCTCCTGGCCGGGACAGACAGGCCCGG
GGGGCGTCTGGGTCTGGACGACCTCATCCTGTCTGACCACTGCAGACCAGTCTCGGAGGTGTCCACCTGCAGC
CGCTGCCTCCTGGGGCCCCGGGCCCCAGCCCCCAGCCCCCTGCCGCCAGCTCGCGGCTCCAGGATTCCTGCAAGC
AGGGGCATCTTGCTGCGGGGACCTGTGTGTGCCCCCGGAACAACTGTGTGACTTCGAGGAGCAGTGCCGAGGGG
GCGAGGACGAGCAGGCCTGTGGCACCACAGACTTTGAGTCCCCCGAGGCTGGGGGCTGGGAGGACGCCAGCGTGG
GGCGGCTGCAGTGCGGCGTGTCTCAGCCAGGAGAGCCAGGGGTCCAGTGACGCTGCTGCTGGGCACTTCCTGT
CTCTGCAGCGGGCTGGGGGACGCTAGGCGCTGAGGCCCGGGTCTCACACCCCTCCTTGGCCCTTCTGGCCCCA
GCTGTGAACTCCACCTGGCTTATTATTACAGAGCCAGCCCCGAGAGGTCTCCTGTAACCTTTGAGCGGGACACAT
GCAGCTGGTACCCAGGCCACCTCTCAGACACACACTGGCGCTGGGTGGAGAGCCGCGGCCCTGACCACGACCACA
CCACAGGCCAAGGCCACTTTGTGCTCCTGGACCCACAGACCCCTGGCCTGGGGCCACAGTGCCCACTGCTCT
CCAGGCCCCAGGTGCCAGCAGCACCCACGGAGTGTCTCAGCTTCTGGTACCACCTCCATGGGCCCCAGATTGGGA
CTCTGCGCCTAGCCATGAGACGGGAAGGGGAGGAGACACACTGTGGTTCGCGGTCCAGGCACCCAGGGCAACCGCT
GGCACGAGGCCTGGGCCACCCCTTCCACACAGCCTGGCTCCCATGCCAGTACCAGCTGCTGTTTCGAGGGCCTCC
GGGACGGATACACGGCACCATGGCGCTGGACGATGTGGCCGTGCGGCCGGGGCCCTGCTGGGCCCCTAATTACT
GCTCCTTTGAGGACTCAGACTGCGGCTTCTCCCCTGGAGGCCAAGGTCTCTGGAGGCGGCAGGCCAATGCCCTCGG
GCCATGCTGCCTGGGGCCCCCAACAGACCATAACCTGAGACAGCCCAAGGGCACTACATGGTGGTGGACACAA
GCCCAGACGCACTACCCCGGGGCCAGACGGCCTCCCTGACCTCCAAGGAGCACAGGCCCTTGGCCAGCCTGCTT
GTCTGACCTTCTGGTACCACGGGAGCCTCCGACAGCCAGGCACCCCTGCGGGTCTACCTGGAGGAGCGCGGGAGGC
ACCAGGTGCTCAGCCTCAGTGCCACGGCGGGCTTGCCTGGCGCTGGGCAGCATGGACGTGCAGGCCGAGCGAG
CCTGGAGGGTGGTGTGTTGAGGCAGTGGCCGAGGCGTGGCACACTCCTACGTGGCTCTGGATGATCTGCTCCTCC
AGGACGGGCCCTGCCCTCAGCCAGGTTCTGTGATTTTGAAGTCTGGCCTGTGTGGCTGGAGCCACCTGGCCGGGC
CCGGCCTGGGCGGATACAGCTGGGACTGGGGCGGGGAGCCACCCCTCTCGTTACCCCAAGCCCCCTGTGGACC
ACACCTGGGACACAGAGGCAGGCCACTTTGCCCTTCTTTGAACTGGCGTGTGGGCCCGGGGCGGGCCGCT
GGCTGCGCAGCGAGCCTCTGCCGGCCACCCAGCCTCCTGCTTCCGCTTCTGGTACCACATGGGTTTTCTGAGC
ACTTCTACAAGGGGGAGCTGAAGGTACTGCTGCACAGTGTCTCAGGGCCAGCTGGCTGTGTGGGGCGCAGGCGGGC
ATCGGCGGCACCAAGTGGCTGGAGGCCAGGTGGAGGTAGCCAGTGCCAAGGAGTTCCAGATCGTGTGTTGAAGCCA
CTCTGGGCGGCCAGCCAGCCCTGGGGCCCATGCCCCTGGATGACGTGGAGTATCTGGCTGGGACGATTGCCAGC
AGCCTGCCCCAGCCCCGGGAACACAGCCGACCCGGGTCTGTGCCAGCTGTGGTTGGCAGTGCCCTCCTATTGC
TCATGCTCCTGGTGTCTGGGACTTGGGGGACGGCGTGGCTGCAGAAGAAGGGGAGCTGCCCTTCCAGAGCA
ACACAGAGGCCACAGCCCTGGCTTTGACAACATCCTTTTCAATGCGGATGGTGTACCCCTCCCGGCATCTGTCA
CCAGTGATCCG**TAG**ACCACCCACAGACAAGGCCCGCTTCTCACGTGACATCCAGCACTTGGTCAGACCCTAGCC
AGGGACCGGACACCTGCCCCGCCAGGCTGGGACAGGCTGCAGGTCTCAGGATATGCTGAGGCTGGGCGTTCCC
TGCCCTGTGCTGACTCTGTTGCTCTGTGAATAAACACCCCTGGCCCATGAGGGCGGCCCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAA

FIGURE 518

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108684
><subunit 1 of 1, 1137 aa, 1 stop
><MW: 122776, pI: 6.00, NX(S/T): 4
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GAPFACDFEQDPCGWRDISTSGYSWLRDRAGAALEGPGPHSDHTLGTDLGWYMAVGTHRG
KEASTAALRSPTLREAASSCKLRLWYHAASGDVAELRVELTHGAETLTWQSTGPWGPWG
QELAVTTGRIRGDFRVTFSATRNATHRGAVALDDLEFWDCGLPTPQANCPPGHHHCQNKV
CVEPQQLCDGEDNCGDLSDENPLTCGRHIATDFETGLGPWNRSEGWSRNHRAGGPERPSW
PRRDHSRNSAQGSFLVSVAEPGTPAILSSPEFQASGTSNCSLVFYQYLSGSEAGCLQLFL
QTLGPGAPRAPVLLRRRRGELGTAWVRDRVDIQSAYPFQILLAGQTGPGGVVGLDDLILS
DHCRPVSEVSTLQPLPPGPRAPAPQPLPPSSRLQDSCKQGHACGDLCPVPEQLCDFEEQ
CAGGEDEQACGTTDFESPEAGGWEDASVGRQWRRVSAQESQGSSAAAAGHFLSLQRAWG
QLGAEARVLTPLLGPSPGSCELHLAYYLSQPREVSCNFERDTCWYPGHLSDTHWRWVE
SRGPDHDHTTGQGHFVLLDPTDPLAWGHSALLSRPQVPAAPTECLSFYHLHGPIQITL
RLAMRREGEETHLWSRSGTQGNRWHEAWATLSHQPGSHAQYQLLFEGLRDGYHGTMALDD
VAVRPGPCWAPNYCSFEDSDCGFSPGGQGLWRRQANASGHAAGWPPTDHTTETAQGHYV
VDTSPDALPRGQTASLTSKEHRPLAQACLTFWYHGSLRSPGTLRVYLEERGRHQVLSLS
AHGGLAWRLGSMVDVQAEARWRVFEAVAAGVAHSYVALDDLLLDQDGPQPQPGSCDFESGL
CGWSHLAGPGLGGYSWDWGGGATPSRYPQPPVDHTLGTEAGHFAFFETGVLGPGGRAAWL
RSEPLPATPASCLRFWYHMGFPEHFYKGEKLVLLHSAQGQLAVWGAGGHRRHQWLEAQVE
VASAKEFQIVFEATLGGQPALGPIALDDVEYLAGQHCQQPAPSPGNATAAPGSVPAVVGSA
LLLLLMLLVLLGLGGRRWLQKKGSCFPQSNTEATAPGFDNILFNADGVTLPASVTSDF
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

Transmembrane domain:

Amino acids 1075-1092

N-glycosylation sites:

Amino acids 203-207;281-285;339-343;756-760

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 514-518;1100-1104

N-myristoylation sites:

Amino acids 32-38;55-61;61-67;106-112;116-122;336-342;350-356;409-415;
523-529;540-546;678-684;707-713;791-797;870-876;921-927;
937-943;954-960;1036-1042;1071-1077

Amidation site:

Amino acids 1093-1097

Cell attachment sequence:

Amino acids 191-194

FIGURE 519

GCAGGGGAGCTCCGAGTGTCACAGGAAGGGAAGTATCAGCTCCTGGCATCTGTAAGGATGCT
GTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTTCTCTGTGGCCACCAGTGG
GTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGATGCTCTCGAGGGAATTCGAAACCTGTGCCTT
CTCCTTTTCTTCCCTGCCTAGAAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGA
TGGCCTGTATTTTCTCCGCACCAAGAATGGTGTGTCTACCAGACCTTCTGTGACATGACTTC
TGGGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCACGAGAATGACATGCGTGGGAAGTGCAC
GGTGGGTGATCGCTGGTCCAGTCAGCAGGGCAACAAAGCAGACTACCCAGAGGGGGATGGCAA
CTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCC
TGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCCAACAAGTCCCCAT
GCAGCATTTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCAACACTGGCTTCCTCCAGAGACT
GGGACATAATCTGTTTGGCATCTACCAGAAATACCCAGTGAAATACAGATCAGGGAAATGTTG
GAATGACAATGGCCCAGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATC
TTATTACTCACCGTATGGTCAACGGGAATTTGTTGCAGGATTCGTTCACTTCCGGGTGTTTAA
TAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAAAGTTACTGGCTGTAACACTGAGCA
TCACTGCATCGGTGGAGGAGGGTTCTTCCCACAGGGCAAACCCCGTCAGTGTGGGGACTTCTC
CGCCTTTGACTGGGATGGATATGGAACACGTTAAGAGCAGCTGCAGTCGGGAGATAACGGA
GGCGGCTGTACTCTTGTCTATAGATGAGACAGAGCTCTGCGGTGTGAGGGCGAGAACCCATC
TTCCAACCCCGGCTATTTGGAGACGGAAAACTGGAATTCTAACAAGGAGGAGAGGAGACTAA
ATCACATCAATTTGCA

FIGURE 520

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108701
><subunit 1 of 1, 325 aa, 1 stop
><MW: 36212, pI: 8.68, NX(S/T): 1
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HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGBRWSSQQGNKA
DYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVFNKSPMQHWRNSALLR
YRTNTGFLQRLGHNLFGLIYQKYPVKYRSGKWCNDNGPAIPVVYDFGDAKKTASYSPYGQ
REFVAGFVQFRVFNNERAANALCAGIKVTGCNTEHHCIGGGGFFPQGKPRQCGDFSADFWD
DGYGTHVKSSCSREITEAAVLLFYR
```

Important features of the protein:

Signal peptide:

Amino acids 1-26

Glycosaminoglycan attachment site:

Amino acids 86-90

N-myristoylation sites:

Amino acids 23-29;88-94;127-133;136-142;265-271

FIGURE 521

GATCAGTGTGTGAGGGAACTGCCATCATGAGGCTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCT
 GTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCA
 TTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACA
 GGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTG
 ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAAATGATTTTTTTGTTGAAA
 TAAGAGGAACTTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCA
 ACTACGATGTAATGCTTATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTG
 TGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAACTTCCAGCTCCACTTTCTTATG
 TACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATCAATGCTTTTCAGTTT
 TGTTCCACTTCTGGATTACGATTACGACTATCATTTTTTGGGAAGAGTTTTATAGTAAGGCATTAGGAAGGCCCA
 CTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCTCAAC
 CATAACCAACCTAACTTTGAGTTTGTGGAGGATTCAGCTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA
 ATTTTGTCCAGAGTTTCAGGGGAAGATGGTATTGTGGTGTCTCTCTGGGGTCACTGTTTCAAAATGTTACAGAAG
 AAAAGGCTAATATCATTGCTTCAGCCCTTGCCAGATCCCACAGAAGGTGTTATGGAGGTACAAAGGAAAAAAC
 CATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAATGATCTTCTTGGTTCATCCCAAAACCA
 AAGCTTTTATCACTCATGGTGGAAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC
 CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAA
 CTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCTCTTATAAAGAGAATGCTATGA
 GATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCTATGC
 GCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTTCAGCACTACTCTATAGATGTGA
 TTGGGTTCTCTGCTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTTATTTTCTGTCAAAAAAT
 TTAATAAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTCCAAATTCAGAAAGACCTGATGGGGTAATCCTG
 TTAATTCAGCCACATAGAATTTGGTGAAAACCTTGCTATTTTCATATTATCTATTCTGTATTATTTATCTTAGCT
 ATATAGCCTAGAAATTCATGATCATGAGGTGTGTGAGTATATCTCATTCTTTCTGTGTATTATTTCTAGGTGTCTTT
 ACTCTCTTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCTATTTCTGATATGACTGTTTTGA
 TGATGTCACTTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGATTATTCCTGGTGTGCGCCCAACAC
 ATGGATATAAAGAGGTAAAAAATTTAAATTCACAAAATTCAGTAAACCACACAAATCAGGTAAGTGTCTATGA
 GATTAGCTGGCTATGAGAAACATAATGATGTTTCTTTTTCAATTTAAATAAGCCTTTCTACATAGCCAGCATCAG
 TGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGCTGTATTTCCATAGAC
 CTCATCTAGATGTGATGGCCTACATTTCTGCCATCACTCAACCAATACTTTTTTCTGTTTTCTTGATGATAAAAA
 GACCTTTCTCATGATTGCCATCAAATAACAAAAGAACTATTTTTTTCTCACATAGAGAACATGTCAGTAAGAT
 ATCAAGGTGAACAGATATTTTGGGATTAGTAACCTATTTGAAATATGTGGTGATAATTACTGAGTTTATAAAAT
 TTATTTGATAGTACACTTAAGAAGATTTATATGTTTATTCTTTAAAAATGATGAATACTCATAATCTTATCTC
 TATAATCAAAAGTATAATTTACTGTAGAAAAATAAAGAGATGCTTGTCTGAAAGTAAGATCAGTGAAGTGCCTT
 TCAGTCTCAATCTTTGAGAATTGTAAATTCATCAAATAATTGCTTACATAGTAAAAATTTAAGGTATTAGAAAAC
 CTGCATAACAAATAGTATTATATATTAAATATTTTGATATGTAAAGCTCTACACAAAGCTAAATATAGTGTAAATA
 ATGTTTACACTAGTAAGCAAAATATGTTAATCTTCTCATTTTTTTACTGTCTATATAATCTTAGTGATATGCCTATT
 AATAGTTTTTAAATAAATAAATTGGCTTATCTGGCTTTTTGAAAATTTTGAATTTCTTACAGATGTTGATTAGGTA
 TATCTACAAATTAATTTCAATTTTAAATGATGATATAAAATAAATAAAGTATTTTTCTGTGTATGTATACA
 ATAAATATAAATAAAATTTGTTTACTGTTTTGAAAGTTTCTTAAGTTTTA

FIGURE 522

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108720
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><MW: 60284, pI: 8.31, NX(S/T): 3
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PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDFVVEIRGT
LKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PCGDLMAELLAVPFVLT LRISVGGNMER
SCGKLPAPLSYVPVPM TGLTDRMTFLERVKNSMLS VLFHFWIQDYDYHFWEEFYKALGR
PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED
GIVVFSLSLGFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQNDL
LGHPKTKAFITHGGMNGIYEAIYHGVP MVGVPIFGDQLDNIAHMKAKGAAVEINFKTMTS
EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAAHD
LTWFQHYSIDVIGFLLTCVATAIFLFTKCF LFSCQKFNKTRKIEKRE
```

Important features of the protein:

Signal peptide:

Amino acids 1-21

Transmembrane domain:

Amino acids 489-510

N-glycosylation sites:

Amino acids 131-135;313-317;518-522

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 67-71;340-344

Tyrosine kinase phosphorylation sites:

Amino acids 122-131;136-144

N-myristoylation sites:

Amino acids 19-25;276-282;373-379;377-383

Amidation site:

Amino acids 338-342

FIGURE 523

GGCTGCGGGGTCGGCACGGAAGATGCACGCGAGGCTCCTGGGGCTCTCGGCCCTGCTGCAGGC
GGCCGAACAGAGCGCGCGCCTTTACACCGTGGCTTACTACTTCACCACAGGACGGCTTCTGTG
GGGGTGGCTGGCCCTTGCTGTCCTCCTGCCCCGGGTTCTTGGTCCAGGCCCTGAGCTACCTGTG
GTTCCGAGCAGACGGGCATCCAGGGCATTGCTCCTTGGTGATGCTGCACCTCCTACAGCTTGG
TGTTTGGAAGCGGCACTGGGACGCTGCACTGACCAGTCTGCAGAAGGAACTGGAGGCTCCCCA
CCGAGGCTGGCTGCAGCTGCAGGAGGCCGACCTGTCGGGCCCTTCGACTCTTGAGGCCCCTGCT
GCAGACTGGGCCCCACCTGCTGCTTCAGACATATGTTTTTCTAGCCTCAGACTTCACAGATATT
GTGCCAGGGGTGAGCACCCTGTTTTCTGCTCCTCACTCTCCTGGGCACTGGTGTCTTACACT
CGCTTCATGGGCTTCATGAAGCCAGGCCACCTGGCCATGCCATGGGCCGCCCTCTTCTGCCAG
CAGCTCTGGAGGATGGGCATGTTGGGAACCCGCGTCTGAGTCTGGTTCTGTTCTACAAAGCC
TACCACTTTTGGGTTTTTGTGGTTGCAGGTGCCCACTGGCTGGTGATGACATTCTGGCTTGTG
GCCAGCAGAGTGACATCATCGACAGCACCTGCCACTGGAGGCTGTTCAACCTGCTCGTGGGG
GCCGTGTACATCCTCTGCTACCTCAGCTTCTGGGACAGCCCTTCTAGAAATAGGATGGTCACG
TTCTACATGGTCATGCTGTTGGAGAACATCATCCTGTTGCTGTTGGCCACCGACTTTCTCCAG
GGGGCATCGTGGACCAGCCTGCAGACCATAGCTGGGGTCTGTCTGGATTTCTGATTGGCAGT
GTCTCACTGGTAATTTATTACAGCCTGCTGCATCCAAAATCCACAGACATCTGGCAGGGCTGC
CTAAGGAAGTCTGTGGCATTGCAGGAGGTGATAAAACAGAGAGAAGAGATTCTCCCCGGGCC
ACAGATCTAGCTGGGAAGAGAACCGAGAGCTCAGGCTCATGCCAAGGGGCAAGTTATGAACCA
ACCATTTTAGGGAAGCCCCCTACCCCTGAGCAGGTCCCCCAGAGGCTGGGCTGGGGACCCAG
GTTGCTGTGGAGGACTCTTTCCTCAGTCATCACCCTGGCTGTGGGTGAAACTTGCCCTAAAA
ACAGGAAATGTGTCTAAGATCAATGCCGCCTTTGGAGATAACAGTCCTGCCTATTGTCCACCT
GCATGGGGGTTGAGTCAACAGGACTACCTGCAGAGAAAGGCCTTGTCTGCCAGCAAGAGCTC
CCATCCTCATCCCGTGACCCCTCAACCTTAGAGAACAGCTCTGCGTTTGAAGGTGTCCCTAAA
GCAGAGGCCGACCCATTGGAAACCTCAAGTTACGTATCTTTTGCCAGCGATCAGCAGGATGAA
GCACCTACCCAGAACCCAGCAGCCACGCAGGGGGAGGGCACCCCAAAGGAAGGAGCTGACGCT
GTTTCTGGGACACAGGGGAAGGGGACAGGTGGGCAGCAGAGAGGAGGGGAAGGACAGCAGAGT
TCCACGTTGTACTTCAGCGCCACTGCAGAAGTGGCCACATCCTCACAACAAGAAGGCAGCCCA
GCTACTCTGCAAACGGCCCACTCTGGAAGGAGGCTGGGAAAGAGCAGCCCTGCCAGCCTGCA
TCGCCCCACCCAGTGGGCTTGGCGCCCTTCCCCGACACCATGGCCGACATTAGCCCCATCCTA
GGCACAGGCCCATGTAGAGGCTTCTGCCCCAGTGCAGGCTTCCCTGGAAGAACCCTCAGTATC
TCAGAGCTAGAGGAGCCGCTGGAGCCCAAAAGGGAGCTAAGTCACCATGCAGCTGTTGGTGTG
TGGGTGTCAATTGCCACAGCTGAGGACTGCCCATGAGCCCTGCCTCACGTCCACCCCTAAGTCT
GAGTCTATCCAAACGGAAGTGCAGCTGCAGGGAACAGATGAAGCAAGAGCCGAGTTTTTTCATC
TGACCACAGTCATGGTGGGATAAGACAACAGGCTGACAAACCAAGCTGGCCATTTGGTACCGT
GAGAAAGGAAATCCCACTTCTGACACCTGTGTCCTTGGGCACATCACTGTCACCTCTGAATCT
CCATCTGCATCCCTGAAAAATGAAGAAACAGGGCTGGATGATTTTGCAGGTCCAATGCAACA
TCACAGACCCCAACCATGCATAGGAGAGACTCTAACATACTTTAGAGGAGGAGAAAGAGATTC
CAGTCAAAATTTGTCTGCTACCTTTTATGAGCTGTAGGTTCCCTTATTTTATCTTTTGTGCTGTG
GCTTCTAGGAAACACAAAGGTAAAACCCAGATTCCCTATTTTATTTGAGGTTCTTGTTACAATT
AGCTTTGCCTCACATTTAGCGGTTATGAATCTCATTTTAATATATTCTAACTGTATTATGTTA
TGAAATCTCTTGGAAGATAATTTGCATGCTTCTGGGAGTAGGTAAGGCCTGTGTGCTTGTA
ATAACTAACATAACTGAAAGTGCAATGTCA

FIGURE 524

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108726
><subunit 1 of 1, 686 aa, 1 stop
><MW: 74981, pI: 6.60, NX(S/T): 2
MHARLLGLSALLQAAEQSARLYTVAYYFTTGRLLWGWLALAVLLPGFLVQALSYLWFRAD
GHPGHCSLVMLHLLQLGVWKRHWDAALTSLQKELEAPHRGWLQLQEADLSALRLLEALLQ
TGPHLLLQTYVFLASDFTDIVPGVSTLFSWSSLSWALVSYTRFMGFMKPGHLAMPWAALF
CQQLWRMGMLGTRVLSLVLFYKAYHFWVFVAGAHWLVMTFWLVAQQSDIIDSTCHWRLF
NLLVGAVYIILCYLSFWDSPSRNRMVTFYVMMLLENIILLLLATDFLQGASWTSLOTIAGV
LSGFLIGSVSLVIYYSLHHPKSTDIWQGCRLKSCGIAGGDKTERRDSPRATDLAGKRTES
SGSCQGASYEPTILGKPPTPEQVPPEAGLTQVAVEDSFLSHHHWLWVKLALKTGNSKI
NAAFQDNTPAYCPPAWGLSQQDYLQKALSAQQELPSSSRDPSTLENSSAFEGVPKAEAD
PLETSSYVSFASDQQDEAPTQNPAAATQGEQTPKEGADAVSGTQGKGTGGQQRGEGQQSS
TLYFSATAEVATSSQQEGSPATLQTAHSGRRLGKSSPAQPASPHPVGLAPFPDTMADISP
ILGTGPCRGFCPSAGFPGRTLSISELEEPLEPKRELSHHAAGVWVSLPQLRTAHEPCLT
STPKSESIQTDCSCREQMKQEPSFFI
```

Important features of the protein:

Signal peptide:

Amino acids 1-17

Transmembrane domains:

Amino acids 35-50;269-287;293-313

N-glycosylation sites:

Amino acids 416-420;467-471

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 344-348

N-myristoylation sites:

Amino acids 188-194;288-294;299-305;335-341;338-344;362-368;
390-396;473-479;529-535;536-542;558-564;603-609;
643-649

Amidation sites:

Amino acids 354-358;568-572

Leucine zipper pattern:

Amino acids 112-134

FIGURE 525A

AGTGCCCTCTGTCATTTAATCTCCACGGAGTCCTGAAGGTGCTTCCCAGGTTTGTCCCCATCACACAGATGAGGC
 AATCGTTCTGTAAAGACTGTCTTGGGTCATTATGTCAGCAATGAAATCGGTGCTGCCATTACTAAACCTTACT
 GTGTGCTGGCATTGTGTATGCATGCATGTGTGTGCGTGCACACGTGTGTGTTTGGGTGTACATGTGCATGTGTGTG
 TTGTGTGCTGTGTGTGCACATGTAGAAAGAAAGTGATGTGTGGGAATGGAGAATTCACCCAGGAGGAGACTG
 TGCCTGGGGCTGCCACGAGAAGTGGTGACACTTCGAGAAACGGGTTCCAAATGCACGTTGCCCTCCAGTTCTCTG
 TGTGACCTTGGGCAAGTCACCTTCAGCTCCCTGAGCTTTGTTTTTAAAAATATTTTTTAAATGTATAAAACCATGG
 ACCATTACATATGAAGAGAAATGTGTGTGCAAAACATTAGTTAATAATCACAAGGTGGAGGAGTGCCTGCTCAGA
 CCCAGAGCTGACACAGGGAACTCTCCAGAAGGCTGCAGGGCTTCCCTCCCAACCTCCAACGGCCCACTTGCTG
 AGCCCGTCTTATCTGTTAGTGGAATGCCATGTGCCACGTTCCCTCAGAAGTAAAGCCACTAGGTAAGTGTGAC
 ACTCTGTGCCAGCTTGGTGCAAGGCCCTTGTGTGTGCTATCTTATTGACCTCCCAAATAGCATGGTAAGGTCA
 GTACTGTCACTTCCCCACTTTGAAGATGAGGAGAGCACAATTTAGATGGAAATGGAGGTACGCGAGTGGAAA
 TAGGATCCAGACAGATTAATCCAAATTCAGCTGAATTTCCATTCCACGCTACGCTTGAAGCTCAATCTCTC
 TTCTGGTTGATTCTCCCCACTTCCCCACCCCCAGATATATCCCATCGCTGCTTGGTGGACAGTAGCCATGACTG
 GGTGTTTGTAAAGGTTGTGAATAATCAGGCTGCTGGTTAGTTTTTACATTTACCTTTCCAGTGAAATGGGGC
 CCCATGAAAAAGGCAGCTCAAGTTGTAAATTACTCAAAGGAAGGACAGAAAGGTCTTCTGTTTGCACCTACCCTA
 AGGATTTGGGGTAGACACTGGGAATTTACTAATTATGAATTCAGTGCTTTCTTGTGAAAGAGAGGCGTGGAA
 TCAACGCTGAGTGAAGGCATCAAGTTTAAAGCTGCTAATTACTTCTGATCATGCAGAATAAAAGCTACGTCCTT
 GAAATACACCAGGCAGCTAAACATAATCTTTCGCTTTCGCTAGTGTGGTTAAGGAATCCAGATGTTACTGCAAT
 AACCCTCCATAAAACAAAGGAACACCCAGCTGTGAGAACTGGCTTCTCAGCATTTCGTCAGAGAGGCTCTTC
 CGGGGCCAGCCCTGGAAGAACCCATCAGGGTTCTGATGGTTGCCCTGTTTCAGCACAGCCCTTATTGGCAGGCAG
 ACGGCTACGGGCACAGCCACAGGCTGAAGGTGAGTCCAGCACACAATTTCTGACAGTGAACAGGAGTAAACATG
 GGACCCACCCGAAACCTTTGTCTGTGACTTCTTAGCAATGGAGGAGCTCTAGGCTCTGGAGAGTTCGGGTAT
 AGGAGACCATGACTTGAGCAGACTGATATAAGTGGAAATGCAACATATTTAGATGGCACAACCTTAATTTAGATTT
 ATCAGTGCTAATATAGAAAAAGCTAGTATTTATTGGGGCTTATTAGATTTTATGCTGAATCCTCACAACCTTACG
 AGGGGGTTCGTTTTACAGACTATGATCTTGCATGATTTCCCCAAGATGCTCATTAAGTATATGGTGAAAGTAGA
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 ACACTTCAGTGCAATTCATGGTTTTTGGAAAAATAACTTGATTTGAGATTGAGACAAATAAGTGCAATTTTAAATG
 TTTATCTTTTATCTTGAAAACTGATATATTTATGAAATGATATGTGCTCACTCAGTGTCAACACTTCAAACAA
 CACAGACAGTACAATGACAAATGGAGATCAGCTCTAATCTCGGCCCCCAATTTAATGCATTGCTGAATATTCTT
 CTGAACATAGTCCATCCCACTGTCCCATGACACAAGACGCTCCAAGGGGCTGAAGATAGAGGGACTTCTGCAG
 TCAAGAGAGCTGGGAACTCTTGACAGTCAATGTGCATTTGGGTATTAAGGCTCTGCAAAGTTCTGCACCA
 AATAAACCTTGGATTGGCTTGATCCAATGCCATGTTTTCCAAAACCTACTTGGCCGTGGGACACCTTAGTCCATA
 ACACAGGTTGGCATTCTTCTAGAGAGTGTGCTGTGAAAAACTGGTCTCACAGCACCGTGCATTTCATCCAGCA
 GGTATTTACCAAGCAGGGACTTTGGGCCAGGTCCGTGCTAGGCTCTGCAGGTGGACCAGCCAGCCCTGACCTCCA
 TGGTGTCTCTTCTCATGGGAGAGGCTGCACAGCAGTCATTGAGAAAAACGAAGAAACACACAGGTACTTTAGATG
 CTGATAATGACTACCATGTGCTAAAAGAGCTCCAGGTGTTGTCTGTTTTGAGACAATCTTCTCGACAATGAGATA
 GAATGAACCATGCAAACTTTGGGGGCTACGATGGTTTTAGGAAAGAGCTAGAGTGAATAATCCTTTGACATATAT
 ACATACAAAATAAGATACATGTGTATAATTTTATGTAATTGACATCACATTATATGCTGGCACCTGCCTTTTTTG
 CTTAATGAAATGTCAAAGGTAATATTACCAATCAATCAATATATTTACCATCGTGTTTAATTTCTGCAGAGCA
 CTTATTCAAGCACATACTGCATTTTTCTTAGTCACTCACTGGTGGGAATAGAAAGTTTTCTCAGGCATGCATTTT
 TCCCCTTCTGAAATGATCTCCTTAGAATAAATCCCCAAATTTGATTGCTGGGTTCAAAGGCATGAACATTTTA
 CATTTTTATACAATAATGTCAAACCTACCTTCCGGAATGATGCTCACTTTACTTTCCCTCCAAGACTGTGTGAAA
 ATGCCCATTTTTCTAAATGCTTACTATGACTGGTTTCCAACCTACATTTTAATTTCTGTTCAATCTGATAGGCAAA
 AAATGATATTTAATTTTTATTGATTGATAATGACCTTGAACGTGCCATTAGCCTTTTGCATGTATTCTTTTAT
 GAAACATCTGTTTCTATCCTTCGTCAATGTTCTCTTCATATGTTAACTTTTCTTATTGATTGTTAGAGCACTT
 TGTATATTGTGAATATTAGCTTTTGTGATCAGAATTATGGAATTGTTGTTGTCTTTAGTTTGTCTTATCAAGTTT
 AAAGCCATTGAGAGATGTTGTAATGTGTATGTTGTTAAATTTATGCTTATTTTGTGTTTTCTGATGCTCATAT
 GTTTAGAATGGTCAAGCAATCCCACTTATGATTACATAAATATTCTCCCATATTTGCTCTTAGCATTTTTTTTC
 TTTTCATGTAACCTTTTGTCTTTTCCAGGAATTTACTTTGCGGTAAGAAATGGGCTGGCTCCAGTTTTATGTTTC
 CCAAATGGTGATTGAGCTGTTCCATTTCCATATCTCCCTTATTAGAAATGACCCTATATATGTTCTAAATA
 TCTGCGTACTTGTGTCCCTTCTCTATAATCTCAGTTCACTCTTTGAGCTATCTTTGATTCCTTTTCAAACCAC
 ACTGCTTTACTGAACTGTCACTCATCTTATACATTTTTTAATCTCAGCAAGACAAGTTTCTAATGCCACTCTTTT
 TCAGAGTTTTTCTGGTGGTTGTAAGATGTTTATTCTTCTGGATAAACTTTAGAATCACTCTTTTTTGTCCAAGGTA
 AAATATATCCACATTGAGATCATACTGAATATACAGACTAATTCAGGAAAAATGTATGTCTTTATTGCATTGA
 GTCTTCTTATCCAATAAAAAAGATATGAATTTCCATGTATTGAAATCTTCACTGAGACTTATTTTTGGCTTTTCA

FIGURE 525B

CATGTCCTGCAAATGTATTGTTAAATTTATTTTAGGTATTTAGGGGAAATGATTTTCTAAAGTTTGTATTTTC
TAGCTTGTTATAATTTACATATGAGATAGTCATTGTTGTATATTATTTATAACTGATCATATTACTGTATTTGTA
TTGTTTAAATAGTTTTCTATTATTTGGGTTTTCTGGAATACAACCTTATTATCTACAAATTATGATTGTTTT
GCCTTTTCCAATGTTCACTGTTTTTATATTCTTGTCGTGATTGCTTTGTTTCAGCACTTCTAGAATAAAGTCAT
GCAATACTAATGA

FIGURE 526

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108728
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10922, pI: 8.81, NX(S/T): 0
MSAMKSVLPLLNPYCVLAFVYACMCVRAHVCVCVYMCVCVLCACVCTCRKKVMCGNGEFQ
PRRRLCLGLPREVVTLRETGSKCTLPSSSLCDLGQVTSAP
```

Important features of the protein:

Signal peptide:

Amino acids 1-28

N-myristoylation sites:

Amino acids 80-86;94-100

Prokaryotic membrane lipoprotein lipid attachment sites:

Amino acids 13-24;34-45

FIGURE 527

GTGAGACTTCTTTCTTCATTGTGGCTAGCTTTGAAAAGACCCCTCTGAACTTCCTAAAGATATC
AAG**ATG**ATATCACCAGACTTGCCCTTTTTGACAATTGTCTTGATCATAGTTAGTTGGACAACCT
TGTGGAGCACTAGCCATACTTCTTTCTTATCTTTACTATGTGTTTAAGGTTGTTTCATCTGCAA
GCCAGCTTAACAACCTTTTAAGAATAGCCAGCCTGTGAATCCCAAACACTCTAGAAGAAGTGAA
AAGAAATCCAATCATCATAAAGACTCCTCAATACACCATCTTCGTTTATCTGCCAACGATGCT
GAAGATAGCCTTCGCATGCACAGTACTGTGATTAACTTACTAACATGGATTGTATTACTCAGC
ATGCCTTCTCTAATTTATTGGCTAAAGAATCTTAGGTATTATTTTAAACTTAATCCTGATCCA
TGTAACCTTTGGCATTATCCTTATTCGACTATGGCAATTCTTGGAATACTTACACTGTT
TCAATAAAATCAAGTAAATTGTTGAAGACTACTTCACAATTTCCACTTCCTCTGGCTGTTGGT
GTGATTGCTTTTGGGTCAGCACATTTATATAGGCTTCCATGCTTTGTCTTCATTCCTCTTTTA
CTCCATGCATTATGCAACTTTATG**TAA**GATTGGACTTAAGGAATGATGAAGATAATTTATGTG
TTTAGGGCCAGTGATAAGAGGGAACACACAGATCCATCAGTATGGACAGCAAGATCCTTTGGA
GAAGACAAGTCTATTTTTACAATATTGAAAATAGGAAATTAGTTTTGTAATGTTTGAGGGAAG
TAGTTGAAGCATGGTTTTGTTTTGTGGTGTGGAATCCATGTACTAATCATTTTTGAAAAATTC
ATGAAGGGATATATGGTGATCACTATCATTGAGGACTCCTGTGCATATAAAATAGTCTGTTTT
ATCAACTGTAAA

FIGURE 528

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108738
><subunit 1 of 1, 196 aa, 1 stop
><MW: 22225, pI: 9.90, NX(S/T): 0
MISPDLPFLTIVLIIVSWTTCGALAILLSYLYYVFKVVHLQASLTTFKNSQPVNPKHSRR
SEKKSNNHHKDSSIHHLRLSANDAEDSLRMHSTVINLLTWIVLLSMPSLIYWLKNLRYYFK
LNPDPCKPLAFILIPTMAILGNTYTVSIKSSKLLKTTSQFPLPLAVGVIAFGSAHLYRLP
CFVFIPLLLHALCNFM
```

Important features of the protein:

Signal peptide:

Amino acids 1-25

Transmembrane domains:

Amino acids 91-108;128-143;167-186

N-myristoylation site:

Amino acids 141-147

FIGURE 529

GCGAGCCGGGTCCCACCATGGCCGCGAATTATTCCAGTACCAGTACCCGGAGAGAACATGTCA
 AAGTTAAAACCAGCTCCCAGCCAGGCTTCCTGGAACGGCTGAGCGAGACCTCGGGTGGGATGT
 TTGTGGGGCTCATGGCCTTCCTGCTCTCCTTCTACCTAATTTTCACCAATGAGGGCCGCGCAT
 TGAAGACGGCAACCTCATTGGCTGAGGGGCTCTCGCTTGTGGTGTCTCCCGACAGCATCCACA
 GTGTGGCTCCCGAGAATGAAGGAAGGCTGGTGCACATCATTGGCGCCTTACGGACATCCAAGCTT
 TTGTCTGATCCAACTATGGGGTCCATCTTCCGGCTGTGAAACTGCGGAGGCACGTGGAGATG
 TACCAATGGGTAGAACTGAGGAGTCCAGGGAGTACACCGAGGATGGGCAGGTGAAGAAGGAG
 ACGAGGTATTTCCTACAACACTGAATGGAGGTCAGAAATCATCAACAGCAAAAACTTCGACCGA
 GAGATTGGCCACAAAAACCCAGTGCCATGGCAGTGGAGTCATTCATGGCAACAGCCCCCTTT
 GTCCAAATTGGCAGGTTTTTCTCTCGTCAGGCCTCATCGACAAAGTCGACAACTTCAAGTCC
 CTGAGCCTATCCAAGCTGGAGGACCTCATGTGGACATCATTGCGCGTGGAGACTTTTTTCTAC
 CACAGCGAAAATCCCAAGTATCCAGAGGTGGGAGACTTGGTGTCTCCTTTTCTATGCTGGA
 CTGAGCGGCGATGACCTGACCTGGGCCCAGCTCACGTGGTCACTGTGATTGCCCGGCAGCGG
 GGTGACCAGCTAGTCCCATTCTCCACCAAGTCTGGGGATACCTTACTGCTCCTGCACCACGGG
 GACTTCTCAGCAGAGGAGGTGTTTCATAGAGAACTAAGGAGCAACTCCATGAAGACCTGGGGC
 CTGCGGGCAGCTGGCTGGATGGCCATGTTTCATGGGCCTCAACCTTATGACACGGATCCTCTAC
 ACCTTGGTGGACTGGTTTTCTGTTTTCCGAGACCTGGTCAACATTGGCCTGAAAGCCTTTGCC
 TTCTGTGTGGCCACCTCGCTGACCCTGCTGACCGTGGCGGCTGGCTGGCTCTTCTACCGACCC
 CTGTGGGCCCTCCTCATTGCCGGCCTGGCCCTTGTGCCCATCCTTGTGTCTCGGACACGGGTG
 CCAGCCAAAAAGTTGGAGTGAAGAGACCTGGCACCCGCGCCGACACCTGCGTGAGCCCTGAGG
 CTGGTTGTACAATGCCCACGCCTGCCTGGCTGCTTTCACCTGGGAGTGCTTTTCGATGTGGGCA
 CCTGGGCTTCCTAGGGCTGCTTCTGAGTGGTCTTTCACGTGTTGTGTCCATAGCTTTAGTCT
 TCCTAAATAAGATCCACCCACACCTAAGTCACAGAATTTCTAAGTTCCTCAACTACTCTCACA
 CCCTTTTAAAGATAAAGTATGTTGTAACCAGGACGCTTAAATGATTCTTTGTGTACCTTTTC
 TGTATATTTCAGAAACCGTTCTGTGCCTGCTGGGAGTAATTCTTTAGCAATTAAGTATTTGG
 TAGCTGAATAAGGGGTGAGAACTTCTGAAACCAGAGATCTGTAATCATCTCTATTGGCCTGGG
 GTGCCTGTGCTATAAATGAGTTTCTTACATGAAAAACACAGCCAGCCCAAGATGACTTATCT
 GGGTTTAGGATTCAATAGTATTCACTAACTGCTTATTACATGAGCAATTTTCATCAAATCTCCA
 AACTCTTAAAGGATGCTTTTCGGAACACAGCTGTATACCTAGATGATGACTAAATGCAAAATC
 CTTGGGCTTTGGTTTTTTTCTAGTAAGGATTTTAAATAACTGCCGACTTCAAAAAGTGTCTTA
 AAACGAAAGATAATGTTAAGAAAAATTTGAAAGCTTTGGAAAACCAAATTTGTAATATCATTG
 TATTTTTTTATTAAAGTTTTGTAATAAATTTCTAAATTATCA

FIGURE 530

1 ></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108743
><subunit 1 of 1, 400 aa, 1 stop
><MW: 44876, pI: 8.32, NX(S/T): 2
MAANYSSSTSTRREHVKVKTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIIFTNEGRALKT
ATSLAEGLSLVVSPDSIHSVAPENEGRLVHIIIGALRTSKLLSDPNYGVHLPVAKLRRHVE
MYQWVETEEESREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHKNPSAMAVESFMA
TAPFVQIGRFFLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKYPEVGDLR
VSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAAEEVFHRE
LRSNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNI GLKAFACVATSLT
LLTVAAGWLFYRPLWALLIAGLALVPILVARTRVPAKKLE

Important features of the protein:

Transmembrane domains:

Amino acids 34-53;365-388

N-glycosylation site:

Amino acids 4-8

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 140-144

Tyrosine kinase phosphorylation sites:

Amino acids 99-107;220-227

N-myristoylation sites:

Amino acids 35-41;93-99;310-316

Cell attachment sequences:

Amino acids 221-224;268-271

FIGURE 531

AAAAAAAAAAAAAAAAAAGAAGCTCTTATGCCAGGAACCTGGAATGGAGACCAAATATATATTG
GTTATATCATAGTATCACAGGGTTACTTTGGCATTGTTGGGAACTTGAGAGAAATGGGCAATAA
CTGTTACTTTAAAAGCTTGGGTGCTGTGATTCTGCCTTCAGCCTCAGCCACTTTTGTGGTGCT
TTGCGTGGCATCAGTACCTCCACTGATTCTTCTGTCTTTCCTCTCTCTCTTCCCCCCTCTTT
CCCTTCTGTTTTTCTCAGATCTAAGGGTTATAATGGAGGGGCAAACCTGCCTGGCTATTTTCTCAG
TAAGACTTCACTGAGTGACTGTTTCAAGCCATGATTTACCCTGCAGTTTAAACAGGCTCAGGAAT
TAGGTCGCATCAGTTGAGCGCGGGTCACTTAGGCCTATAATCATCATCAGACGGCAATTAAAG
GACCATTTCTGCCTTTTTTCACTATTACATCCCCCGCCTGTAGCCAGCCTGCCATACAGTAGA
TACTCAATAAATATTTGCTGAATGATAACCAATAA

FIGURE 532

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108758  
<subunit 1 of 1, 100 aa, 1 stop  
<MW: 10316, pI: 8.52, NX(S/T): 0  
MGNNCYFKSLGAVILPSASATFVVLCVASVPPLILLSFLSLFPPSFPSVFLRSKGYNGGA  
NCLAISDKTSLSDCSAHDLPCLTGSGIRSHQLSAGHLGL
```

Important features of the protein:

Signal peptide:

Amino acids 1-47

N-myristoylation site:

Amino acids 58-64

FIGURE 533

CGGGGTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGCTCAG
 CTGAGCCCATGAGCTCCCAGAGCTAACCCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGG
 TAGTCCCCATCCTGGAGGGGCAGGCTCTGCGCATCTGCTCCTGGC**ATG**GCGCTGCGGCACCTC
 GCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGTCCATGGAGAACACGGCCCAGCTG
 CCCGAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCCAGGCGCAAGTCTGTGTGGT
 CCAGGCTGTTACAGGCGCTGGAACGCCGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGA
 ACCCTCCCAGCCTACAACGGCTCCGAGTGTAAGCTTTGCTGGCCCCGGGTGCGCCATTCCCC
 ATGAACAGAAGCTCAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCCTCC
 CTCTTCCTGGGCACGTTCTTCATTAGCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCTTCTAC
 CTCAAGCGCTCCAGTAAACTCCCAGGGCCTGCTACAGAAGAAACAAAGCTCCGGCCCTGCAG
 CCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCTCAGACGTGGGGTCTGCAGGAAAG
 GAGGACCCACCACGACAGGGCAGACCCCAATACCTGCTCCTCCT**TGA**AGTCCAGCTCCACCC
 GAGGACAGACGCAGCCGGCCTCCGCCAGGCCCCTCCTGAGCAGCCATCGCTTCAGTGGTGTGG
 GTCAGGCGGACCCAAGAGTCAGCCCGTACGGAAGCCGCGCTACGTCAGGCGGGAGCGGCCCT
 GGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGAGGCCCGTATCAGCAATGTCTGACCTGG
 AGGCCGAGACCACGCCACGCAC'TTGGCGGCAGGGACCCGAGGCCGACCCCTTGGCGGGAACC
 AGCACAAAGTGTTGGCATCGCCCGCGCCCGGGACAGTCTGGGCACAGCCTCGGCTCTGGGT
 CCCTCCGCCTCCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCCTGAGGCTCCTCCCCACCAC
 AGCCATCTCGTTTATCGGACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGC
 CTTGGGGGGTCCGGGCCCCCCCCAGGAAACACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGG
 CACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCAGGGGCTCTGCTGCCGTGCCCTC
 CAGAGCCCACAGCGGGCAGGACTCCTCCAGCACCACCACACCCAGTGGCCCCGAGACCCCTCTG
 AGAACAGTGAGGCTGGTCCCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGC
 CTAGGAACCAGCTGCCTGAGACCAGGGTGCCTCTGGGCTGTCCTCCCGCGTGGCGGAGACCCC
 AAGCACGCAGCCACCCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAG
 CAGAAATTCATTGTGCAGAAAAGTCCCTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACC
 CCCATGCCTGGCTGATCCCTGCCCACGTGGGGCAGGCCACATCTAACCCCCACAAGTCACTG
 CCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCCTGGGGTCCCTCCCGGAGTTCCTGG
 GAGAAAGGCGCCGTGCTGGCCGCCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCAGA
 CGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCC
 TTCGGGGTCCCCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTG
 GGCCAGCGGGAACGTGGGGGCACTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 534

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108765
><subunit 1 of 1, 189 aa, 1 stop
><MW: 19464, pI: 9.60, NX(S/T): 4
MALRHLALLAGLLVGVASKSMентаQLPECCVDVVGVNASCPGASLCGPGCYRRWNADGS
ASCVRCGNGTLPAYNGSECRSFAGPGAPFFPMNRSSGTPGRPHPGAPRVAASLFLGTFFIS
SGLILSVAGFFYLKRSSKLPRACYRRNKAPALQPGEAAAMIPPPQSSDVGSAGKEDPPRQ
GRPPIPAPP
```

Important features of the protein:

Signal peptide:

Amino acids 1-18

Transmembrane domain:

Amino acids 111-129

N-glycosylation sites:

Amino acids 38-42;68-72;75-79;92-96

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 134-138

N-myristoylation sites:

Amino acids 11-17;36-42;43-49;59-65;69-75;122-128

FIGURE 535

TGGATCTGCGGGAATGTGGGCTGGAGAGGTCCTGCCGTGGTACCAGCCTCCAGCCTGCCCCCA
GGACTGCCCCCTGACCCAGGCGCGCCCGCTGCTCGGTGGCAGGAGGGCCGGCGGAGCGCCATGG
CCTGCATCCTGAAGAGAAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTTTTCCTGC
TGGTTGTGCGTCTTGTAATGAAGTGAATTTCCCATTTGCTACTAAACTGCTTTGGACAACCTG
GTACAAAGTGGATAACCATTTCTCCTACACATACAGGCGGCCCTTCGAACTCACTATGGATACA
TAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAACCT
CAGGTCAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAA
TGAACAATGCCCCCACCAAAGGTTATGAAGAAGATGTCGGCCGCATGACCATGATTGAGTTG
TGTCCCATACAGCGTTCCTCTTTTGCTAAAAAACCTGATTATTTTTTCAAGGAAGCGAATA
CTACTATTTATGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTT
ACAACATGTTGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGA
AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAACTGGGAAGGACAGTACAGAGTGAC
CATGCAGTGTTGATTGATCGAACAGCAACCACCACATACATGTCCTGCCCCACCACAAAAGGA
AGGAAGGAATAAAAGAAAGAAAGAAAGAAACAAACAAACAAACAAACAAACTAAGCAAGACA
AAACAAATACCCATGTCAGTGGTTCAAAGATTAAGATTGTGGCTTTGTGTAAAGTTCTTTCCC
TTTGTAGACTTGCTGCATAATTATTCAGGTATGATGGTTACAGTTTTTAAAAAGGAAGGAAA
TTGTGGTATGTGGTATGTAAATATTTTTAAATGTTGTCTCTCTGTTTTGATCAGTTTTTGT
TATTCAATTTGTCTTTATTAAATCTTATCAAAGCA

FIGURE 536

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108783
><subunit 1 of 1, 210 aa, 1 stop
><MW: 24022, pI: 9.51, NX(S/T): 1
MACILKRKSVIAVSFIAAFLFLLVRLVNEVNFPLLLNCFGQPGTKWIPFSYTYRRPLRT
HYGYINVKTQEPLQLDCDLCAIVSNSGQMGQKVGNEIDRSSCIWRMNNAPTKEYEEDVG
RMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVGII
PNAQIYVTTEKRMSYCDGVFKKETGKDSTE
```

Important features of the protein:

Signal peptide:

Amino acids 1-27

N-glycosylation sites:

Amino acids 148-152

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 6-10;191-195;201-205

N-myristoylation sites:

Amino acids 41-47;87-93;91-97;167-173;178-184

FIGURE 537

GTTTTATTGACAATACATGCATCATATCTTTTGACTTTGAAGGATATCTCATGTCAAAGGAAT
CAAGTTATGATTTATAGAGGATTCAGCTGGAATACCTTGTGGGTGCTGGCTGAGGGTGGCAAA
ACGCCTACCGAGACATGAAGGTTTTAGCCACTAGTTTTGTCTTGGGAGCCTGGGGTTGGCCT
TCTACCTGCCCTTTGGTGGTGACTACACCTAAAACACTGGCCATCCCTGAGAAGCTGCAAGAAG
CTGTGGGGAAAGTTATCATCAATGCCACAACCTGTACTGTACCTGTGGCCTTGGCTATAAGG
AGGAGACCGTCTGTGAGGTGGGCCCTGATGGAGTGAGAAGGAAATGTCAGACTCAGCGCTTAGAA
TGTCTGACCAACTGGATCTGTGGGATGCTCCATTTCACCATTCTCATTTGGCAAGGAATTTGAG
CTTAGCTGTCTGAGTTTCAGACATCTTGGAGTTTGGACAGGAAGCTTTCCGGTTTCACCTGGAGA
CTTGCTCGAGGTGTCATCTCCACTGACGATGAGGTCTTCAAACCTTTCAAGCCAACTCCCAC
TTTGTGAAGTTTAAATATGCTCAGGAGTATGACTCTGGGACATATCGCTGTGATGTGCAGCTG
GTAAAAAACTTGAGACTTGTCAAGAGGCTCTATTTTGGGTTGAGGGTCCCTTCCTCAACTTG
GTGAATCTGAATTTCCATCAGTCACTTACTGAGGATCAGAAGTTAATAGATGAGGGATTGGAA
GTTAATCTGGACAGCTACTCCAAGCCTCACCACCCAAAGTGGAAAAAGAAGGTGGCGTCAGCC
TTGGGAATAGGAATTGCCATTGGAGTGGTTGGTGGCGTGTGGTGAGGATTGTCCTCTGTGCG
CTAAGGGGGGGCCTGCAGCAGTGACAGCTTCAAGAACTTAACAGCCTTGCTCCTGAAGAACTG
GCTGCCCAGGAAGCCAAGCTAGCTTTTTAGGGGAGTGTTCAGCTGCTGGTAGTGGATCAGCT
TAGAGGGAACACTCCACAGCCAAAAGAATGAGTGGGAGAAATGGAGGGGACAATCTCCTGGG
AGCTATGCGCAGTAACCTAACTTCCTTATGTCCCATGGATCTTTCCTGATCTTCCCTGCCCA
TTGGGTACCCAGGAACTGCAAGCATTGCCTGTGTTTCTGGGAAGAGTTCTAAGAAGCTTGCA
TTCATTTTCTACCTTTATGACTTGGATGCCTCCCCACCTCCATTTCCCCTCTTCTGAGCTGT
GTATTCATGTAGAGGGATGTATTCAGCCTTTTGTAGTGAACATTTTTTTTCAATAAAAGTAATT
CACAGTAA

FIGURE 538

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108789
><subunit 1 of 1, 255 aa, 1 stop
><MW: 28440, pI: 8.92, NX(S/T): 1
MKVLATSFVLGSLGLAFYLPLVVTTPKTLAIPEKLQEAVGKVIINATTCTVTCGLGYKEE
TVCEVGPDGVRRKCQTQRLECLTNWICGMLHFTILIGKEFELSCLSSDILEFGQEAFT
WRLARGVISTDDEVFKPFQANSHFVKFKYAQEYDSGTYRCDVQLVKNLRLVKRLYFGLRV
LPPNLVNLNFHQSLTEDQKLIDEGLEVNLDSYKPHHPKWKKKVASALGIGIAIGVGGV
LVRIVLCALRGGLQQ
```

Important features of the protein:

Signal peptide:

Amino acids 1-30

Transmembrane domain:

Amino acids 225-244

N-glycosylation site:

Amino acids 45-49

N-myristoylation sites:

Amino acids 126-132;156-162;204-210;229-235;231-237;235-241

FIGURE 539

GCGCTCATCACTGGCTGGGGACAGAGCCGGGCACCAAGGAGCGACAGGATCCCGAAGAGAGAG
AGAGAAGGCAGCGAGGGAAGGAGGACCCCGGCAGGCAGCAGCATGAAATTCAGCCCAGCGCAC
TACCTGCTGCCTCTCCTGCCTGCGCTGGTCCCTCAGCACCAGACAGGACTATGAAGAGCTAGAA
AAGCAGCTGAAAGAAGTCTTTAAGGAGCGAAGCACCATTCTTCGTCAGCTGACAAAGACATCA
AGAGAACTTGATGGAATTAAAGTCAATCTTCAGTCCTTAAAAAACGATGAGCAGTCTGCCAAA
ACTGATGTTTCAGAACTTCTGGAATTAGGACAGAAACAAAGAGAAGAAATGAAGTCTCTTCAG
GAGGCCCTGCAAAATCAGCTTAAGGAGACATCAGAGAAAGCAGAAAAACACCAGGCTACTATT
AATTTTTTAAAGACTGAAGTTGAAAGAAAGAGCAAAATGATCCGAGACCTCCAGAATGAGGAT
TCAAGGAAGAGACCAAGAGATCTCCAGTGGAAGATAGTCTCCATGAGGACCATGTCAATATAC
TTATTGATGTATCTCTAGTACCTAGAATAGTGGAGATTTATATTAGATACAAAATAAATATGT
GTGGAATTAATTAATAA

FIGURE 540

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108806
><subunit 1 of 1, 159 aa, 1 stop
><MW: 18865, pI: 9.76, NX(S/T): 0
MKFSPAHYLLPLLPAVLSTRQDYEELEKQLKEVFKERSTILRQLTKTSRELDGIKVNLO
SLKNDEQSAKTDVQKLLELGQKQREEMKSLQEALQNQLKETSEKAEKHQATINFLKTEVE
RKSKMIRDLQNEDSRKRPRDLQWKIVSMRTMSIYLLMYL
```

Important features of the protein:

Signal peptide:

Amino acids 1-22

N-myristoylation site:

Amino acids 54-60

FIGURE 541

[illegible]

FIGURE 542

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108936
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19472, pI: 5.71, NX(S/T): 0
MSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADSTIMDIQVPTRAPDAVYTELQPTSPT
PTWPADETPQPQTQTQQLEGTDGPLVTDPEETHKSTKAAHPTDDTTLSERPSPSTDVQTD
PQTLKPSGFHEDDPFFYDEHTLRKRGLLVAAVLFITGIIILTSKGKCRQLSRLCRNRCR
```

Important features of the protein:

Signal peptide:

Amino acids 1-21

Transmembrane domain:

Amino acids 147-162

Tyrosine kinase phosphorylation site:

Amino acids 45-52

N-myristoylation site:

Amino acids 146-152

FIGURE 543

CGGCTCGAGGTGAGAAGGAAACTGCAAGAGTGGGGCAGAGAACCAGAGTGTCTAGAGCAAAACC
TCCTCTATCTGCACATCCTGGGGACGAACCGGGCAGCCGGAGAGCTGCGGCCGCCCCAGTCCC
GCTCCGCCCTTTGAAGGGTAAAACCCAAGGCGGGCCTTGTTCTGGCAGAAGGGACGCT**ATGA**
CCGCAGAATTCCTCTCCCTGCTTTGCCTCGGGCTGTGTCTGGGCTACGAAGATGAGAAAAAGA
ATGAGAAACCGCCCAAGCCCTCCCTCCACGCCTGGCCAGCTCGGTGGTTGAAGCCGAGAGCA
ATGTGACCCTGAAGTGTCTAGGCTCATTTCCAGAATGTGACATTTGTGCTGCGCAAGGTGAACG
ACTCTGGGTACAAGCAGGAACAGAGCTCGGCAGAAAACGAAGCTGAATTCCCCTTCACGGACC
TGAAGCCTAAGGATGCTGGGAGGTACTTTTGTGCCTACAAGACAACAGCCTCCCATGAGTGGT
CAGAAAGCAGTGAACACTTGCAGCTGGTGGTCACAGATAAACACGATGAACTTGAAGCTCCCT
CAATGAAAACAGACACCAGAACCATCTTTGTGCGCCATCTTCAGCTGCATCTCCATCCTTCTCC
TCTTCCTCTCAGTCTTCATCATCTACAGATGCAGCCAGCACGGTTCATCATCTGAGGAATCCA
CCAAGAGAACCAGCCATTCCAACTTCCGGAGCARGAGGCTGCCGAGGCAGATTTATCCAATA
TGGAAAGGGTATCTCTCTCGACGGCAGACCCCCAAGGAGTGACCTATGCTGAGCTAAGCACCA
GCGCCCTGTCTGAGGCAGCTTCAGACACCACCCAGGAGCCCCCAGGATCTCATGAATATGCGG
CACTGAAAGTGT**AG**CAAGAAGACAGCCCTGGCCACTAAAGGAGGGGGGATCGTGCTGGCCAAG
GTTATCGGAAATCTGGAGATGCAGATACTGTGTTTCCTTGCTCTTCGTCCATATCAATAAAAT
TAAGTTTCTCGTCTTA

FIGURE 544

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119510
><subunit 1 of 1, 236 aa, 1 stop
><MW: 26079, pI: 5.05, NX(S/T): 3
MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHAWPSSVVEAESNVTCLKCAHSQNVTFVL
RKVNDSGYKQEQSSAENEAEFPFTDLKPKDAGRYFCAYKTTASHEWSESSEHLQLVVTDK
HDELEAPSMKTDTRTIFVAIFSCISILLFLSVFIIYRCSQHGSSEESTKRTSHSKLPE
QEAAEADLSNMERVSLSTADPQGVTYAELSTSALSEAASDTTQEPPGSHEYAALKV
```

Important features of the protein:

Signal peptide:

Amino acids 1-16

Transmembrane domain:

Amino acids 135-153

N-glycosylation sites:

Amino acids 44-48;55-59;64-68

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 171-175

Tyrosine kinase phosphorylation sites:

Amino acids 61-69;87-95

N-myristoylation sites:

Amino acids 12-18;203-209

FIGURE 545

GGCGGCCCGGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTTCTGACAGCTGCGCGCGATCCTG
CTCTCTCTCAGCCGCCTGTGGACATGCGCAAAGGGCCCTCTCCTGAGTCCAGATGATGCTCAT
ACCAATGGCTTCAGTGATGGCGGTGACTGAACCGAAATGGGTCTCGGTCTGGAGCCGCTTCCT
CTGGGTGACGCTGCTGAGCATGGTGCTGGGGTCCCTGCTGGCCCTGCTGCTGCCGCTGGGGGC
TGTGGAGGAGCAGTGCTTGGCTGTGCTCAAAGGCCTCTACCTGCTCAGGAGCAAACCGGACAG
GGCGCAGCATGCCGCCACCAAGTGCACCAGCCCGTCCACGGAGCTCAGCATCACCTCCAGGGG
CGCGACGCTGCTGGTGGCCAAGACCAAGGCCTCTCCAGCGGGTAAGTTGGAAGCCAGAGCTGC
CCTGAACCAGGCCCTGGAGATGAAGCGCCAGGGCAAGCGGGAAAAAGCCCAAAGCTCTTCAT
GCACGCCCTCAAGATGGACCCGGACTTCGTGGACGCGCTCACCGAGTTTGGCATCTTCTCGGA
AGAAGACAAGGACATCATCCAGGCGGACTACTTGTACACCAGAGCATTGACCATCTCACCCCTA
CCATGAGAAAGCACTGGTCAACCGCGATCGGACACTGCCTCTTGTGGAAGAGATCGACCAGAG
GTATTTTCAGCATCATCGACAGCAAAGTGAAGAAGGTCATGTCCATCCCCAAGGGGAACTCAGC
TCTGCGCAGGGTCATGGAGGAGACCTACTACCATCACATCTACCACACAGTGGCCATCGAGGG
CAACACCCTCACCTCTCGGAAATCAGGCACATCCTGGAGACCCGCTACGCCGTGCCCGGGAA
GAGCCTGGAGGAGCAGAACGAGGTCATAGGCATGCATGCAGCCATGAAGTACATCAACACGAC
TCTGGTTTCGCGCATCGGCTCCGTCACCATCAGCGACGTGCTGGAGATCCACAGGCGGGTGCT
GGGCTACGTGGACCCCGTGAAGCCGGCAGGTTTCGGACAACACAGGTCCTGGTCGGACACCA
CATCCCTCCCCATCCGCAGGATGTGGAAAAGCAGATGCAGGAGTTTGTACAGTGGCTCAACTCC
GAGGAAGCCATGAACCTGCACCCAGTGGAGTTTGCAGCCTTAGCCCATTTATAAACTCGTTTAC
ATCCACCCTTTTATTGATGGCAACGGGAGGACCTCCCGTCTGCTCATGAACCTCATCCTCATG
CAGGCGGGCTACCCGCCCATCACCATCCGCAAGGAGCAGCGGTCCGACTACTACCACGTGTTG
GAAGCTGCCAACGAGGGCGACGTGAGGCCTTTTATTTCGCTTCATCGCCAAGTGTACTGAGACC
ACCCTGGACACCCTGCTTTTTGCCACAACCTGAGTACTCGGTGGCACTGCCAGAAGCCCAACCC
AACCACTCTGGGTTCAAGGAGACGCTTCCTGTGAAGCCC**TAA**CCCTAGAAATCCTCAGTGACA
AAGGCTGTCCTGAGGTAGGAAA

FIGURE 546

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119517
><subunit 1 of 1, 458 aa, 1 stop
><MW: 51778, pI: 7.81, NX(S/T): 2
MMLIPMASVMAVTEPKWVSVWSRFLWVTLLSMVLGSLLALLLPLGAVEEQCLAVLKGLYL
LRSKPDRAQHAATKCTSPSTELSITSRGATLLVAKTKASPAGKLEARAALNQALEMKRQG
KREKAQKLFMHALKMDPDFVDALTEFGIFSEEDKDIIQADYLYTRALTISPYHEKALVNR
DRTLPLVEEIDQRYFSIIDSKVKKVMSIPKGNALRRVMEETYHHIYHTVAIEGNTLTL
SEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLEIHRRVLGY
VDPVEAGRFRTTQVLVGHHPHPQDVEKQMGEFVQWLNSEEAMNLHPVEFAALAHYKLV
YIHPFIDGNGRTSRLLMNLIILMQAGYPPITIRKEQRSDYYHVLEAANEGDVRPFIRFIK
CTETTLDTLLFATTEYSVALPEAQPNHSGFKETLPVKP
```

Important features of the protein:

Signal peptide:

Amino acids 1-46

N-glycosylation sites:

Amino acids 275-279;446-450

Tyrosine kinase phosphorylation sites:

Amino acids 216-225;217-225;244-232

N-myristoylation sites:

Amino acids 35-41;235-241;266-272;368-374

Amidation site:

Amino acids 119-123

FIGURE 547

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGGGCA
 TGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTGAGCTGG
 CCTACTTCAGACAGCCAGGGCCCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGTGGCCCCCTTG
 GCATTTCCACAAGACGCCAAGATGGAGATTCCCATGGGGACCCAGGGCTGCTTCTCAAAGAGC
 CTCCTGCTCTCAGCCTCAATCCTGGTCCTCTGGATGCTCCAAGGCTCCCAGGCAGCTCTCTAC
 ATCCAGAAGATTCCAGAGCAGCCTCAAAGAACCAGGACCTTCTCCTGTCAGTCCAGGGTGTC
 CCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAGACGTACGGAGGCACGAGGCTA
 TTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGATGGCAGTGCCATGGGACAGCGAGAC
 ATCGTGGGCTTCCCCAATGGTTCCATGCTGCTGCGCCGCGCCAGCCTACAGACAGTGGCACC
 TACCAAGTAGCCATTACCATCAACTCTGAATGGACTATGAAGGCCAAGACTGAGGTCCAGGTA
 GCTGAAAAGAATAAGGAGCTGCCAGTACACACCTGCCACCAACGCTGGGATCCTGGCGGCC
 ACCATCATTGGATCTCTTGCTGCCGGGGCCCTTCTCATCAGCTGCATTGCCTATCTCCTGGTG
 ACAAGGAAGTGGAGGGGCCAGAGCCACAGACTGCCTGCTCCGAGGGGCCAGGGATCTCTGTCC
 ATCTTGCTGCTCGGCTGTATCCCCAGTGCCTTCAGTGACGCCCAGCACATGGATGGCGACCACA
 GAGAAGCCAGAATTGGGCCCTGCTCATGATGCTGGTGACAACAACATCTATGAAGTGATGCCC
 TCTCCAGTCTCTCCTGGTGTCCCCCATCAGTGACACAAGGTCCATAAACCCAGCCCGGCCCTG
 CCCACACCCCCACACCTGCAGGCGGAGCCAGAGAACCACCAGTACCAGCAGGACCTGCTAAAC
 CCGGACCCTGCCCCCTACTGCCAGCTGGTGCCAACTTCTCTGATGGGTCTGGGCCAGGCCAGC
 CAGGGAGAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCTCACACCTGAGACCAGCAGGACAAG
 GCCATTGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCACATGGGGCA
 GGTGTCCTGGCAGGGGGACAGGAGACTGTAACAGGCCCAGGTCCTTGTGCAGCCCCTGAATGC
 ACGCCCGCCTTCGGTCTGTTCTTCAAGCAAGCTGGCCTGGGCCATGTGCCTGTGAAAGGCAG
 GCTCTGGCCCCCTTCCATGCCAAAGTCCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGC
 CTCAGGCCTGCCTCCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCTCAATGCCCTACCCC
 AACTCCACTAGTGACCCTCAGAGTCTTCTCCCCTTAGGACAAGGCAGACACCCACCATGCGG
 GCCTCAGGTGGCAGAGAGGCCCAGCCTCACAGGCCTGTGGCCCCACACACCAGTCCCAGCAAG
 GTGACCACGGCTGCTGGACCCCTTCCCTGTTTCAGGCAGGCCCAGCCCCCTCTCAGAACCTGCTG
 CCAGCTGCTGGTCTTGGCCCCCACCCTGAATCTTACTGAGTCCCTCTGGGCAGCAGCTCCCTT
 CTCCACCCCAACCCAGCACCCGTCCCAAATGTGGCCTCAGCTTGTCTCTCCCTTCCCCAACT
 ATGCATTCATTCAGCAATAAATGAGCCTTTGCTGCA

FIGURE 548

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119535
><subunit 1 of 1, 300 aa, 1 stop
><MW: 32638, pI: 6.02, NX(S/T): 1
MEIPMGTOGCFSKSLLLSASILVLWMLQGSQAALYIQKIQEQPKNQDLLLLSVQGVPDF
QDFNWYLGEETYGGTRLFTYIPGIQRPQRDGSAMGQRDIVGF PNGSMLLRR AQPTDSGTY
QVAITINSEWTMKAKTEVQVAEKNKELPSTHLPTNAGILAATIIGSLAAGALLISCIAYL
LVTRNWRGQSHRLPAPRGQGSLSILCSAVSPVPSVTPSTWMATTEKPELGP AHDAGDNNI
YEVMPSPVLLVSPISDTRSINPARPLPTPHLQAE PENHQYQQDLLNPD PAPY CQLVPTS
```

Important features of the protein:

Signal peptide:

Amino acids 1-32

Transmembrane domain:

Amino acids 159-178

N-glycosylation site:

Amino acids 104-108

N-myristoylation sites:

Amino acids 6-12;29-35;55-61;91-97;157-163;165-171

FIGURE 549

GCCACTCACACCATCTGCTAATGGGACAGCTCACTCTTCCCTCCAAACCATGGCCTTGGCTCA
AGAGCTTCCCTGTTTCTGGAATGTTCTTTCCTCCAGCTCCAGGTGTTGAAATTCTGCCTGGTC
TGGGTCTCCTGTTGAAGGACGCCCTCCACTGGGAAGGATCCTCTTGCCTTCACCACTTGTCTT
CACCAGCCCCCTGCTCCCCCTCTTCCCTCTTGGGGCTGTTGTCGTTGTTGATACTTTTTTTTTTGT
GTGTTTGACACACATCTTCTTCTCACCTCTAACACAGTTCTCAACCACAGCACTTTTGTCCC
TGGAGATGTTGGCAGTGTCCAGAGGCGTGTGATGGTCCCACTGGGGTGGGGGTGCTGCTGGCA
CCAGATGGTAGGGAGATGCCAGGGGTGCTGCTCCACACCCTATGGGACACTGCACAGTACACC
TGGCCTGTGTCCCCACAGCGAGAGCTGGCCCTGGGCAGGCGTGGTCCCTGCGGTGTGTGTTG
GTTGGGATCCTCCACAGTGACAGACGGTGCCTCTGCCCACGTTTCCACACAGCTCTTTTGCT
TGTGGAGCTCACCCCTTTGCAGAGAGCTCATTTCCCTGCGGTCTTTGGCCTGCAGAAGTAAAA
TGAGGGGTGGTGAATTACACCCCTGCTGGTTACACATGGAAACTCAGGAGTGAGAATTTTGT
GGAGAGCAAGAGAGGTGAGACTGGGGTGTGGCTGCCAGCCAGGCGGTCCCTCAGCCCCCTGGA
GAAGCGGGGTGGGGCCTGCACACCGAGTCTTCCAGTGAGTCCAGTGATGCTCTCTCCTCTTC
CTCCAGTCACCTTTCTCTCCAGTGCCACTACTGCGCTTTCGATGCAGAATAATTCAGTATTT
GGCGACTTGAAGTCGGACGAGATGGAGCTGCTCTACTCAGCCTACGGAGATGAGACAGGCGTG
CAGTGTGCGCTGAGCCTGCAGGAGTTTGTGAAGGATGCTGGGAGCTACAGCAAGAAAGTGGTG
GACGACCTCCTGGACCAGATCACAGGCGGAGACCACTCTAGGACGCTCTTCCAGCTGAAGCAG
AGAAGAAATGTTCCCATGAAGCCTCCAGATGAAGCCAAGGTTGGGGACACCCTAGGAGACAGC
AGCAGCTCTGTTCTGGAGTTCATGTGATGAAGTCTATCCCGACGTTTCTGTGGATATCTCC
ATGCTCAGCTCTCTGGGGAAGGTGAAGAAGGAGCTGGACCCTGACGACAGCCATTTGAACCTG
GATGAGACGACGAAGCTCCTGCAGGACCTGCACGAAGCACAGGCGGAGCGCGGCGGCTCTCGG
CCGTCTGCTCAACCTCAGCTCCCTGTCCAACGCCTCCGAGAGGGACCAGCACCCACCTGGGAAGC
CCTTCTCGCCTGAGTGTGCGGGAGCAGCCAGACGTCACCCACGACCCCTATGAGTTTCTTCAG
TCTCCAGAGCCTGCGGCCTCTGCCAAGACCTAACTCTAGACCACCTTCAGCTCTTTTATTTTA
TTTTTTTAGTTTTATTTTGCACGTGTAGAGTTTTTGTTCATCAGACAAGGACTTTTGATCCTGTC
CCCTTTGGCATGCGGGAAGCAGCCGCGGGGAGGTAATGAATTGTCTGTGGTATCATGTCAGCA
GAGTCTCCAAGCCCCACGAACCCTGAGGAGTGGAGTCATACGCGAAGGCCATATGGCCATCGT
GTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGGAGTCATACACGAAG
GGCGTGTGGCCATCGTGTGAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGG
AGTCATACGCGAAGGGTGTGTGGCCAGGCTGCAGAGCTGCGTGCCGTTTGTGTCCGAGCATCA
CGTGTGGCTCCAGCCCTTGTCTTCTGCCAGTGTAGACACCTCTGTCTGCCCCACTGTCTGGGG
TCGCTCTTGGGAGGCACAGGCATGGGTGTGTCTGGCCTCATTTCTGTATCAGTCCAGTGTGTTT
CTGTCTAGTTTGTGTCTCCAGGCAGGCCATGGTAGGGGCCCTCGCAGGGGCCATTGGGGAGC
ACAGGGCCAGGCTGGGGTGAAGGAGAGCTCCCTGTTTTCTGTTTAATTGATGAGCCTGGGAAA
GGAGTGTGTTCTGCCTGCCCCGTTACAGTGGAGCGTTCCGTGTCCATAAAACGTTTTTCTAACTG
GGAA

FIGURE 550

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119537
><subunit 1 of 1, 104 aa, 1 stop
><MW: 11136, pI: 8.20, NX(S/T): 0
MLAVSRGVLMVPLGLGVLLAPDGREMPGVLLHTLWDTAQYTWPVSP TARAGPGQAWSLRC
VLVGILHSDRRCALPTFPHSSFACGAHPFAESSFPCGLWPAEVK
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

N-myristoylation sites:

Amino acids 53-59;64-70;97-103

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 74-85

FIGURE 551

CGCCCTTAGCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCAT
GACCCCTGGCCCTGGGTACCTTGCCCTGCCTTCCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAAGTGAACCTG
GCTGTTCTCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCTTGTCTCTC
CAACCGCATCCACCACCTCCATGATTCTGACTTTGCCCCACCTGCCAGCCTGCGGCATCTCAACCTCAAGTGGAA
CTGCCCCGCCGTTGGCCTCAGCCCCATGCACCTTCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGT
GCCACCCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATC
CCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCCT
ATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGG
CCTGGGCAGCCTCACCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGGCCCCGCAACCTGCCTTCCAGCCT
GGAGTATCTGCTGTTGTCTTACAACCGCATCGTCAAACCTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCG
TGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCAGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTT
CCCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGCTTGAAGGCCTGGTGTGGAAGGACAGTTCTCTCTC
CTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCTCTACAA
ATGCATCACTAAACCAAGGCCCTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCTTCAATTACCAAAA
GAGGTGTCTTTGCCCCACCTGTCTCTGGCCCCCTTCCCTCGGGAGCCTGGTGGCCCTGAAGGAGCTGGACATGCA
CGGCATCTTCTTCCGCTCACTCGATGAGACCAGCTCCGGCCACTGGCCCCGCTGCCCATGCTCCAGACTCTGCG
TCTGCAGATGAACTTCATCAACCAGGCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCT
GTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTG
GCTGCAGCTTGGGGACCTTGCTCCGGCCCCAGTGGACACTCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCAC
CCTCAACTTCACCTTGGATCTGTACGGAAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCAGCTCTCGCA
CCTGCAGTGCCTGCGCCTGAGCCACAACCTGCATCTCGCAGGCAGTCAATGGCTCCAGTTCTTCCGCTGACCGG
TCTGCAGGTGCTAGACCTGTCCACAATAAGCTGGACCTCTACCACGAGCACTCATTACGGAGCTACCACGACT
GGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTGGCATGCAGGGCGTGGGGCCACAACCTCAGCTTCTGTCG
TCACCTGCGCACCCCTGCGCCACCTCAGCCTGGCCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAG
TACGTGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCA
CTTCTTCCAAGGCCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCCTGCACACCCCTCCTGCCCCAAC
CCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAG
CCTCCACTTCTTCCCCAACTGGAAGTCTCGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCT
GCCTGCTGGCACCCTGGCTCCGGAGGCTGGATGTGAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTC
CAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCC
CCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGA
CTTCTGCTGGAGGTGCAAGCTGCGCTGCCCGTCTGCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCA
GGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCCCTCTC
GCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACTCTGTGGCTGGGACCTCTGGTACTGCTT
CCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTACGATGC
CTTCGTGGTCTTCGACAAAACGAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCGAGCTGGAGGA
GTGCCGTGGGGCGCTGGGCACTCCGCTGTGCCCTGGAGGAACGCGACTGGCTGCCCTGGCAAAACCCCTCTTTGAGAA
CCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCACACGGACCGGTCAGTGGTCTCTT
GCGCGCCAGCTTCTGCTGGCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGTGGTGATCCTGAG
CCCTGACGGCCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCTCTCTGGCCCCA
CCAGCCAGTGGTCAAGCAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACAACACCACCTTCTATAA
CCGGAACCTTCTGCCAGGGACCCACGGCCGAATAGCCGTGAGCCGGAATCCTGCACGGTGCCACCTC

FIGURE 552

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119714
><subunit 1 of 1, 1032 aa, 1 stop
><MW: 115799, pI: 8.61, NX(S/T): 12
MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWFLKSVPHFSMAA
PRGNVTSLSLSSNRIHHLHDSDFAHLPRLHLNLKWNCPVGLSPMHFPCMTIEPSTFL
AVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDGNCY
KNPCRQALEVAPGALLGLGSLTHLSLKYNLTVVPRNLPSLEYLLLSYNRIVKLAPEDL
ANLTALRVLDVGGNCRCDHAPNCPMECPRHFPQLHPDTFSHLRLEGLVLKDSLSWLN
ASWFRGLGNLRVLDLSENFYKCI TKTKALQGLTQLRKLNLSFNYQKRVSFHLSLAPSF
GSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYV
DLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPN CSTLNFTLDLS
RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHS
FTELPRLEALDLSYNSQPFGMQGVGHNF SFVAHLRTLRLHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWL DLSQNLHTLLPQTLRNLPKSLQVLRL
RDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGF
FSKAKELRELNLSANALKTVDH SWFGPLASALQILDVSANPLHCACGA AFMDFLLEVQAA
VPGLP SRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGV PMLHHL CG
WDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVDKTS AVADWVYNELRGQLEECRG
RWALRLCLEERDWLP GKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLL E
DRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNH HF
YNRNFCQGPTAE
```

Important features of the protein:

Signal peptide:

Amino acids 1-30

Transmembrane domain:

Amino acids 818-835

N-glycosylation sites:

Amino acids 64-68;129-133;210-214;242-246;300-304;340-344;
469-473;474-477;513-517;567-571;694-698;731-735

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 347-351

Tyrosine kinase phosphorylation site:

Amino acids 863-871

N-myristoylation sites:

Amino acids 27-33;41-47;63-69;193-199;361-367;409-415;
563-569;607-613;695-701;794-800;929-935;945-951;
1010-1016

Amidation site:

Amino Acids 974-978

Leucine zipper patterns:

Amino acids 204-226;644-666;814-836

FIGURE 553

GGCGTGGGACGTGCTGCGGCGTCCTAGCTGGCTTACAGGGCGGCGGGCGGGGTGTGTGTCTCT
GTTAAGAGTGCTACTCGCCCGGGGTGATCTGTGCATGCCACTCCTGGGTCAGACGGTGAGGT
CGGCGTCTGCGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGAGACAGGCCCGGCGCCCCCT
CCGAGGCTAGACGGCCCCAGCTTCGCGGGGATC**ATGG**CATTGCTGGTGGACCGAGTGCGGGGC
CACTGGCGAATCGCCGCGGGCTCCTGTTCAACCTGCTGGTGTCCATCTGCATTGTGTTCTCT
AACAAATGGATTTATGTGTACCACGGCTTCCCCAACATGAGCCTGACCCTGGTGCACCTTCGTG
GTCACCTGGCTGGGCTTGTATATCTGCCAGAAGCTGGACATCTTTGCCCCCAAAGTCTGCCG
CCCTCCAGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTCACTAACCTTTCT
CTGCAGAACAAACACCATAGGCACCTATCAGCTGGCCAAGGCCATGACCACGCGGGTGATCATA
GCCATCCAGACCTTCTGCTACCAGAAAACCTTCTCCACCAGAATCCAGCTCACGCTGATTCT
ATAACTTTAGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTAATTTCTTGGAATGGTG
TTTGCTGCTCTTGGTGTTTTAGTTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAGCAT
GAATTACAAGTGAACCAATGCAGCTGCTGTACTACCAGGCTCCGATGTCATCTGCCATGTTG
CTGGTTGCTGTGCCCTTCTTTGAGCCAGTGTTTGGAGAAGGAGGAATATTTGGTCCCTGGTCA
GTTTCTGCTTTGCTTATGGTGCTGCTATCTGGAGTAATAGCTTTCATGGTGAACCTTATCAATT
TATTGGATCATTGGGAACACTTCACCTGTCACCTATAACATGTTCCGACACTTCAAGTTCTGC
ATTACTTTATTTCGGAGGATATGTTTTATTTAAGGATCCACTGTCCATTAATCAGGCCCTTGGC
ATTTTATGTACATTATTTGGCATTCTCGCCTATACCCACTTTAAGCTCAGTGAACAGGAAGGA
AGTAGGAGTAAACTGGCACAAACGTCCT**TAA**TGGGTTTTTTGTGGAGAAAAGAATGTTGTCCCA
AGAAGATAAAAAATATTGTTAAGTGTGCAAGTTATTA

FIGURE 554

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125170
><subunit 1 of 1, 313 aa, 1 stop
><MW: 35066, pI: 9.39, NX(S/T): 5
MALLVDRVRGHWRIAAGLLFNLLVSICIVFLNKWIYVYHGFPNMSLTLVHFVVTWLGLYI
CQKLDIFAPKSLPPSRLLLLALSFCGFVVFTNLSLQNTTIGTYQLAKAMTTPVIIAIQTF
CYQKTFSTRIQLTLIPITLGVILNSYYDVKFNFGLGMVFAALGVLVTSLYQVWVGAKQHEL
QVNSMQLLYYQAPMSSAMLLVAVPFFEPVFEGGGIFGPWSVSALLMVLLSGVIAFMVNLS
IYWIIGNTSPVTYNMFGHFKFCITLFGGYVLFKDPLSINQALGILCTLFGILAYTHFKLS
EQEGSRSKLAQRP
```

Important features of the protein:

Signal peptide:

Amino acids 1-27

Transmembrane domains:

Amino acids 46-60;75-90;153-167;192-208;221-237

N-glycosylation sites:

Amino acids 43-47;92-96;97-101;238-242

N-myristoylation sites:

Amino acids 17-23;57-63;140-146;155-161;162-168;283-289

FIGURE 555

GTTAGGCAGAGCCAAGGTGGTTGCAGACCTGGAATCAGAACAGCTTTTAGACCAACCTGAAAG
 CAGGAATGTAAGCACTGTTTACAGAGATTTTCGTCTTTGGCTTATTGTGCCTGCAGAGTCTAG
 TGCTTCTTTGCCAGCTGTGCTGACTCAGCACTCCATGCCTGTTTTCTGGAACCACTCCCTGGA
 GCTGGGCCATGTTTTGATTGACAGTGTGGAGCTAGCCCAGCAAGTACTCTACATGCAACCCCC
 CACCCAGGCACTACCTCTGCTCCTCCTCCATGGCCTCCTGCTACACCGGCAGCTCTATGGAAC
 AAGGCTGCAGGCACACAGGGGGCGCTGGAGTCAAGTGACTCTAACCCAGGTTCTTCAGACCCA
 AGACCAGCTGTGGGCAAGTCTTAGCAATCCCCGTGCTGCCATGCAAGAGCTGGCTGCTTCAGT
 TTTCTACGGGGGTCTCTGGGGGACACTGAGGACAGGGAGGCCCTGATTAGCCTCACACAAGC
 CTGCCTGAGCCCCAGTAGTGGGAGCTGGGTCCAGCCACACACCTCAGTCTTTGCTGGCCAC
 GCTCATGCCCCCTCCAGCTAAGGGAGCTGGATGCAATGGCAGAGTGCAAGGCCCAAGCTGCACC
 TACTGCCCTCACCACCTTGAACCCCCGGCTCTGCGGACTGAGTGAGGGCCCCCAAGCCTGGCTGT
 TGGCAGCCAGAGTCGCGCTCTCTTGAGTGGCTGCAGCGGAGTTACCCGTGTGGGTTCTTG
 AGTCTCGAAGAGGCGCCAGCTTGCGGAAAGGCGACTGCGGCAACGCCTAGTGCAAGTCAACCG
 GAGGCTGGAGTCACTGCAGGATCTGCTGACCCACGTGATTCGCCAAGACGAGTCCGACGCCCC
 GTGGTCAGTGCTGGGGCCAAATGCACGGCGGCCTCTGGAGGGCGTCTTAGAGACCGAGGCTCT
 AGAACTGAGCCAGTTGGTGGGCACGCTACAACGCGACCTTGATTGCCTGTTGCAGCAGCTGAA
 GGGCGCACCCCCGTGCCCTCCCGCGCTGTGCTGCGGTGGCCCACGCTCTCTGGACTGGCCG
 CCTACCCCTTGCCCTTGGCGACCTCATGCGCCGGCCGGTCCGCAGCCGCCCTGGCACTGGCTGCG
 ACAGTTGTGCGCCGTGGGCAACTGTTGGTTTCGTTACTTGGGCGTGGGCGCGGACGCGAGCAG
 TGATGTACCAGAGCGCGTCTTCCACCTGTCAGCCTTTCGCCACCCGCGCCGCCTGCTGCTGGC
 ATTGCGTGGGGAAGCTGCCCTGGACCAGAATGTGCCCAGCTCGAATTTCCCTGGTAGCCGAGG
 CTCGGTCTCCAGTCAGCTCCAGTATAAACGTCTGGAGATGAACAGCAACCTCTGCACTTCAG
 GGTGGAGAATGGTCCAAATCCCACGGTTCAGAGAGAGGGCTGCTGCTGATCGGGCTACAGGT
 CCTACATGCGGAGTGGGACCCAATAGCTGGAGCCTTGCAAGACAGTCCTTCCAGCCAACCCAG
 CCCTCTGCCTCCCGTCAGCATCAGCACACAGGCCCCGGGCACCAGTGACCTGCCAGCCCCAGC
 CGACCTGACTGTGTACTCGTGTCTGTGTACATGGGAGGGCCCCCTTGGCACCGCTAAGCTGCA
 GAGCAGGAACATCGTGATGCATCTGCCTTTACCCACCAAGCTCACCCCCAACACCTGTGTCCA
 AAGGAGGGTCCATGTGTGCAGCCCACCCCTGTCTTGAGCCCGTCTACCAAATAAAGTTGTAG
 TGATTCCA

FIGURE 556

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129594
><subunit 1 of 1, 162 aa, 1 stop
><MW: 17598, pI: 6.58, NX(S/T): 1
MPVFWNQSLELGHVLIDSVELAQQVLYMQPPTQALPLLLHGLLLHRQLYGTRLQAHRGR
WSQVTLTQVLQTQDQLWASLSNPRAAMQELAASVFYGGPLGDTEDREALISLTQACLSPS
SGSWVQPHTPQSLLATLMPLPAKGAGCNGRVQGPDAPTALTT
```

Important features of the protein:

Signal peptide:

Amino acids 1-45

N-glycosylation site:

Amino acids 6-10

N-myristoylation sites:

Amino acids 97-103;144-150

FIGURE 557

GACCTTGAGCCCTCGAAAGCGACATGGCGGTTCTCTTAAAGCTGGGCGTTCTCTGCAGTGGCC
AAGGAGCTCGAGCTCTCCTACTCCGAAGCCGGGTGGTCAGACCCGCTTATGTGTCAGCATTTC
TCCAGGACCAGCCTACCCAAGGACGGTGTGGTACCCAGCACATTACCTGTCACCAAGCCACC
ACTCTGGTTCCAAGGCTGCATCTCTCCACTGGACCAGTGAGAGGGTTGTCAGTGTCTGCTCT
TGGGGCTGATCCCTGCTGGGTACTTGAATCCCTGCTCTGTGGTGGACTACTCTCTGGCTGCAG
CCCTCACCCCTGCACAGTCACTGGGGCCTTGGACAAGTGGTTACCGACTACGTTTCATGGGGACA
CCCTGCCGAAGGCTGCCAGGGCAGGCCTCTTGGCACTCTCAGCTTTGACCTTTGCTGGGCTTTGC
TACTTCAATTACCACGATGTGCGCATCTGCAGAGCGGTTGCCATGCTGTGGAAGCTCTGACCCT
GGGTGCAGCACTTTGATTGTGTGCCTCCTTGCCCTCTGCTTTACCAATGCCGTTACCTCGCAG
TGAGGGGGGATGAAGGATAAGCCCATTGGTGGGCAGAATGTCTTCTAATTACATGGTTATTTT
CAGAATTTATTTGTTGAGGAAGAGGTTTGAGGAGTTAGGTTTCGACCATTTCGTGAGTCTGTGTT
CCATACTCCACTGAGTGTGGGCACCTAGCTCACAGCCTCGCGGTGAGACTGAACATTTTCATGAG
CTCATGTTGCCTTTGACCACCATTTCTTAAGGAGAGCCAGCTGATTGCTGTCAGGATAAGAGC
ATCTCTTCAGCCAGGAGGGAGGCCTGTTCCCTCCTGAGTTAGACTTTGCATGAAGCTCGAAAG
TATTCCCTTTGGAACCTCCCATTCTTGTTTCAGGTGACACCAGCTCTGTTGATGGCTCTGCTTC
TAGGGAACATTTAATCAGGAGATGCTCTCAATGACTAATTTGTCTAAGTCTTAGGAAGGAGGT
TGAGGAAAGCTGGATTTAGACAAGTTCAATTTAGGGAGTTCTCCTTGTTTGTGGATTAAAATA
TGACAGATTGCAAACAGACTACTCTTCAAATGTATCTCAATTGTGCAGAAGTGAGCTGTCCAA
AAGTATAAGACTAAGTGATAAACTGTCTTCCCACCGTGGGAGTTGTTAATGAGAAAGAAAGTG
TACTCTGAAAAACAAGGGGG

FIGURE 558

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129793
><subunit 1 of 1, 159 aa, 1 stop
><MW: 17014, pI: 9.38, NX(S/T): 0
MAVLLKLGVLCSGQGARALLRSRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSERVVSLLLLGLIPAGYLNPCSVVDYSLAAALTLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALTTFAGLCYFNYHVDVGICRAVAMLWKL
```

Important features of the protein:

Signal peptide:

Amino acids 1-15

Transmembrane domains:

Amino acids 71-88;126-140

Glycosaminoglycan attachment site:

Amino acids 12-16

N-myristoylation sites

Amino acids 8-14;58-64;78-84;108-114;148-154

FIGURE 559

CCCAGCCCCGCGTTCGGCTGCTCTCGAGGAGGCCGGAGTCCCCGGAGACGATGCGCCCCGCGC
 AGCCGCTGCGCCTGCGGGAGCCGGCTGCCCTTGAGATGGAGTTGCTGCCTCTTTGGCTCTGC
 CTGGGTTTTACTTCTTGACCGTGGGCTGGAGGAACAGAAGCGGAACAGCCACAGCAGCCTCC
 CAAGGAGTCTGCAAGTTGGTGGGTGGAGCCGCTGACTGCCGAGGGCAGAGCCTCGCTTCGGTG
 CCCAGCAGCCTCCCCCCCCACGCCCCGGATGCTCACCCTGGATGCCAACCCCTCTCAAGACCCTG
 TGGAATCACTCCCTCCAGCCTTACCCTCTCCTGGAGAGCCTCAGCCTGCACAGCTGCCACCTG
 GAGCGCATCAGCCGCGGCGCCTTCCAGGAGCAAGGTACCTGCGCAGCCTGGTCTGGGGGAC
 AACTGCCTCTCAGAGAACTACGAAGAGACGGCAGCCGCCCTCCACGCCCTGCCGGGCCTGCGG
 AGGCTGGACTTGTGAGGAAACGCCCTGACGGAGGACATGGCAGCGCTCATGCTCCAGAACCTC
 TCCTCGCTGCGGTCCGTGTCCCTGGCGGGGAACACCATCATGCGGCTGGACGACTCCGTCTTC
 GAGGGCCTGGAGCGTCTCCGGGAGCTGGATCTGCAGAGGAACTACATCTTCGAGATCGAGGGC
 GGCGCTTTCGACGGCCTGGCTGAGCTGAGGCACCTCAACCTGGCCTTCAACAACCTCCCCTGC
 ATCGTGGACTTCGGGCTCACGCGGCTGCGGGTCTCAACGTCAGCTACAACGTCCTGGAGTGG
 TTCCTCGCGACCGGGGGAGAGGCTGCCTTCGAGCTGGAGACGCTGGACCTGTCTACAACCAG
 CTGCTGTTCTTCCCCTGCTGCCCCAGTACAGCAAGTTGCGGACCCTCCTGCTGCGCGACAAC
 AACATGGGCTTCTACCGGGACCTGTACAACACCTCGTCGCCGAGGGAGATGGTGGCCCAGTTC
 CTCCTCGTGGACGGCAACGTGACCAACATCACCACCGTCAGCCTCTGGGAAGAATTCTCCTCC
 AGCGACCTCGCAGATCTCCGCTTCTTGACATGAGCCAGAACCAGTTCAGTACCTGCCAGAC
 GGCTTCTGAGGAAAATGCCTTCCCTCTCCACCTGAACCTCCACCAGAATTGCCTGATGACG
 CTTACATTCGGGAGCACGAGCCCCCGGAGCGCTCACCAGCTGGACCTGAGCCACAACCAG
 CTGTGCGAGCTGCACCTGGCTCCGGGGCTGGCCAGCTGCCTGGGCAGCCTGCGCTTGTTCAAC
 CTGAGCTCCAACCAGCTCCTGGGCGTCCCCCTGGCCTCTTCGCCAATGCTAGGAACATCACTAC
 ACTTGACATGAGCCACAATCAGATCTCACTTTGTCCCCTGCCAGCTGCCTCGGACCGGGTGGG
 CCCCCCTAGCTGTGTGGATTTAGGAATATGGCATCTTTAAGGAGCCTGTCTCTGGAGGGCTG
 TGGCCTGGGGGCATTGCCAGACTGCCCATTTCAAGGGACCTCCCTGACCTACTTAGACCTCTC
 AAGCAACTGGGGGGTTCTGAATGGGAGCCTCGCCCCACTCCAGGATGTTGCCCCCATGTTACA
 GGTCTGTCTCTCAGGAACATGGGCCTCCACTCCAGCTTTATGGCGTTGGACTTCTCTGGGTT
 TGGGAATCTCAGGGACTTAGATCTGTCGGGGAATTGCTTGACCACCTTCCCAAGGTTTGGGGG
 CAGCCTGGCCCTGGAGACCCTGGATCTCCGTAGAAACTCGCTCACAGCCCTTCCCCAGAAGGC
 TGTGTCTGAGCAGCTCTCGAGAGGTCTGCGGACCATCTACCTCAGTCAGAATCCATATGACTG
 CTGTGGGGTGGATGGCTGGGGGGCCCTGCAGCATGGGCAGACGGTGGCCGACTGGGCCATGGT
 CACCTGCAACCTCTCCTCCAAGATCATCCGCGTGACGGAGCTGCCCCGAGGTGTGCCTCGGGA
 CTGCAAGTGGGAGCGGCTGGACCTGGGCCTGCTCTACCTCGTGCTCATCCTCCCCAGCTGCCT
 CACCCTGCTGGTGGCCTGCACTGTCTGCTCCTCACTTTTAAGAAGCCTCTGCTTCAGGTCAT
 CAAGAGCCGCTGCCACTGGTCTCCTCCGTTTACTGACCTGGCTGTGTGCCAAGACTCGAAATTCG
 GTCCGCACACAACAGGACACTTTCTCTGCCAGCTTTCAAGATGTGATGCAGAGGCCAAGTCTG
 ACGAATTGAAGTTTCAATTAAAATTTAATATGTTTCCATTCCTCATCGCCACCCCCACCCCG
 CCCCCACCACCGCCCAAGTCTTTTCCATCATTATAATTCATCCTTATTATCTTGGTAAAT
 ATTTATTAAGTGACTTTTTTCAGAAATAAAAGGCAACGTGTCTCATAAATATTTTTTAAAAAA
 AAAAAAAAAAAAAA

FIGURE 560

><subunit 1 of 1, 692 aa, 1 stop
><MW: 76366, pI: 6.07, NX(S/T): 11
MELLPLWLCLGFHFLTVGWRNRSQTATAASQGVCKLVGGAADCRGQSLASVPSSLPPHAR
MLTLDANPLKTLWNHSLQPYPLLESLSLHSCHLERISRGAFQEQGHLRSLVLGDNCLSEN
YEETAAALHALPGLRRLDLSGNALTEDMAALMLQNLSSLRSVSLAGNTIMRLDDSVFEGL
ERLRELDLQARNYIFEIEGGAFDGLAELRHLNLAFNNLPCIVDFGLTRLRLVNLVSYNVLEW
FLATGGEAAFELETLDLSHNQLLFFPLLPQYSKLRITLLLRDNNMGFYRDLYNTSSPREMV
AQFLLVDGNVTNITTVSLWEEFSSSDLDLRLFDMSQNFQYLPDGFRLKMPSLSHLNLH
QNCLMTLHIREHEPPGALTELDLSHNQLSELHLAPGLASCLGSLRLFNLSNQLLGVPPG
LFANARNITTLDMSHNQISLCPLPAASDRVGPPSCVDFRNMASLRSLSLEGCGLGALPDC
PFQGTSLTYLDLSSNWGVNLGSLAPLQDVAPMLQVLSLRNMGLHSSFMALDFSGFGNLRD
LDLSGNCLTTFPRFGGSLALETDLRLRNSLTALPQKAVSEQLSRGLRTIYLSQNPYDCCG
VDGWGALQHGQTVADWAMVTCNLSSKIRVTELPGGVPRDCKWERLDLGLLYLVLIPLSC
LTLVACTVIVLTFKKPLLQVIKSRCHWSSVY

Important features of the protein:

Signal peptide:

Amino acids 1-18

Transmembrane domain:

Amino acids 651-672

N-glycosylation sites:

Amino acids 21-25;74-78;155-159;232-236;292-296;309-313;
312-316;408-414;427-431;500-504;622-626

Glycosaminoglycan attachment site:

Amino acids 533-537

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 566-570

N-myristoylation sites:

Amino acids 24-30;39-45;45-51;141-147;199-205;245-251;
308-314;396-402;416-422;420-426;471-477;
484-490;497-503;522-528;545-551;555-561;610-616

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 657-668

Leucine zipper patterns:

Amino acids 48-70;492-514

FIGURE 561

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAACAT
GGCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG
CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTG
CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT
GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAC
TTGGGCTGGAAGTGTTGAACACAGTTTTTGGATATTTTCCAAAAGATTTGATCAAGGTA
TAAATACACGGAAGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG
AGGAAGAGATGATTTTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGA
CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA
GGAGTCTCGGGGGCGTGAACCTGACCCCTGTGCCTGAGCCCGAGGCATT
GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA
GAGCCACCCTCACACCAGCGGTCCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC
TTTTGAAGAAATTCTGCACGATAAATTGAAAGTGCCGGAAGCGAAAGCAGAACTGGCAATAG
TTCTCCTGCCTCGGTGGAGCGGAGAAGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAG
TCAGAGAGGAAGTGGACAGTGCCTTATTATTACAGCAAAGGATTTTCGTTGGCATCAAAATCT
AAGTTTGTTTTACAAAGATTGTTTTTAGTACTAAGCTGCCTTGGCAGTTTGCATTTT
GAGCCAAACAAAATATATTATTTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

FIGURE 562

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131639
><subunit 1 of 1, 303 aa, 1 stop
><MW: 33900, pI: 4.81, NX(S/T): 2
MAAAPGLLFWLFLVGLALWWVPGQSDLSHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPD
CRFVNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADET
DFVCFEGGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELD PVP
EPEAFRADSEEDGEAFSESTEGLOQQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDK
LKVPGSESR TGNSSPASVEREKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYK
DCF
```

Important features of the protein:

Signal peptide:

Amino acids 1-22

N-glycosylation site:

Amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 67-76

N-myristoylation sites:

Amino acids 205-211;225-231;277-283

Amidation site:

Amino acids 28-32

FIGURE 563

GCCAGCCGTGGGATTAGGCTTCGCCGGCTACGATTGCGGCCCCCATCTTCTGACTTTTCCTCG
TGTGACCCATCTTTTCAAATTCCTTACCTGAGGAAGGAGCCCGATTACAAGGATATTTACCT
GCTCCTACCCTGATCTAGGGACGAGGATGGGAAGACCGCCTGTGGCCATGAGCCCTCCCCGGT
GCTCCTGGGGCTAAGGCTGGGGCTGCAGCCATGGGGCTGGGTCAGCCCCAGGCCTGGTTGCTG
GGTCTGCCCCACAGCTGTGGTCTATGGCTCCCTGGCTCTCTTCACCACCATCCTGCACAATGTC
TTCTTGCTCTACTATGTGGACACCTTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGG
GTCGGAGAGACAGTGTTTTCTCCTCTGGAACAGCCTCAATGACCCTCTCTTCGGTTGGCTCAGT
GACCGGCAGTTCCTCAGCTCCCAGCCCCGCCTGTGTGGAGAGGAGCTGCTTGTGGGCAGTGAG
GAGGCGGACAGCATCACCTTGGGCCGGTATCTCCGGCAGCTGGCACGCCATCGGAACTTCCTG
TGGTTCGTGAGCATGGACCTGGTGCAGGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTCGG
GACGCCAAGGTGGAAAGACCGCTTGAGCCCAGGAGTTCGAGGCTGCAATTGAGTTATGATTGCA
CCACTGCACTCCAGCCTGGGCGGCAGAGAAAGGCTCCATCTCTAAAAAAGAAGAGCTAAGTG
CTGTACCTAAAACATGCAGTATATAAACTGGCTGAACTTAGAAATAAACTGTTTTCATGTTAT
GAAAA

FIGURE 564

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131649
><subunit 1 of 1, 153 aa, 1 stop
><MW: 17603, pI: 7.42, NX(S/T): 0
MGLGQPQAWLLGLPTAVVYGSLALFTTILHNVFLLYYVDTFVSVYKINKMAFWVGETVFL
LWNSLNDPLFGWLSDRQFLSSQPRLCGEELLVGSEEADSITLGRYLRQLARHRNFLWFVS
MDLVQVQWLTPVIPALRDAKVERPLEPRSSRLQ
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

N-myristoylation sites:

Amino acids 4-10;12-18;93-99

Leucine zipper pattern:

Amino acids 102-124

FIGURE 565

CGGCACGAGTAAATGGAGATAATATCACCATGCACTCAGCCCTAGCCACTGCATTGCTGTTA
CTGATACCATTACTGCTGCTACGTCGTTTTTTTGATGGCTCAGCCCTTAGGGAAGGGGGATCA
AGGGAGAAGCCCGGACCTTCCCGCAGGAGGTGGGCTGGGCACAGCCCTGAACCATGGAGGTCA
CCCACCCTGAGGTCGGGACCTGGGTTCCCTTCCTATCCACTGGGGGTCCCAGCCTTTGTCTTC
ATCTCTCCAGGTCCCAGCCCTTCACAGTGGGCACTTCCCTGCCTGTGACGGAGGCCCCAGCCA
TCTCC

FIGURE 566

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131652
><subunit 1 of 1, 89 aa, 1 stop
><MW: 9688, pI: 11.49, NX(S/T): 0
MHSALATALLLLIPLLLLRRFFDGSALREGGSREKPGPSRRRWAGHSPEPWRSPTLRSGP
GFPSYPLGVPAFVFISPGSPSQWALPCL
```

Important features of the protein:

Signal peptide:

Amino acids 1-18

Glycosaminoglycan attachment site:

Amino acids 58-62

FIGURE 567

AGTCTAGCAGGAAAGGAGAGGGAGCTTTCCCCGAAGACCCTCCTGGACCAGCCCCAGGCTCCT
GTGCTGGTTGCACGCCAGGGCCTGTACTGACCACCTCCACGTGCCACTGGGGCTGTAAGGAGGA
ATGGCGGCCGTGGGCAGCCTGCTTGGCCTGGCAGCCTCTTCCTGGCTAGGGGGCCAGAACGCC
TCTGACCACAGCCTGTGGCTCCTGAGGAAGCCCCGAGGCTCATCCTGCCCCGGCACGGGTCAC
CAGCTCTGCCGGCTGAGGCAGAGCACCGTGAAGGCCACCGGACCTGCACTCCGCCGCCTGCAC
ACATCCTCCTGGCGAGCTGACAGCAGCAGGGCCTCACTCACTCGTGTGCACCGCCAGGCTTAT
GCACGACTCTACCCCGTGCTGCTGGTGAAGCAGGATGGCTCCACCATCCACATCCGCTACAGG
GAGCCACGGCGCATGCTGGCGATGCCCATAGATCTGGACACCCTGTCTCCTGAGGAGCGCCGG
GCCAGGCTGCGGAAGCGTGAGGCTCAGCTCCAGTCGAGGAAGGAGTACGAGCAGGAGCTCAGT
GATGACTTGTCATGTGGAGCGCTACCGACAGTTCTGGACCAGGACCAAGAAG**TGA**CCGTGGCTC
CAGCCACCCCGGACATTGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGC

FIGURE 568

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131658
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18903, pI: 11.08, NX(S/T): 1
MAAVGSELLGLAASSWLGGQNASDHSLLWLLRKPRGSSCPGTGHQLCRLRQSTVKATGPALR
RLHTSSWRADSSRASLTRVHRQAYARLYPVLLVKQDGSTIHIRYREPRRMLAMPIDLDTL
SPEERRARLRKREAQLQSRKEYEQELSDDLHVERYRQFWTRTKK
```

Important features of the protein:

Signal peptide:

Amino acids 1-18

N-glycosylation site:

Amino acids 20-24

N-myristoylation sites:

Amino acids 5-11;9-15;17-23;18-24

FIGURE 569

GGTGCCAAGGGTTCGGGGGGGAGCACTGAGGCTTTAGCAGCTCTCCTGTATCCTCATTTGCAT
CCTCCTGTAGCAGCTGGAAAATTCAGATTACAGGTGAAATTCCTGGCTGGCAATCTTCTGTA
TATGGACACAGTGATGTGCCAGAAGGGCTTTGCATCCCTGAGACTGAAGGAAGCTCCATTTTT
GGAGCCCTCCCACACCTTGCTCTGTGTGCCTCTCATTCTGATTTGAATTCTTATTTTTGCTATA
TGATGAAGCTGTAATCCTAAGTTTAAAAAGGGGAGTAGGTATTGACATCATGGTAGAAATAGG
CTGTCTTATGGAAGTGTAGTTAGGGATCACAGCCTATTGGACCAGCCCCAGCCTTAGCAGCAG
TTCTGTACACTGATTCTTCCAGATTAGTCTACGTTCCCTCGAACAGACCTATGCCATGGGTTA
CAACTACAATTTGTTGTGCGATTAGAGTTAACTTACAGACTCTCAAAACCCCATTTCTTTGGGT
TAGGCAACTTCCAGAAGTAGTCATTTATTTGAATTTTAGTCTAAGATCAACTGAATTAGGGAG
GTTTGAAAGTGTAAGCAATCGTACATTCCCAAACACTTTGTAAAGAAGGAATGGGTAGTG
TCAACTAAAGGAAATGGTGTGCATCCAGCAAAAGAAAGAGACCGAAAGCAAAGTCATAAACC
ATGCCCACGAGCTCAGCTGTCTGTCTCGTGTCTCTCCATACCCTTGTTGACTGTGCTCATA
TTAGCCAGAGACCTAAGTGCTCTTGAGGATGTCCCTGGGGCCCCCTCCCCCTCCGCTGTCAC
TGTCTACTTCTGATCCTCTCTTCTGTGTCAGGAGAGGTCCAGGCCTTCTATGAGGACCTGAGT
GGCCGGCAGTACGTGAATGAAGTCTTCAACTTCAGCGTGGACAAGCTCTATGACCTCCTCTTC
ACCAACTCGCCCTTCCAGCGGGATTTTCATGGAGCAGCGGCGCTTCTCTGATATCATCTTCCAT
CCATGGAAAAAGGAGGAGAAATGGAAACCAGAGCCGAGTGATTCTTTACACCATCACCTTACC
AACCCTCTGGCTCCCAAACTGCCACTGTGAGGAGACACAGACCATGTACAAGGCGAGCCAG
GAGAGTGAATGTTACGTGATAGATGCCGAAGTCTCACCCACGACGTGCCCTACCACGACTAC
TTCTACACAATCAATCGCTACACGCTCACCCGTGTGGCTCGGAACAAGAGCCGACTCAGGGTC
TCCACAGAGCTGCGCTATCGAAAACAGCCCTGGGGGTTAGTGAAAACGTTTCATCGAGAAGAAC
TTCTGGAGTGGGCTGGAGGACTACTTCCGCCATTTAGAGAGCGAGCTGGCCAAAACGGAGAGC
ACTTATTTGGCTGAGATGCACAGACAATCTCCAAAGAGAAGGCCAGCAAGACTACAACGGTG
CGGAGGAGGAAGCGTCCCCATGCCACCTGCGAGTCCCTCACCTGGAAGAGGTGATGAGCCCG
GTCACCACGCCCACAGATGAGGATGTGGGCCACAGGATCAAACATGTGGCAGGTTCCACACAG
ACGCGGCATATCCCGGAGGACACCCCCAACGGTTTCCACCTGCAGAGCGTGTCCAAGCTGCTG
CTGGTTATCAGCTGTGTTCTGGTGCTGCTGGTCATCCTTAACATGATGCTCTTCTACAAACTC
TGGATGTTGGAATACACCACGCAGACCTCACTGCCTGGCAGGGTCTAAGGCTCCAAGAAAGG
TTACCCAGTCTCAGACAGAATGGGCCAGCTCTTAGAGTCCCAACAAAAGTACCACGATACT
GAGCTCCAAAAATGGAGGGAAATCATCAAATCCTCAGTGATGCTCCTTGACCAGATGAAGGAC
TCGCTCATCAACCTTCAGAACGGCATCAGGTCCCGCGACTACACGTCGGAAAGTGAAGAAAAG
AGGAATCGCTATCATTGACAAGGCAGGAACAGGGTGGCTGCAAGAGGCCTGTGCAATACATGT
ACATAGACCATATAAATATATATATATAAATATATATATATACAGAATATAAATATATATATT
ATATACAGATTTTAAAAAAGAGATAATGCCTATGTACCAGGGAGAAGGAGCGGGCCCTCCCGC
GCCCTGTGCTGGCCGGAGCAGCGTTTTCTTATGGTGGAGCAGCTGAGGAGGGCAGGAACCGCC
TCTCAGCACCGACCTCCCCTGATCTCCCTCCTCCACCCCTCTGTTCCCCACCCCTTCCCTTGC
TGGCCATTCTTGCTTTTGAAGGGAAATGTTGAGCCAAAGTTATGCCTGCGAAGACCCTAAG
GTCTCAAAAAGAAGTCTTAAGACGGCATTGCTTAAGGTGCTTCATTCCCTAATCCCCTTTTGA
TTTGTTCCTCAAAATAAAAGAGAATCTTTCTTCCCTAAAAA

FIGURE 570

><subunit 1 of 1, 425 aa, 1 stop
><MW: 49786, pI: 8.84, NX(S/T): 3
MPTSSAVLLRVLSIPLLTVLILARDLSALGGCPWGPLPLRCHCLLPDPLFCAGEVQAFYE
DLSGRQYVNEVFNFSDKLYDLLFTNSPFQDFMEQRRFSDIIFHPWKKEENGNSRVIL
YTITLTNPLAPKTATVRETQTMKASQSECYVIDAEVLTHDVPYHDYFYTINRYTLTRV
ARNKSRLRVSTELRYRKQPWGLVKTFIEKNFWSGLEDFRHLSESELAKTESTYLAEMHRQ
SPKEKASKTTTVRRRKRPHAHLRVPHLEEVMSPVTTPTDEDVGHRIKHVAGSTQTRHIPE
DTPNGFHLQSVSKLLLVISCVLVLLVILNMMLFYKLWMLEYTTQTLTAWQGLRLQERLPQ
SQTEWAQLLESQOKYHDTLQKWREI IKSSVMLLDQMKDSLINLQNGIRSRDYTSESEK
RNRVH

Important features of the protein:

Signal peptide:

Amino acids 1-28

Transmembrane domain:

Amino acids 312-334

N-glycosylation sites:

Amino acids 73-77;114-118;183-187

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 97-101

Tyrosine kinase phosphorylation sites:

Amino acids 144-153;188-196

N-myristoylation sites:

Amino acids 201-207;291-297

Leucine zipper pattern:

325-347

FIGURE 571

GTAGAGAGTGAAGCAGCAAGACTGCAGAGCCTCATCAAGAAGTGTGGAGTGAAGGGAAGGCTTCAGATGGACAAT
 TTGTGTGCTGGGAAAAAATGGAATGTGCTGCAAATTTCCCTGTGGATAAGGGTGGACGGCTGCTCTGTCAACTT
 TGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCATCGTGAGAAGCGAGACAC
 TAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTGCATCGAGAGGGATGAGGTTTCGGAATGTTTTCCG
 GGAGCTGCAGATCATGCAAGGGCTGGAGCACCCCTTCTGGTCAATCTGTGGTACTCCTTCAGGATGAGGAGGA
 CATGTTTCATGGTGGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTACAGA
 GGGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTACCACATCATCCACAG
 AGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACATGTTTACATTACAGACTTCAACATAGCGACGGT
 AGTGAAAGGAGCAGAAAGGGCTTCTCCATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCAGGTGTA
 CATGGACAGAGCCCCGGATACTCGTACCCTGTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCG
 GGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCATCGATGAAATCCTTAACATGTTCAAGGTGGAGCGTGT
 CCAGTACTCTCCAGTGGTGCAAGGGGATGGTGGCCCTGCTGAGGAAGCTCCTGACCAAGGATCCTGAGAGCCG
 CGTGTCCAGCCTTCATGACATACAGAGCGTGCCCTACTTGGCCGACATGAACGGGACGCGGTGTTCAAGAAGGC
 ACTGATGCCCCGCTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCCACATTTGAGCTTGAAGAGATGATTCT
 AGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGATGGCACAAAGGACAGCTG
 CCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCGGAGGAATTATCATATTC AACAGAGAGAAGCT
 CAGGAGGCAGCAGGGACAGGGCAGCCAGCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCT
 CCAGGACGGGTGCAACAACAACCTCCTCACCCACCTGCACCCGTGGCTGCAGCAGCTGAGCCACACTTGTTG
 CTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCTCTTTGTGCCCTGATGGTCCCTGTCTC
 ACCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGAGCTGGGAAGCCTGGGTTCTGGTCCCATCTCCAT
 GACTGATTACGTGTGACCTCAGACAAGTCACGCCCTCTCTGTGCCCTCCGTTTTCTGCATCTGCCAAAGGGGTTA
 AACACTTCTGCCCCACTTCAAATTACAAGATTATGGGGAGAACCCTAATAGGTAGGAAACATGAAAAACCTTTGA
 TATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCCATTCCCCAAAGCAATCAA
 ACCGTGATGACTTTGCAATTTGGCACATCCTAGCTTGTAGAGGGCACTTCGAAAAACACAGCCCTGACAGCAA
 AATAAAGGTCTGATATGTTGGCCCTTCTATGGAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTT
 CATGTGCATTCTCTGGCAGGCCACAGTCTTCTGAGCTTGTAAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
 AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCTCATTTAAGAAGACTATCCTTACCTTTTAGTTTCAGCAGTCCT
 CACCACCACCATATCCCAGTGCTGGGATGGCACACAGGTGTCCATTGAGATGAGAGTTGGGTGCTGAGCATTG
 GTTACTCCTGCAGAGTGAATCAGCACCCCATCCAAGTGGCCCGAAAGCCAGACCTGCAGCAGAACTCTCCAAC
 TCTCTATCAGCTTTAGGGTTTTCTCTCCTGGGAAGGGTGTAAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
 ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAGAAAGTTTATTTCAGG
 AGGAAAATGGGTTACACAAAAAGCAAACCTACATTCTGATCTGCTCAGGGAGAAGCTTGCTTTGAACTGGAAGA
 TGTTGGGATGAGCAGGGAAAGCTTAGACTTTGGAGTCAGGTTTGTGTTTCAAGATCCAGCCCTGCTGGCTACTAAC
 TAACTGGGAGACCTTAGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCTTCATTTTTAAACAGGGATAATAAA
 ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTGGATGACTCATAGAAT
 GGCCTTTTTTGTGAGCATAATCGTCATCATTATTTAGATACTTTCTTCTTCACTCACCCAGCAGGTGAGTTTTT
 TGTGCAAAACAACTGTTTAGGATCTTCAAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGC
 TGAAGTTCGACTGTGTTTTTATTTTTTATCCAACCTCCATTTTCACTTTTTTACATGATTACTCAATCCTTGGG
 GCTGTCCATGTCATCTCTTAGATTTCTTAAAGACATTTTAAATGTATGGTTAGGTTTTATATTTTTTATTTTTAA
 AAAAGAAATAGTCAGTGTCTTCTCCTTTCAACCGAGACTATTTCTGGATTGTGTGCTCCTCGTCAGTTGACTTGT
 TTTGCACACTTTTCTTTACTTCATGTCCCATCAACAACCGTCTGCTCCCACTCCCCAGGAAATAAGGGGC
 CTGCTCCTCTCCCTACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTTGGGCTGAGTTCACGAA
 TTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTCTCTGGTTCTGTTCAAGTTGGCATTCTTGTGTTG
 GAATAAACTATTTCTTGG

FIGURE 572

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA136110
<subunit 1 of 1, 364 aa, 1 stop
<MW: 42195, pI: 7.40, NX(S/T): 1
MKYMNKQKCIERDEVNRFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY
HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV
VKGAERASSMAGTKPYMAPEVFQVYMDRGPYSGYSYPVDWWSLGITAYELLRGWRPYEIHVS
TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA
VFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTDKSCPLNGH
LQHCLETVREEFIIFNREKLRRQQGQGSQLLDTSRGGGQAQSKLQDGCNNNLLTHTCTR
GCSS
```

Important features of the protein:

N-glycosylation site:

Amino acids 285-289

N-myristoylation sites:

Amino acids 123-129;290-296;337-343;339-345;348-354

Serine/Threonine protein kinases active-site signature:

Amino acids 92-105

FIGURE 573

CTCCAGTTTCGCCGACTGTAACATGTTTCATCCAGTTTCAGTATGTTTTGTATGCAAGTTGGAAATAAATAAACGTC
CTGAACTGGATGAAACATGTTACAGTCGGCCGAAACATGAGAGGCTGTGTGAGAAGCTGCAGCCGCCGGCAGAGG
AGACCTCAGCATCATCTAGAGCCCAGCGCTGGCCCTGCCTCCGCCGCGCCGCCGCGTGCCTGTTCTGTT
CCTGCTACTGTCCACCTAAACAACCTCCCGTTACACGGACAAGTGAAACATCTGTGGCTGTCTCTCTCTTTCTTC
CTCCTCTTCCAACCTCTCTCTCTCTCCACTTCCCAGCCGCAGCAGAAAGCCCCCAACCCAACCTGACGCTGGCA
CAACTGCAAACGGTGTCTATCCGCACAACCTTTATCTCGCTCTCTCGGGCTCCCCTAAGGCATTTGGACCCATCGCCGC
GTCTTTTATTTTTGCAAAGTTGCATCGCTGTACATATTTTTGTCCCCGCCACCTCCCTCTGTCTCTGGAGTGCCC
TACAGCCCCGCAAACCTCTCTGAGCTGCGCCCTAGTGCCCCCTGCTGGGCAGTGGCGTTCCCCCCCATCTCCC
GCGCCAGCCCCGCTGCTCTGGGCAGACGATGCTGAAGATGCTCTCTCTTAAGCTGCTGCTGCTGGCCGTGGCT
CTGGGCTTCTTTGAAGGAGATGCTAAGTTTGGGGAAAGAAACGAAGGGAGCGGAGCAAGGAGGAGAAGGTGCCTG
AATGGGAACCCCCGAAGCGCCTGAAAAGGAGAGACAGGAGGATGATGTCCAGCTGGAGCTGCTGAGTGGGGGA
GAGATGCTGTGCGGTGGCTTCTACCCCTCGGCTGTCTGTCTGCTGCGGAGTGACAGCCCGGGGCTAGGGCGCCTG
GAGAATAAGATATTTCTGTTACCAACAACACAGAATGTGGGAAGTTACTGGAGGAAATCAAATGTGCACTTTGC
TCTCCACATTTCTCAAAGCCTGTTCCACTCACCTGAGAGAGAAGCTTTGGAAAGAGACCTAGTACTTCTCTGCTC
TGCAAAGACTATTGCAAAGAATTCTTTTACACTTGCCGAGGCCATATTCCAGGTTTCTTCAAACAACCTGCGGAT
GAGTTTGTCTTTACTATGCAAGAAAAGATGGTGGGTTGTGCTTTCCAGATTTTCAAAGAAAACAAGTCAGAGGA
CCAGCATCTAACTACTTTGGACCAGATGGAAGAATATGACAAAGTGGAAGAGATCAGCAGAAAAGCACAACACAAC
TGCTTCTGTATTCCAGGAGTTGTGAGTGGGCTGCGGCAGCCCGTTGGTGCCCTGCATAGTGGGGATGGCTCGCAA
CGTCTCTTCATTCTGGAAGAAAGAGTTATGTGAAGATACTTACCCCTGAAGGAGAAATTTCAAGGAGCCTTAT
TTGGACATTACAAACTTGTTCAAAGTGGAATAAAGGAGGAGATGAAAGAGGACTGCTAAGCCTCGCATTCCAT
CCCAATTACAAGAAAATGGAAGTTGTATGTCTTATACCAACCAAGAACGGTGGGCTATCGGGCCCTCAT
GACCACATTTCTAGGGTTGTGGAATACACAGTATCCAGAAAAATCCACACCAAGTTGATTTGAGAACAGCCAGA
GTCTTTCTTGAAGTTGCAGAACTCCACAGAAAGCATCTGGGAGGACAACCTGCTCTTTGGCCCTGACGGCTTTTGT
TACATCATTTCTGGTGATGGGATGATTACACTGGATGATATGGAAGAAATGGATGGGTAAAGTGATTTTACAGGC
TCAGTGCTACGGCTGGATGTGGACACAGACATGTGCAACGTGCCTTATTCATACCAAGGAGCAACCCACACTTC
AACAGCACCAACCCAGCCCCCGAAGTGTTTGTCTATGGGCTCCACGATCCAGGCAGATGTGCTGTGGATAGACAT
CCCACTGATATAAACATCAATTTAACGATACGTGTTTCAGACTCCAATGGAAAAACAGATCATCAGCCAGAATT
CTACAGATAATAAGGGGAAAGATTATGAAAGTGAGCCATCACTTTTAGAATTCAGCCATTGAGTAATGGTCCT
TTGGTTGGTGATTTGTATACCGGGGCTGCCAGTCAGAAAGATTGTATGGAAGCTACGTGTTTGGAGATCGTAAT
GGGAATTTCTAACTCTCCAGCAAAGTCTGTGACAAAGCAGTGGCAAGAAAAACCACTCTGTCTCGGCACTAGT
GGGTCCTGTAGAGGCTACTTTTCCGGTCACATCTTGGGATTTGGAGAAGATGAAC TAGGTGAAGTTTACATTTTA
TCAAGCAGTAAAGTATGACCCAGACTCACAATGGAAAACCTACAAAATTGTAGATCCCAAAAGACCTTTAATG
CCTGAGGAATGCAGAGCCACGGTACAACCTGCACAGACACTGACTTCAGAGTGCTCCAGGCTCTGTGAAACGGC
TACTGCACCCCCACGGGAAAGTGCTGCTGCAGTCCAGGCTGGGAGGGGACTTCTGCAGAACTGCAAAATGTGAG
CCAGCATGTCTGTCATGGAGGTGTCTGTGTTAGACCGAACAAGTGCCCTCTGTAAAAAAGGATATCTTGGTCTCAA
TGTGAACAAGTGACAGAAACATCCGCAGAGTGACCAGGGCAGGTATTCTTGATCAGATCATTTGACATGACATCT
TACTTGCTGGATCTAACAAGTTACATTGTATAGTTTCTGGGACTGTTTGAATATTCTATTCCAATGGGCATTTAT
TTTTTATCTGTCTATTAAAAAAGACTGTTATCCTGCTACACACTCCTGTGATTTTATTCTCTTTATTAA
TTTAAAAATAATTTCCAGAAATGTGCAGATCCTCTGTGTGTATGTGAGCATGTTTGTTCACATATGCACATACAC
ATACTCATAACCCCTATATGCGTTGTTGCATAACAGATGATTTTTTAAATATATACTTCCCTTATGCAAAGTAAT
TTACACAGAAATTCATTGTAAATTGATAATGGATTTTTTATGTTACTAGAAGAGATTATTTGACTTCCAGGAA
TTTTCTGTCTGTAATCACTAAAGTCAACTTTAATAGAGTTTTGAAACAGTACTGTGCAATCCGATGGATCTAATT
AAAAAAAGGCAATATTTTTATATTAAAGTACTATACTAGGAGAGAATGTTTCAGAACTCCCTGATGAATTTCTA
AGTGAGCAACTTGATATAAAATTTGTAATCTTCATTTTTGTGAGTGATCCAGTTACAGAATGCTACACACTTACC
TTTTTATTGGCTGAGAAATCTGGTTATTTTATCTTAATCTCAAGATTGTTTTCAAGTGTTTTATAATTAAATCAT
AATAGCATATTTTAAATCAAAAA

FIGURE 574

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139592
><subunit 1 of 1, 882 aa, 1 stop
><MW: 98428, pI: 8.89, NX(S/T): 5
MKHVTVGRNMRCVRSRQRRPQHHLEPSAGPASACAAA VAVSVPATVPPKQLPLHG
QVNICGCPLLFLLFQLLLLLPLPSRSRKPPTQLTLAQLQTVSSAQLYLAPRAPLRHWTH
RRVFYFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCALVPLLGSVPPHPPAPSPCCSG
QTMLKMLSFKLLLLLAVALGFFEGDAKFGERNEGSGARRRRCLNGNPPKRLKRRDRMMSQ
LELLSGGEMLCGGFYPRLSCLLRSDSPGLGRLENKIFSVTNNTTECGKLLLEEIKCALCSPH
SQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCTRGHIPGFLQTTADEFCFYARKDGGL
CFPDFPRKQVRGPASNYLDQMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDG
SQRLFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLLSLAFHPNYKKNGK
LYVSYTTNQRWAIGPHDHILRVVEYTVSRKNPHQVDLRTARVFLEVAELHRKHLGGQLL
FGPDGFLYIILGDGMITLDDMEEMDGLSDFTGSVLRDLVDVTDMCNVPYSIPRSNPHFNST
NQPPFVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRSSARILQIIKGKDYESEF
SLLEFKPFSNGPLVGGFVYRGCQSERLYGSYVFGDRNGNFLTLOQSPVTKQWQEKPLCLG
TSGSCRGYFSGHILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEECRATV
QPAQTLTSECSRLCRNGYCTPTGKCCSPGWEGDFCRTAKCEPACRHGGVCVRPNKCLCK
KGYLGPQCEQVDRNIRRVTRAGILDQIIDMTSYLLDLTSYIV
```

Important features of the protein:

Transmembrane domains:

Amino acids 63-80;186-201

N-glycosylation sites:

Amino acids 152-156;281-285;598-602;629-633;641-645

Glycosaminoglycan attachment site:

Amino acids 417-421

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 856-860

N-myristoylation sites:

Amino acids 12-18;413-419;457-463;698-695;720-726;723-729

EGF-like domain cysteine pattern signatures:

Amino acids 805-817;837-849

FIGURE 575

CGGCTCGAGAGCGGGGCAAACCTGCTTGGCACCTCTTCAATAGGTGACATTCAATGATAGATCT
 CTGGCTTCTGCTCTGTTTGTCTGGTTGCCCTGGAAAGCCTGCTGCTCAGCCCATGCCCCGG
 GACTTCTCCACCCTCACCAGGACATTCTTTCCATCTCTTGTCTCCTGTGTGCAAGTCCCTTT
 CTCCTGGATTCCATGTCTTGAATGTTTCTTAATTTACTTCCTCATTTTGGCAGAGGATGTCCT
 CCAGTTGTTTTCTGGGAATGCTAATATGCAAGTGAACCAGTGAACCTGCAGTTCTGCCACACA
 GGGTTAATAACCAATCAGATTCTCTCTTTTCAAGATGGTTAACATAACAGACACCAAGAAAGG
 GAAGAGGAGCCGACAGCAGAGGGGAAGCTGAAAAGACGCACAAAGAATGGCCATAAAAGATA
 TGAGCAACCCAGCTTTCCAGACAGTCACTTTTCCAGTGGTCATACCTGGTCTGGAAGATTCC
 CCCATCATCTCGAATAAAGCTGTTGTTGCTTTTAACTCCATGGAGAGACCGAATGGAGTGAGC
 CCAGCAGGGCATGCTGGGCAAGAGAGGTCCCCGAGTCCCAAATAAGAATTTCAACTAGTATA
 AAACGAGGCAGCGAACCACACGTGGAAGTCTGATAACCGCTTGCAGAAGGGAATTGAATAGAT
 GTCTCCCTATTGGTAAGGATGTGGTTTTATTGACTTGAAATAACAAAGCCCGCAAGCAACAAC
 TGATCATCCGCGGGATGCTGCCACAAGGAATAATTGAGCACTCATTTCAGACACAGGGGAAACC
 ACTGCCTCTTTAGTCTTTCTCCAGATTCCAACAGTCACTGTTACAGCATTTACCTTGTTT
 ACCTCCCTGAGAAGACGTTGCAGCTCACTCACCCAGTGGGCACTGGGAGCCTCTGCTCAGGT
 GGGAGACAGATGCCCCCACATGCACATCTGGTGTATTGAAGCAGATACTGGGGCTTCATAA
 ACACAGAAGGGGCAGGGAAGTAGCCCCAGGGCATAGTGTGGGGCCTCTGACTAAAAGTAGCTT
 GCAAACCCCTGCCTATAACAGCCACTTCTGGCAGTCATTGTGCCACTTAGGAGCCCTCCTCA
 CCGCTCTTCTTTAGTTCCTTCACTCTGTATAGACCCTGCCAGAGCAGCTCAGGGTGGAGCAG
 CTGCAGCATGGGACCTGCTCCAGGCAAGGCCCTATGCTACACAGTCCCTGGGGGTGAGGATT
 CCAGAGGAGTCAATTCCCTACCCGCCCTTCCAGGGGATGGCCGAGATGAGCGTTCCACAGGG
 AAAGTGAAAGTTGCAAGGCTGTTGCGGAAACACCAGGGGTTCCATTTAGGTCTTGCTGCTCAT
 CTCACAGAAAGCCAGTCACTGAGACAAGTATTGTGAGGGAAGAAGGCTTTATCCAGGTGCTAC
 AGACAGGGTGAACAAGAGATCAGTCTCAAATCCATCATCATCACTGACTAAAATTAGGGGTT
 TATATAGCAGGGAAGAAATGTAACTACATGTGGGAAAACAGGGATTAAACGAGGGGCAAGGAAG
 AGGAGTTGGCCAACAGGCAGCAGGTGGTCACCTGGGGAATCATGATGGGTGAGGGGTCTGGCT
 TCTCACTTTCCAGATGTGGGGATCTGGTAAATTTAGTTCCTTGATAACCGTCTGGGAGGATTG
 CTGGCTGGTTTCTGAGAAAGGAATTCAGATGACATAAATGTAAATTTCTCCTTGGGTTTCAA
 GACTGAGAGGGTCAATTTCTAGGTTTATTCAAGAAAAACCATAAACATCAGTTCTATGGGACA
 ATTGGGCCCATTTCAGGCTCTGAGGATAAGGGTTAATGAGGGGACAGAGTCGCCTGGAGAAG
 TTCCTGGGGCTTACAAGAACTAGAGAGGCTTCCTGGCAAAGCTCTATGCTGTCTATCCTCT
 CTTCTCTCCTTGACAGGAAGATTCCAGTATAATAGACCCGAGGTGAAAAGGCTTTTGTTCATA
 AGTAGAAAACCTGAAGGGGGGTGGGAGGCACATGGATTGTAACCAGAGACCGCTTGGCCTGCAG
 GCAAATGCTGTACCTTCAGTTGCACCCCTCACTTGTTACAGCTGTTTCTGATAAGCACTTGTTG
 CAGCCCCATCAGCACCTCGATTTCTTCTTGGTGAGTCCATGGGAACAGCCCCACTGCAACAA
 CCCATTCTGCTCTCCTCTTCTCTTAAACCTCAACCTCCTCCTACCTGGCAGTCCACAGGCC
 TACAGCTTCTCCTCAGTGGGAAAGACATCAGCTTGGAAAACCACTTGGAAGCCAACGTTATC
 CTAGAAAAGCTTTTAAATGACCCAGCAGGACAAGTCTCCGGATGGCCTTGGCCAACCCGGTG
 CTTCCCTCTTTTCTTGGTTGTAGTTCTCAGAATAACTAGAGAATGTACTGGGAGTGTGTCTCT
 GAGATAAGGAGGAACCTGTCTAAACCTGGACTCTGTTCCCATCACACCTAGAACAGGATGTCC
 TGCAACGCTTTAGCCCAATGATCCAAGTTGCCCTGGGGTATAAACTTGACAGCAGAGGGCG
 TTCAGGGTCCCTCAGCTGCAGTGTGAAGTGGGACACACAGGTGAGACTCCATCTGCCCTGGGC
 AGGTTCTTGAGCCTTGGGGGACCAGTTCACCTACATCCAGGCTTCTGTTGTCCCTTGCTG
 CCTGTAAGGAATAAAGTTGCTTTGCTTA

FIGURE 576

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139608
><subunit 1 of 1, 80 aa, 1 stop
><MW: 8927, pI: 3.77, NX(S/T): 0
MIDLWLPA LFVLVALESLLLSPCPGTSSTLTRTFFPSLVSCVQVPFSWIPCLECFLIYFL
ILAEDVLQLFSGNANMQVNQ
```

Important features of the protein:

Signal peptide:

Amino acids 1-29

Transmembrane domain:

Amino acids 47-62

N-myristoylation sites:

Amino acids 25-31

FIGURE 577

ATCGGTTAGCGCCTTGCCATGATTAATCCAGAGCTGCGGGATGGCAGAGCTGATGGCTTCATA
CATCGGATAGTTCCCAAGTTGATACAAAAGTGGGAAGATTGGCCTTATGTGCTTCCTGAGTATT
ATTATTACTACAGTTTGCATTATTATGATAGCCACATGGTCCAAGCATGCTAAACCTGTGGCA
TGTTCAGGGGACTGGCTTGGAGTGAGAGATAAGTGTTTCTATTTTTCTGATGATACCAGAAAT
TGGACAGCCAGTAAAATATTTTGTAGTTTGCAGAAAGCAGAACTTGCTCAGATTGATACACAA
GAAGACATGGAATTTTTGAAGAGGTACGCAGGAAGTATGCACTGGATTGGACTAAGCAGG
AAACAAGGAGATTCTTGGAATGGACAAATGGCACCACATTCAATGGTTGGCCATCAAACCTCC
AAATGGTCTTGCAACTGGAGCCTCCGACAATGGCTTCTTCTGCTGGGACCCCTTAGATAGGCC
TCTGAGGGAGCTCTGACTGCCGTTTCCCCAAAACAATGTCCCCTGTCAGCAGGAAGCAGTTAA
ATCAGTCTTCATCCTTATCCTTAATATAACGGCAGTTAGATGTACTTCTTTAGAGGGAGTAAA
TTTATCAATTCAGAGCAATTCATCCTCCTCTTTCCATCTTTGATTACAGTTAATAGGCTATA
AATTTTGATAATGTAGAATAAACTACAGAAAACCTTCTTG

FIGURE 578

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143292
><subunit 1 of 1, 160 aa, 1 stop
><MW: 18576, pI: 9.29, NX(S/T): 3
MINPELRDGRADGFIHRIVPKLIQNWKIGLMCFLSIIITTVCIIMIATWSKHAKPVACSG
DWLGVRDKCFYFSDDTRNWTASKIFCSLQKAELAQIDTQEDMEFLKRYAGTDMHWIGLSR
KQGDSWKWTNGTTFNGWPSNSKWSCNWSLRQWLLLLGPLR
```

Important features of the protein:

Signal peptide:

Amino acids 1-42

N-glycosylation sites:

Amino acids 78-82;130-134;146-150

N-myristoylation site:

Amino acids 131-137

FIGURE 579

TGAAGGCCTGTGAGTGAGGAATGCCTCTCACCAGCTGTGCCTGAGCTGCAGCACTCCAGCCAC
TGCTGTCTCCTTAGCTGCTCACATAATGGACTTTTACAGTTCAGGATTCCACTGCAATGAGC
TGGTGGAGGAATAATTTCTGGATCATCTTAGCTGTGGCCATCATTGTTGTCTCTGTGGGCCTG
GGCCTCATCCTGTACTGTGTCTGTAAGTGGCAGCTTAGACGAGGCAAGAAATGGGAAATTGCC
AAGCCCCTGAAACACAAGCAAGTAGATGAAGAAAAGATGTATGAGAATGTTCTTAATGAGTCG
CCAGTTCAATTACCGCCTCTGCCACCGAGGAATTGGCCTTCTCTAGAAGACTCTTCCCCACAG
GAAGCCCCAAGTCAGCCGCCCGCTACATACTCACTGGTAAATAAAGTTAAAAATAAGAAGACT
GTTTCCATCCCAAGCTACATTGAGCCTGAAGATGACTATGACGATGTTGAAATCCCTGCAAAT
ACTGAAAAAGCATCATTTTTGAAACAGCCATTTCTTCTTTTTTGGCAAAACTGAAGAGGGTTTAC
ACAACTTATTTTAAAACAATCAAGAATGGTTGAACTTCAGTAGGTCTCTGGGCCCTGAAAGCC
AGTGGTGATTTTATGAAGCTCTATAAGATAAAGCACTTCCCAAACCTTAGATGAAGACACCCC
TGCGATCGGATGACTGCAGCCAGAGGAGACACATGGGTGCTCGGCTCTGAGGACTTAGAGGGG
TCAGCCTTGTGCTGTTGAGGAAACTTTCCATGGGAAGGACCACGGGGCTCCATGGCTCCCACC
TGTGGGAAACTACTCATTTCTTGGCATTCTTTCCCCCTTCATTCCCTTTGGTTTGCATGGTTC
TGAGTGATATTAAATCTCAGCATTGTTGGTTGTGCAAAAAAAAAA

FIGURE 580

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144844
><subunit 1 of 1, 145 aa, 1 stop
><MW: 16618, pI: 5.26, NX(S/T): 1
MDTFTVQDSTAMSWWRNFWIILAVAIIVSVGLGLILYCVCKWQLRRGKKWEIAKPLKH
KQVDEEKMYENVLNESPVQLPPLPPRNWPSLEDSSPQEAPSQPPATYSLVNKVKNKKTVS
IPSYIEPEDDYDDVEIPANTEKASF
```

Important features of the protein:

Signal peptide:

Amino acids 1-35

Tyrosine kinase phosphorylation site:

Amino acids 61-70

Amidation site:

Amino acids 48-52

FIGURE 581

GGCCGCCTCCGCGGGGCTGTGGGAAGCTTGGGCTGTCCCAGGACCGTCAGTCTCCTCCTCTGA
CCCTCCCTTTTCCCCTTGTGTGTAGGGCCGCGTCCCACCCCCACCTCGCCGGAGTCCGGGGCG
GCCCCGGTGTCCCCTCCGAGCCTGCTGCACTCCACGTCCCCCTACCAGGGCTCCAGCCCCCAG
GGAAATCTCCGACCAGGCCCGCCAGGAGCCAGATCCAGGCTCCTGGAAGAACCATGTCCGGC
AGCTACTGGTCATGCCAGGCACACACTGCTGCCCAAGAGGAGCTGCTGTTTGAATTATCTGTG
AATGTTGGGAAGAGGAATGCCAGAGCTGCCGGCTGAAAATTACCCAACCAAGAGAAATCTGCAGG
ATGGACTTTCTGGTCCTCTTCTTGTTCTACCTGGCTTCGGTGCTGATGGGTCTTGTTCTTATC
TGCCTCTGCTCGAAAACCCATAGCTTGAAAGGCCTGGCCAGGGGAGGAGCACAGATATTTTCC
TGTATAATTCCAGAATGTCTTCAGAGAGCCGTGCATGGATTGCTTCATTACCTTTTCCATACG
AGAAACCACACCTTCATTGTCTGACCTGGTCTTGCAAGGGATGGTTTATACTGAGTACACC
TGGGAAGTATTTGGCTACTGTGAGGAGCTGGAGTTGTCTTGCAATTACCTTCTTCTGCCCTAT
CTGCTGCTAGGTGTAAACCTGTTTTTTTTTACCCTGACTTGTGGAACCAATCCTGGCATTATA
ACAAAAGCAAATGAATTATTATTTCTTCATGTTTATGAATTTGATGAAGTGATGTTTCCAAAG
AACGTGAGGTGCTCTACTTGTGATTTAAGGAAACCAGCTCGATCCAAGCACTGCAGTGTGTGT
AACTGGTGTGTGCACCGTTTCGACCATCACTGTGTTTGGGTGAACAACTGCATCGGGGCCTGG
AACATCAGGTACTTCCTCATCTACGTCTTGACCTTGACGGCCTCGGCTGCCACCGTCGCCATT
GTGAGCACCACTTTTCTGGTCCACTTGGTGGTGATGTCAGATTTATAACCAGGAGACTTACATC
GATGACCTTGGACACCTCCATGTTATGGACACGGTCTTTCTTATTTCAGTACCTGTTCTGACT
TTTCCACGGATTGTCTTCATGCTGGGCTTTGTGCTGGTTCTGAGCTTCCTCCTGGGTGGCTAC
CTGTTGTTTGTCTGTATCTGGCGGCCACCAACCAGACTACTAACGAGTGGTACAGAGGTGAC
TGGGCCTGGTGCCAGCGTTGTCCCCTTGTGGCCTGGCCTCCGTCAGCAGAGCCCCAAGTCCAC
CGGAACATTCACCTCCCATGGGCTTCGGAGCAACCTTCAAGAGATCTTTCTACCTGCCTTTCCA
TGTCATGAGAGGAAGAAACAAGAATGACAAGTGTATGACTGCCTTTG

FIGURE 582

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144857
><subunit 1 of 1, 344 aa, 1 stop
><MW: 39787, pI: 7.44, NX(S/T): 2
MDFLVLFYFLASVLMGLVLICVCSKTHSLKGLARGGAQIFSCIPECLQRAVHGLLHYL
FHTRNHTFIVLHLVLQGMVYTEYTWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTLCG
TNPGIITKANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHCV
WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVVMSDLYQETYIDDLGHLHVM
DTVFLIQYLFLTFPRIVFMLGFVVVLSFLLGGYLLFVLYLAATNQTNEWYRGDWAQCQR
CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
```

Important features of the protein:

Signal peptide:

Amino acids 1-29

Transmembrane domains:

Amino acids 100-116;201-217;256-275

N-glycosylation sites:

Amino acids 65-69;284-290

N-myristoylation sites:

Amino acids 32-38;77-83;120-126;322-328

Cell attachment sequence:

Amino acids 292-298

DHHC zinc finger domain:

Amino acids 140-204

FIGURE 583

CCGCGGAAGTGGCAGGCGTTTCAGAGCGTCAGAGGCTGCGGATGAGCAGACTTGGAGGACTCCAGGCCAGAGACT
 AGGCTGGGCGAAGAGTCGAGCGTGAAGGGGGCTCCGGGCCAGGGTGACAGGAGGCGTGCTTGAGAGGAAGAAGTT
 GACGGGAAGGCCAGTGCGACGGCAAATCTCGTGAACCTTGGGGGACGAATGCTCAGGATGCGGGTCCCCGCCCTC
 CTCGTCTCTCTTCTGCTTCAGAGGGAGAGCAGGCCCGTCGCCCCATTTCTGCAACAGCCAGAGGACCTGGTG
 GTGCTGCTGGGGAGGAAGCCCGCTGCCGTGTGCTCTGGGCGCTACTGGGGGCTAGTTCACTGGACTAAGAGTGGG
 CTGGCCCTAGGGGGCCAAAGGGACCTACCAGGGTGGTCCCGTACTGGATATCAGGGAATGCAGCCAATGGCCAG
 CATGACCTCCACATTAGGCCCCGTGGAGCTAGAGGATGAAGCATCATATGAATGTCAGGCTACACAAGCAGGCCTC
 CGCTCCAGACCAGCCCAACTGCACGTGCTGGTCCCCCAGAAGCCCCCAGGTGCTGGGCGGCCCCCTCTGTGTCT
 TTGGTTGCTGGAGTTCTTGCAGAACCTGACATGTGCGAGCCGTGGGGATGCCCGCCCTACCCCTGAATTGCTGTGG
 TTCCGAGATGGGGTCCCTGTTGGATGGAGCCACCTTTTCATCAGACCCCTGCTGAAGGAAGGGACCCCTGGGTCACTG
 GAGAGCACCTTAACCTGACCCCTTTCAGCCATGATGATGGAGCCACCTTTGTCTGCCGGGCCGGAGCCAGGCC
 CTGCCACAGGAAGAGACACAGCTATCACACTGAGCCTGCAGTACCCCCAGAGGTGACTCTGTCTGCTTCGCCA
 CACACTGTGACAGGAGGGAGAGAAGGTCAATTTCTGTGTCAGGCCACAGCCAGCCTCCTGTACAGGCTACAGG
 TGGGCAAAAGGGGGCTCTCCGGTGTCTGGGGCCCCGCGGCCAAAGGTTAGAGGTCTGTGGCAGACGCCCTCGTTCTG
 ACTGAGCCCGTGTCTTCCGAGGTGAGCAACGCCGTGGGTAGCGCCAACCGCAGTACTGCGCTGGATGTGCTGTTT
 GGGCCGATTCTGACAGGCAAGCCGAGCCCGTGTCCGTGGACGTGGGGGAAGACGCTTCCTTCAGCTGCGCCTGG
 CGCGGGAACCCGCTTCCACGGGTAACTTGGACCCGCGCGGTGGCGCGCAGGTGCTGGGCTCTGGAGCCACACTG
 CGTCTTCCGTCCGTGGGGCCCCGAGGACGACGGCGACTATGTGTGACAGCTGAGGCTGGGCTATCGGGCTGCGG
 GCGGGCGCCGCGGAGGCTCGGCTGACTGTGAACGCTCCCCAGTAGTGACCGCCCTGCACTCTGCGCCTGCCTTC
 CTGAGGGGGCCCTGCTCGCTCCAGTGTCTGGTTTTCGCTCTCCCCGCCCCAGATGCCGTGGTCTGGTCTTGGGAT
 GAGGGCTTCTTGGAGGCGGGTTCGACGGGCCGGTCTTCTGGTGGAGACATTCCCTGCCCCAGAGAGCCGCGGGGA
 CTGGGTCCGGGCTGATCTCTGTGCTACACATTTCCGGGACCCAGGAGTCTGACTTTAGCAGGAGCTTTAACTGC
 AGTGCCCGGAACCGCTGGGCGAGGGAGGTGCCAGGCCAGCCTGGGCCGTAGAGACTTGCTGCCCACTGTGCGG
 ATAGTGGCCGGAGTGGCCGCTGCCACCACAACCTCTCCTTATGGTCATCACTGGGGTGGCCCTCTGCTGTGGCGC
 CACAGCAAGGCCCTCAGCCTCTTTCTCCGAGCAAAAGAACCTGATGCGAATCCCTGGCAGCAGCGACGGCTCCAGT
 TCACGAGGTCTGAAGAAGAGGAGACAGGCAGCCGCGAGGACCGGGCCCCATTGTGCACACTGACCACAGTGAT
 CTGGTTCTGGAGGAGGAAGGACTCTGGAGACCAAGGACCAACCAACGGTTACTACAAGTCCGAGGAGTCAGT
 GTGAGCCTGAGCCTTGGCGAAGCCCCCTGGAGGAGTCTCTTCTGCCACCACCCTCCCCCTTGGGCCCCCAGGG
 ACCCTACCTTCTATGACTTCAACCCACACCTGGGCATGGTCCCCCCTGCAGACTTTACAGAGCCAGGGCAGGC
 TATCTCACCACACCCACCCCTCGAGCTTTCACCAGCTACATCAAACCCACATCCTTTGGGCCCCCAGATCTGGCC
 CCGGGGACTCCCCCTTCCCATATGCTGCCTTCCCCACACCTAGCCACCCGCGTCTCCAGACTCACGTGTGACAT
 CTTTCCAATGGAAGAGTCTGGGATCTCCAATTGCCATAATGGATTGTTCTGATTCTTGAGGAGCCAGGACAAG
 TTGGCGACCTTACTCTCCAAACTGAACACAAGGGGAGGGAAGATCATTACATTTGTCAGGAGCATTGTGTATA
 CAGTCAGCTCAGCCAAAGGAGATGCCCAAGTGGGAGCAACATGGCCACCCAATATGCCACCTATTCCCCGGTG
 TAAAAGAGATTCAAGATGGCAGGTAGGCCCTTTGAGGAGAGATGGGGACAGGGCAGTGGGTGTTGGGAGTTTGGG
 GCCGGGATGGAAGTTGTTTCTAGCCACTGAAAGAAGATATTTCAAGATGACCATCTGCATTGAGAGGAAAGGTAG
 CATAGGATAGATGAAGATGAAGAGCATAACAGGCCCCACCTGGCTCTCCCTGAGGGGAACCTTGTCTCGGCCAAT
 GGAAATGCAGCCAAGATGGCCATATACTCCCTAGGAACCCAAATGGCCACCATCTTGATTTTACTTTCTTAAA
 GACTCAGAAAGACTTGGACCCAAGGAGTGGGGATACAGTGAGAATTACCACTGTTGGGGCAAAATATTGGGATAA
 AAATATTTATGTTTAAATAAAAAAAGTCAAAGAGAAAAAAA

FIGURE 584

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145841
><subunit 1 of 1, 708 aa, 1 stop
><MW: 75093, pI: 6.65, NX(S/T): 3
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LALGGQRDLPGWSRYWISGNAANGQHDHLHIRPVELEDEASYECQATQAGLRSRPAQLHVL
VPPEAPQVLGGPSVSLVAGVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEG
TPGSVESTLTTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVTLSASPHTVQE
GEKVIIFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVADASFLETPVSCEVSNVAVGSA
NRSTALDVLFGPILQAKPEPVSVDVGEDASFSCAWRGNPLPRVTWTRRGAQVLGSGATL
RLPSVGPEDAGDYVCRAEAGLSGLRGGAEARLTVNAPPVVTALHSAPAFRLRGPRLQCL
VFASAPADAVVWSWDEGFLEAGSQGRFLVETFPAPESRGGLGGLISVLHISGTQESDFS
RSFNCSARNRLGEGGAQASLGRDLLPTVRIVAGVAAATTTLLMVITGVALCCWRHSKAS
ASFSEQKNLMRIPGSSDGSSSRGPEEEETGSREDRGPIVHTDHSDLVLEEEGTLETKDPT
NGYYKVRGVSVSLSLGEAPGGGLFLPPPSPLGPPGTPTFYDFNPHLGMVPPCRLYRARG
YLTPHPRAFTSYIKPTSFGPPDLAPGTPPFPPYAAFPPTPSHPRLQTHV
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

Transmembrane domain:

Amino acids 511-531

N-glycosylation sites:

Amino acids 143-147;301-305;484-488

N-myristoylation sites:

Amino acids 48-54;60-66;79-85;139-145;180-186;183-189;355-361;383-389;
387-393;460-466;473-479;494-500;495-501;514-520;528-534;
554-560;592-598;608-614

Amidation site:

Amino acids 500-504

Cell attachment sequence:

Amino acids 149-152

Multicopper oxidases signature 1:

Amino acids 445-466

Immunoglobulin domain:

Amino acids 326-377

FIGURE 585

GCGCGCTGAGGAAGCCGTGTGCCTGGGATGCCAAGAGCCAGAGAATGGATCTTCTCCGAGTG
 GGGACATTGCTGACAATCCCGGCTTCCCGAGGCGGCTAAGAACAGGCAGTTTGTGTGCGGCTGG
 CTGCAGATACCCAGAGGCACAAAGAGACCGAAGCCACCCGGAGGGACCCACGGACGGACAGAT
 GGTAGGCGCGAACCCGAGAGGACCGGCGGAGGCTGAGCACCGAGAGCCGCCAAGGAAGAGAAA
 CTAACCACAGCCAAGTTACCCCGCCGGCTTTCCTTCGCTGCGCTAAGGA**ATG**AAACCCTTCCA
 GCTCGATCTGCTCTTCGTCTGCTTCTTCCTCTTCAGTCAAGAGCTGGGCCTCCAGAAGAGAGG
 ATGCTGTCTGGTGCTGGGCTACATGGCCAAGGACAAGTTTCGGAGAATGAATGAAGGCCAAGT
 CTATTCTTCAGCCAGCAGCCCCAGGACCAGGTGGTGGTGTGCGGGACAGCCAGTGACGCTACT
 TTGCGCCATCCCCGAATACGATGGCTTCGTTCTGTGGATCAAGGACGGCTTGGCTCTGGGTGT
 GGGCAGGGACCTCTCAAGTTACCCACAGTACCTGGTGGTAGGGAACCACCTGTCAGGGGAGCA
 CCACCTGAAGATCCTGAGGGCAGAGCTGCAAGACGATGCGGTGTACGAGTGCCAGGCCATCCA
 GGCCGCCATCCGCTCCCGCCCCGCACGCCTCACAGTCCTGGTGCCGCTGATGACCCCGTCAT
 CCTGGGGGGCCCTGTGATCAGCCTGCGTGCAGGGGACCTCTCAACCTCACCTGCCACGCAGA
 CAATGCCAAGCCTGCAGCCTCCATCATCTGGTTGCGAAAGGGAGAGGTCATCAATGGGGCCAC
 CTACTCCAAGACCCTGCTTCGGGACGGCAAGCGGGAGAGCATCGTCAGCACCCCTCTTCATCTC
 CCCTGGTGACGTGGAGAATGGCCAGAGCATCGTGTGTGCTGCCACCAACAAAGCCATCCCCGG
 AGGAAAGGAGACGTCGGTCACCATTGACATCCAGCACCCCTCCACTGGTCAACCTCTCGGTGGA
 GCCACAGCCAGTGCTGGAGGACAACGTCGTCACTTTCCACTGCTCTGCAAAGGCCAACCCAGC
 TGTACCCAGTACAGGTGGGCCAAGCGGGGCCAGATCATCAAGGAGGCATCTGGAGAGGTGTA
 CAGGACCACAGTGGACTACACGTACTTCTCAGAGCCCGTCTCCTGTGAGGTGACCAACGCCCTG
 GGCAGCACCAACCTCAGCCGCACGGTTGACGTCTACTTTGGGCCCCGGATGACCACAGAACCC
 CAATCCTTGCTCGTGGATCTGGGCTCTGATGCCATCTTCAGCTGCGCCTGGACCGGCAACCCA
 TCCCTGACCATCGTCTGGATGAAGCGGGCTCCGGAGTGGTCTTGAGCAATGAGAAGACCCTG
 ACCCTCAAATCCGTGCGCCAGGAGGACGCGGGCAAGTACGTGTGCCGGGCTGTGGTGGCCCCGT
 GTGGGAGCCGGGGAGAGAGAGGTGACCCCTGACCGTCAATGGACCCCCCATCATCTCCAGCACCC
 CAGACCCAGCACGCCCTCCACGGCGAGAAGGGCCAGATCAAGTGCTTCATCCGGAGCACGCCG
 CCGCCGGACCGCATCGCCTGGTCTGGAAGGAGAACGTTCTGGAGTCCGGGCACATCGGGGCGC
 TATACGGTGGAGACCATCAGCACCGAGGAGGGCGTCATCTCCACCCTGACCATCAGCAACATC
 GTGCGGGCCGACTTCCAGACCATCTACAACCTGCACGGCCTGGAACAGCTTCGGCTCCGACACT
 GAGATCATCCGGCTCAAGGAGCAAGGTTTCGGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGAG
 TCTGTGCCGATGGCCGTCATCATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCTCTGCTCCTT
 ATGGCAACCATCGTGGCGTTCTGCTGTGCCCGTTCCAGAGAAGTACGGGAGGGAGATCCGGG
 ATCTCAGGGAGGGGGACAGAGAAAAAGGCCAGGCTTAGGCTGCCCCGGAGAGCAAGTAAGCAG
 GAGTGCAATGAACAGGGGTCC**TAA**CAGTGCTGTGAGCTCCTGGGGCAGGGAGTGGGTCTGATG
 CATCGGTGTATGTGAGCCTGGGCAACATGGCGCCTGGCAGAGTGGGCGCTAGGCTGAGGTTGA
 CCTGGACTAGACTGAACTTCATCTGCAGGGCAGCCAGCATTTTGGATTGAACACATAGCTCTT
 TCAGTCAGGAACTGTACAGAAAGATAGGGGGAAAAGCGGTTTGTGGTTTGATCCTTGCTCTAC
 AAGAGCTGTTAGTCTAGAGAGACCCATCTCTACAACAAAATAAAAATAAAGAGCTGCTAGTC
 TCACCAGAAAAGCAGGTCACTCACACAGCTGTGGGGGAGTGGGTGGGGAAGCAATAAAGGAAT
 TGCTTTGAGAAAACCTTAA

FIGURE 586

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA148004
><subunit 1 of 1, 600 aa, 1 stop
><MW: 65308, pI: 8.35, NX(S/T): 5
MKPFQLDLLFVCFFLFSQELGLQKRGCCLVGYMAKDKFRRMNEGQVYSFSQQPQDQVVV
SGQPVTLLCAIPEYDGFVLWIKDGLALGVGRDLSSYPQYLVVGNHLSGEHHLKILRAELQ
DDAVYECQAIQAAIRSRPARLTVLVPPDDPVILGGPVISLRAGDPLNLTCHADNAKPAAS
IIWLRKGEVINGATYSKTLRLDGKRESIVSTLFI SPGDVENGQSIVCRATNKAIPGGKET
SVTIDIQHPPVLNLSVEPQPVLLEDNVVTFHCSAKANPAVTQYRWAKRGQIIKEASGEVYR
TTVDYTYFSEPVSCVETNALGSTNLSRTVDVYFGPRMTTEPQSLLVDLGSDAIFSCAWTG
NPSLTIVWMKRGSGVVL SNEKTLTLKSVRQEDAGKYVCRAVVPRVGAGEREVTLTVNGPP
IISSTQTQHALHGEKGQIKCFIRSTPPPDRIAWSKENVLESGTSGRYTVETISTEEGVI
STLTISNIVRADFQTIYNCTAWNSFGSDTEIIRLKEQGSEMKSGAGLEAESVPMAVIIGV
AVGAGVAFLVLMATIVAFCCARSQRSTGGRSGISGRGTEKKARLRLPRRASKQECNEQGS
```

Important features of the protein:

Signal peptide:

Amino acids 1-17

Transmembrane domain:

Amino acids 534-555

N-glycosylation sites:

Amino acids 167-171;253-257;324-328;498-502

Glycosaminoglycan attachment sites:

Amino acids 523-527;574-578

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 204-208;370-374;588-592

Tyrosine kinase phosphorylation sites:

Amino acids 40-49;300-308;389-397

N-myristoylation sites:

Amino acids 45-51;62-68;84-90;103-109;192-198;236-242;
374-380;436-442;478-484;539-545;543-549;
568-574

Amidation site:

Amino acids 202-206

Leucine zipper pattern:

Amino acids 8-30

FIGURE 587

CAAAAAAGGAGCATGTCTTCATCCATGAGAGGCCTCGAAAAATCAATGGTATTTGCATTTCTC
CCAAGAAGGTTGCTTGCCAAAACCTTTCGGCCATTTTCTGCTTTCAGAGTGAGACAAAGTTCA
AAATGACAGTCTGTCTGAGCTCATTGAAGGCACTAGATACCCTGCCTGCAGGTACCACTATTCCC
CCACAGAGGGGTTTGTCTTGTCACTTGTGATGACTTGAGGCCAGATAGTTTCCTTGGCTATG
TTAAATAACTCAAGATCAGCTACCGAGTCTGAGATCTCTTCTCTCATGGCATTGGAGCTGGCT
GTGCCTGAGGCAGACCTGGACCGTGGACATGGGGCAATGCCTTGAGCGGAAGGGGAAGCCACT
GAATTTTGGGTGTCACCAGGTAAACAGAGCCCTCAGCATCTGAATAGAACTGAACAGGAACA
GAAGAGATTACACTACATCTGAGATGGAGACCTTTCCTCTGCTGCTGCTCAGCCTGGGCCTGG
TTCTTGACAGAAGCATCAGAAAGCACAAATGAAGATAATTAAAGAAGAATTTACAGACGAAGAGA
TGCAATATGACATGGCAAAAAGTGGCCAAGAAAAACAGACCATTGAGATATTAATGAACCCGA
TCCTGTTAGTTAAAAATACCAGCCTCAGCATGTCCAAGGATGATATGTCTTCCACATTACTGA
CATTCAGAAGTTTACATTATAATGACCCCAAGGGAAACAGTTCGGGTAAATGACAAAGAGTGTT
GCAATGACATGACAGTCTGGAGAAAAGTTTCAGAAGCAAACGGATCGTGCAAGTGGAGCAATA
ACTTCATCCGCAGCTCCACAGAAGTGATGCGCAGGGTCCACAGGGCCCCCAGCTGCAAGTTTGTA
CAGAATCCTGGCATAAGCTGCTGTGAGAGCCTAGAACTGGAAAATACAGTGTGCCAGTTCACT
ACAGGCAAACAATTCCCCAGGTGCCAATACCATAGTGTTACCTCATTAGAGAAGATATTGACA
GTGCTGACAGGTCAATCTCTGATGAGCTGGTTAGTTTGTGGCTCTAAGTTGTAATCCACAG
AGCTTTAGGACTAGGGTCTTACTAAAGAAGGACCTCTTCTTGTTCAATCTTGTTTAAACCTTT
CCTTAATATCTACTCTTTAGCACTATAGTGAACCTCTGATTATTTATTCTAACTGGAGGAGTG
AAAAATCCAAAATTGTGGATAATTCAATTAAAAGTTATGACTGATACCG

FIGURE 588

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149893
><subunit 1 of 1, 199 aa, 1 stop
><MW: 22427, pI: 6.46, NX(S/T): 3
METFPLLLLSLGLVLAEASESTMKIIKEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVK
NTSLSMKDDMSSTLLTFRSLHYNDPKGNSSGNDKECCNDMTVVRKVSEANGSCKWSNNF
IRSSTEVMRRVHRAPSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKI
LTVLTGHSLSWLVCGSKL
```

Important features of the protein:

Signal peptide:

Amino acids 1-16

N-glycosylation sites:

Amino acids 61-65;89-93;111-115

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 105-109

N-myristoylation sites:

Amino acids 12-18;88-94;144-150

Microbodies C-terminal targeting signal:

Amino acids 197-201

FIGURE 589

CAGTCCTGCCGGGACGGTGAGCGCATTTCAGCACCCCTGGACAGCACCGCGGTTGCGCTGCCTCC
AGGGCGGCCCCGGGCTGCTCCTGCTCCGCAGAGCTACGCCCCTCCCCCGGGTGCCCCGGACCC
TGCACTTGCCGCCGCTTTCTCTCGCGCTGCTCTGGACCTTGCTAGCCGGCTCTGCACCTCCCAG
AAGCCGTGGGCGCGCCGCTCAGCTGCTCCATCGCCTCACTTTCCCAGGCTCGCGCCCGAAGCA
GAGCCATGAGAACCCCAGGGTGCTGGCGAGCCGCTAGCGCCATGGGCCCCGGCGAGGCGCTG
CTGGCGGGTCTCCTGGTGATGGTACTGGCCGTGGCGCTGCTATCCAACGCACTGGTGCTGCTT
TGTTGCGCCTACAGCGCTGAGCTCCGCACTCGAGCCTCAGGCGTCCTCCTGGTGAATCTGTCT
CTGGGCCACCTGCTGCTGGCGGCGCTGGACATGCCCTTCACGCTGCTCGGTGTGATGCGCGGG
CGGACACCGTCGGCGCCCCGGCGCATGCCAAGTCATTGGCTTCCTGGACACCTTCCTGGCGTCC
AACGCGGCGCTGAGCGTGCGGGCGCTGAGCGCAGACCAGTGGCTGGCAGTGGGCTTCCCACTG
CGCTACGCCGGACGCCTGCGACCGCGCTATGCCGGCCTGCTGCTGGGCTGTGCCTGGGGACAG
TCGCTGGCCTTCTCAGGCGCTGCACTTGGCTGCTCGTGGCTTGGCTACAGCAGCGCCTTCGCG
TCCTGTTGCTGCGCCTGCCGCCCCGAGCCTGAGCGTCCGCGCTTCGCAGCCTTCACCGCCACG
CTCCATGCCGTGGGCTTCGTGCTGCCGCTGGCGGTGCTCTGCCTCACCTCGCTCCAGGTGCAC
CGGGTGGCAGCAGACACTGCCAGCGCATGGACACCGTCACCATGAAGGCGCTCGCGCTGCTC
GCCGACCTGCACCCCAGTGTGCGGCAGCGCTGCCTCATCCAGCAGAAGCGGCGCCGCCACCGC
GCCACCAGGAAGATTGGCATTGCTATTGCGACCTTCCTCATCTGCTTTGCCCCGTATGTCATG
ACCAGGCTGGCGGAGCTCGTGCCCTTCGTACCGTGAACGCCAGTGGGGCATCCTCAGCAAG
TGCCTGACCTACAGCAAGGCGTGGCCGACCCGTTACGTA CTCTGCTCCGCCGGCCGTTTC
CGCCAAGTCCTGGCCGGCATGGTGCACCGGTGCTGAAGAGAACCCCGCGCCAGCATCCACC
CATGACAGCTCTCTGGATGTGGCCGGCATGGTGCACCAGCTGCTGAAGAGAACCCCGCGCCCA
GCGTCCACCCACAACGGCTCTGTGGACACAGAGAATGATTCTGCCTGCAGCAGACACACTTGA
GGGCTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAGGGCACTGGCCCTG
CCACAGAGATGCCACTGGGGACCCCCAGACACCAGTGGCTTGACTTTGAGCTAAGGCTGAG

FIGURE 590

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149930
><subunit 1 of 1, 363 aa, 1 stop
><MW: 39332, pI: 10.42, NX(S/T): 3
MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLSLGHLLLAALDM
PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRLRP
RYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG
FVLPLAVLCLTSLQVHRVARRHCQRMDTVMTKALALLADLHPSVRQRCLIQKRRRHRAT
RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLRRP
FRQVLAGMVHRLKRTPRPASTHDSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
QTH
```

Important features of the protein:

Signal peptide:

Amino acids 1-24

Transmembrane domains:

Amino acids 46-60;85-103;130-150;175-192;246-264

N-glycosylation sites:

Amino acids 47-51;348-352;355-359

Tyrosine kinase phosphorylation site:

Amino acids 286-295

N-myristoylation sites:

Amino acids 66-72;124-130;128-134;132-138;139-145;244-250;
349-355

G-protein coupled receptor proteins:

Amino acids 72-112

7 transmembrane receptor (rhodopsin family):

Amino acids 22-294

FIGURE 591

AACATGGCTGCGGCGCCTGGGCTGCTCGTCTGGCTGCTCGTGCTCCGGCTGCCCTGGCGGGTG
 CCGGGCCAGCTGGACCCCAGCACTGGCCGGCGGTTCTCGGAGCACAACTCTGCGCGGACGAC
 GAATGCAGCATGATGTACCGCGGTGAGGCTCTTGAAGATTTACAGGCCCGGATTGTCGTTTT
 GTGAATTTTAAAAAAGGTGATCCTGTATATGTTTACTATAAACTGGCAAGAGGATGGCCTGAA
 GTTTGGGCTGGAAGTGTTGGACGCACTTTTGGATATTTTCCAAAAGATTTAATCCAGGTAGTT
 CATGAATATACCAAAGAAGAGCTACAAGTTCCAACAGATGAGACGGATTTTGTGTTTGTGAT
 GGAGGAAGAGATGATTTTCATAATTATAATGTAGAAGAACTTTTAGGGTTTTTGGAACTGTAC
 AATTCTGCAGCTACAGATTCTGAGAAAGCTGTAGAAAAAACTTTACAGGATATGGAAAAAAC
 CCTGAATTATCTAAGGAAAGGGAACCTGAACCTGAACCAGTAGAAGCCAACTCAGAGGAAAGT
 GATAGTGATTCTCAGAAAACTGAGGATCTTCAGGAACAGTTTACAACCTCAGAAGCACCAC
 TCCCATGCAAACAGCCAAGCAAATCATGCTCAGGGAGAGCAGGCTTCATTTGAATCTTTTGAA
 GAAATGCTGCAAGATAAACTAAAAGTGCCAGAAAGTGAAAACAACAAACCAGCAATAGTTCT
 CAGGTCTCAAATGAACAGGATAAGATTGATGCCTATAAACTTTTGAAAAAGAAATGACTCTA
 GACTTGAAAACCAAATTTGGCTCAACAGCTGATGCACTTGTATCTGATGATGAGACAACCAGA
 CTCGTTACTTCATTAGAAGATGATTTTGATGAGGAATTGGATACTGAGTATTATGCAGTTGGA
 AAGGAAGATGAGGAGAACCAAGAAGACTTTGATGAGTTGCCATTACTTACCTTTACAGATGGG
 GAAGATATGAAAACCTCAGCAAAGTCTGGCGTTGAGAAATATCCAACAGATAAAGAGCAGAAT
 TCAAATGAAGAGGACAAGGTTCACTAACTGTGCCCCCTGGCATCAAAAATGATGATAAAAT
 ATACTAACCAACCTGGGGGGACACTATCTTCTCTATTGTACAGGAGGTGAAGAAACAAGAGAT
 ACGATGGATTTAGAGAGCTCTAGTTCAGAGGAAGAAAAAGAAGATGATGATGATGCATTAGTC
 CCAGATAGCAAACAGGGGAAACCACAGTCAGCAACAGATTATAGTGACCCTGACAATGTAGAT
 GATGGTCTTTTTATTGTAGACATTCCTAAAACAAATAATGACAAAGAAGTAAACGCAGAACAT
 CACATTAAAGGAAAAGGGAGGGGAGTTCAGGAATCCAAGAGGGGCCTGGTACAAGATGAGACA
 GAATTAGAGGATGAAAATCAAGAAGGCTTTAAAACAGAGCCCATAAACTATGACCTCTGAGG
 TTTCATTGGAAAGAAAGTGTACTGTGCATTATCCATTACAGTAAAGGATTTCAATTGGCTTCAA
 AATCCAAAAGTTTATTTTAAAAGGTTTGTGTTAGAACTAAGCTGCCTTGGCAGTGTGCATTT
 TTGAGCCAAACAATTCAAAAATGTCATTTCTTCCCTAAATAAAAAATCACCTTTTAAGCTAGAG
 CGTCCTTACAACTTTGAAATGTGCAATAAAGAATACCTGTGTTTTAGCTAATGTAGCATATGT
 AATTGCAAAATGATTTAGAATGTCATGAAAAATATGAACATTTCTGTGGAAATGCTTTAAGA
 ACATGTATTTCCATTATCCTATTTTTAGTGTACACCAGCTGAATACGGAGCAATGGTGTATTAT
 AAGCGTTTTTTTAACTATCTGGTCACAAAGACTGTTACGCTAAAAATGTTTACTAAAAGATC
 ACTAACTATCTCCCTCTTGCTGAAGTTCCTTGTAGTAATAGCTCATAAAAAATTTGTTTATT
 AATATTTAAAAA

FIGURE 592

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150157
><subunit 1 of 1, 499 aa, 1 stop
><MW: 56471, pI: 4.31, NX(S/T): 2
MAAAPGLLVWLLVLRPLWRVPGQLDPSTGRRFSEHKLCADDECSMMYRGEALEDFTGPDC
RFVNFKKGDPVYVYYKLARGWPEVWAGSVGRFTGYFPKDLIQVVHEYTKHEELQVPTDETD
FVCFDGGRRDDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEP
VEANSEESDSVFSSENTEDLQEQFTTQKHSHANSQANHAQGEQASFESFEMLQDKLKVP
ESENKTSNSSQVSNEQDKIDAYKLLKKEMTLDLKTkFGSTADALVSDDETTRLVTSLED
DFDEELDTYYAVGKEDEENQEDFDELPLLTFTDGEDMKTPAKSGVEKYPTDKEQNSNEE
DKVQLTVPPGIKNDDKNILTTWGDITFSIVTGGEETRDMDLESSSSEEEKEDDDDALVP
DSKQKGKQSATDYSDDPNVDDGLFIVDIPKTNNDKEVNAAEHHIKKGGRGVQESKRGLVQD
ETELDENQEGFKTEPIKL
```

Important features of the protein:

Signal peptide:

Amino acids 1-22

N-glycosylation sites:

Amino acids 245-249;249-253

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 66-72

N-myristoylation sites:

Amino acids 392-398;469-475

Amidation site:

Amino acids 28-32

Aminoacyl-transfer RNA synthetases class-II signature 1:

Amino acids 47-70

FIGURE 593

GGGCCAGTAGAGTGTGTCTGGGTCTGAGTGACTACATCAAAGCTCCCAGCCTTGAAAAAC
ACATGCTGTTCCCAGGCCTCAAGATATTGAAACATTAATTAGATAATTTAAAGTAGCGTTTTTC
TTCTACAATGTCTGAAGAAGTGACCTACGCGACACTCACATTTTCAGGATTCTGCTGGAGCAAG
GAATAACCGAGATGGAAATAACCTAAGAAAAAGAGGGCATCCAGCTCCATCTCCCATTTGGCG
TCATGCTGCTCTGGGTCTGGTAACTCTTTGCCTGATGTTGCTGATTGGGCTGGTGACGTTGGG
GATGATGTTTTTGCAGATATCTAATGACATTAACTCAGATTCAGAGAAATTGAGTCAACTTCA
GAAAACCATCCAACAGCAGCAGGATAACTTATCCCAGCAACTGGGCAACTCCAACAACCTTGTC
CATGGAGGAGGAATTTCTCAAGTCACAGATCTCCAGTCTACTGAAGAGGCAGGAACAAATGGC
CATCAAACCTGTGCCAAGAGCTAATCATTCTACTTTCAGACCACAGATGTAATCCATGTCTTAA
GATGTGGCAATGGTACC AAAATAGTTGCTACTATTTTACAACAAATGAGGAGAAAACCTGGGC
TAACAGTAGAAAGGACTGCATAGACAAGAACTCCACCCTAGTGAAGATAGACAGTTTGGGAAGA
AAAGGATTTTCTTATGTCACAGCCATTACTCATGTTTTTCGTTCTTTTGGCTGGGATTATCATG
GGACTCCTCTGGCAGAAGTTGGTTCTGGGAAGATGGCTCTGTTCCCTCTCCATCCTTGACGT
CTCTAACTATTGAGGGTAAACACAAGCTTTCCATGGAATCCTGGGAAAATTAATAATGATTGT
GAGAATTATAAATACAGACATAAAAAGAGGAGTACAACATACTGAGAAAAGAGCTCCAGTAAC
AAATATTGAAAGGAGATTTAGTACTAAAGAACTTGACCAGATCAATGGATCCAAAGGATGTGC
TTATTTTCAAAAAGGAAATATTTATATTTCTCGCTGTAGTGCTGAAATTTTTTGGATTTGCGA
GAAGACAGCTGCCCCAGTGAAGACTGAGGATTTGGATTAGTATGCTTCTTCCAAATTCTCCAA
GAAGTAAGAGACTTGTGAGTAAGCTCATATGAGGAAAGAGGAAACTACGGTACCAGAGCAAGG
GCGAATTCTGCA

FIGURE 594

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150163
><subunit 1 of 1, 232 aa, 1 stop
><MW: 26754, pI: 5.80, NX(S/T): 3
MSEEVTYATLTFQDSAGARNNRDGNLRLKRGHPAPSPIWRHAALGLVTLCLMLLIGLVTL
GMMFLQISNDINS DSEKLSQLQKTIQQQQDNLSQQLGNSNNLSMEEEFKLSQISSLLKRQ
EQMAIKLCQELIIHTSDHRCNPCPKMWQWYQNSCYFFTNEEKTWANSRKDCIDKNSTLV
KIDSLEEKDFLMSQPLLMFSFFWLGLSWDSSGRSWFWEDGSVPSPSLYVSNY
```

Important features of the protein:

Transmembrane domain:

Amino acids 42-62

N-glycosylation sites:

Amino acids 91-95;101-105;176-180

N-myristoylation sites:

Amino acids 17-23;97-103

FIGURE 595

CGGACGCGTGGGGAAGAGGAGGAGGAGGAAGAAGACGTGGACAAGGACCCCCATCCTACCCAG
AACACCTGCCTGCGCTGCCGCCACTTCTCTTTAAGGGAGAGGAAAAGAGAGCCTAGGAGAACC
ATGGGGGGCTGCGAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCTTCTTGCCCTATGCTGACA
GCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTTGCTTGATACAACAAC
GTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATG
GATGAACATAATAGGCCCATTCACACATACCAGGTATGTAATGTAATGGAACCAACCAAAAC
AACTGGCTTCGTACAAACTGGATCTCCCGTGATGCAGCTCAGAAAATTTATGTGGAAATGAAA
TTCACACTAAGGGATTGTAACAGCATCCCATGGGTCTTGGGGACTTGCAAAGAAACATTTAAT
CTGTTTTTATATGGAATCAGATGAGTCCCACGGAATTAAATTCAGCCAAACCAGTATACAAAG
ATCGACACAATTGCTGCTGATGAGAGTTTTACCCAGATGGATTTGGGTGATCGCATCCTCAA
CTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTTATCTGGCTTTTCAA
GACATTGGGGCGTGCAATGCCCTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCTTCACT
GTCGTAACCTTGGCCATGTTTCCTGATACCATTCCAAGGGTTGATTCTCCTCTTTGGTTGAA
GTACGGGGTTCTTGTGTGAAGAGTGCTGAAGAGCGTGACACTCCTAACTGTATTGTGGAGCT
GATGGAGATTGGCTGGTTCCTCTTGGAAGGTGCATCTGCAGTACAGGATATGAAGAAATTGAG
GGTTCTTGCCATGGAGCCTCCAAAGGCCGCTGCTTCT**AG**TTGGCCATCTTGGCCCCACCCGA
AACAGTAACCTTTGAAGAATAAAAGAAAAAGCAAAGAGTAGCATTACTAAATATTAAACGG
TTACATTTACAAAAA

FIGURE 596

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA153579
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32368, pI: 5.32, NX(S/T): 0
MGGCEVREFLLQFGFFLPMLTAWPGDCSHVSNQVVLDDTTTVLGELGWKTYPLNGWDAI
TEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWI SRDAAQKIYVEMKFTLRDCNSIPWVLGT
CKETFNLFYMESESHGIKFKPNQYTKIDTIAADESFTQMDLGDRILKLNTEIREVGPIE
RKGFYLAFAQDIGACIALVSVRVFYKKCPFTVRNLMFPDTIPRVDSSSLVEVRGSCVKSA
EERDTPKLYCGADGDWLVLPLGRCICSTGYEEIEGSCHGASKGRCF
```

Important features of the protein:

Signal peptide:

Amino acids 1-22

N-myristoylation sites:

Amino acids 192-198;274-280;278-284

Receptor tyrosine kinase class V signature 1:

Amino acids 192-209

Ephrin receptor ligand binding domain:

Amino acids 34-207

FIGURE 597

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTACAGGACTCCCA
GGACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGG
ATTCCAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTTGGGGGGGGG
CAGCACAGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTT
GCTGTCTTGGCACTGGGCCGAAGCCAGTGGTCTTTCTCTGGAGAGGCTTGTGGGGCCTCA
GGACGCTACCCACTGCTCTCCGGGGCCTCTCCTGCCGCCTCTGGGACAGTGACATACTCTGCCT
GCCTGGGGACATCGTGCCTGCTCCGGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCT
GGTGTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGC
CGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGAGGAGCAGCTGACTCAGG
GGTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCC
TACTGCCCGCTGCGTCTCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTC
TGTGGGCTCTGTGGTATATGACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTC
CTATACTCAGCCCAGGTACGAGAAGGAACTCAACCACACACAGCAGCTGCCTGCCCTGCCCTG
GCTCAACGTGTGAGCAGATGGTGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCA
CTTCGGCCTCTCCCTGTACTTGAATCAGGTCAGGGCCCCCAAAACCCCGGTGGCACAAAA
CCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTGCCTCTGTATTCA
GGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCTTTCAGGGAGGACCCCG
CGCACACCAGAACCTCTGGCAAGCCGCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCT
GGACGCACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCC
CTGCCAGCCACTGGTCCCACCGCTTTTCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTT
CCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAAGTGAACAGCTCGGAGAAGCTGCAGCT
GCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTTGGAGAC
ACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCCAGTGGCTGTACTTCACTACC
CAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTACAAGACCTGCAGTCAGG
CCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCCATGGACAAATA
CATCCACAAGCGCTGGGGCCTCGTGTGGCTGGCCTGCCTACTCTTTGCGCTGCGCTTTCCCT
CATCCTCCTTCTCAAAAAGGATCACGCGAAAGGTGGCTGAGGCTCTTGAAACAGGACGTCCG
CTCGGGGGCGGCCGCCAGGGGCCGCGCGGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTT
CGAGCGCCTGGTGGGCGCCCTGGCGTCCGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGA
CCTGTGGAGCCGTCTGAACTGAGCGCGCAGGGGCCCGTGGCTTGGTTTACGCGCAGCGGCG
CCAGACCCTGCAGGAGGGCGGCGTGGTGGTCTTGCTCTTCTCTCCCGGTGCGGTGGCGCTGTG
CAGCGAGTGGCTACAGGATGGGGTGTCCGGGGCCCCGGGGCGCACGGCCCGCACGACGCCTTCCG
CGCCTCGCTCAGCTGCGTGCTGCCCGACTTCTTGCAGGGCCGGGGCGCCCGGCAGCTACGTGGG
GGCCTGCTTCGACAGGCTGCTCCACCCGACGCCGTACCCGCCCTTTTCCGCACCGTGCCTGT
CTTCACTGCCCTCCCAACTGCCAGACTTCTGGGGGCCCTGCAGCAGCCTCGCGCCCCCGG
TTCCGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAG
CTACTTCCATCCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGG
GGCGGGGGACGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

FIGURE 598

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA164625
><subunit 1 of 1, 705 aa, 1 stop
/><MW: 76970, pI: 6.00, NX(S/T): 9
MPVPWFLLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWDSIILCLPGDIVPAPGP
VLAPTHLQTELVLRQCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRN
ASLQAQVVLVSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYT
QPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWH
KNLTGPQIITLNLHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLT
LQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCV
QVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRA
ARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILL
LKKDHAKGWLRLLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAV
DLWSRRELSAQGPVAFHQAQRQTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGP
HDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDLFLG
ALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

Transmembrane domain:

Amino acids 453-473

N-glycosylation sites:

Amino acids 118-122;186-190;198-202;211-215;238-242;
248-252;334-338;357-360;391-395;

Glycosaminoglycan attachment site:

Amino acids 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 552-556

N-myristoylation sites:

Amino acids 107-113;152-158;319-325;438-444;516-522;612-618;
692-698;696-702;700-706

FIGURE 599

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA
TCCCTAAGTTTCAACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTGAGTCCCCTGGGGAAGAACTAA
ATGTCACAACGGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTGAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCTGGAGCCAA
GTGCAGGAGCACCACTCGCCATGTCTCAGGCACAACCCAACTCAGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCCAATAGCTCATTCAGTGCCTTGATTCCTTTTGCCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTCTTTTGTGTTGGAAAA
TCAAGTACTTCTTTGAATGATGATCTTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

FIGURE 600

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFLH
YDCGNKTVTPVSPPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 601

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTT
GCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCA
CCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATG
GGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCCGGC
GCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT
GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACCAGCTCT
CCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGT
TGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGTCTGCAGCATGTGGCTGAAAAAC
TCTGTCTGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGA
AATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAAT
ATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAACAAGAAGACCTGGAATTTG
CCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGCGCCCTGACA
GTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAACTGTTCCATATTATAA
TAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAA
AGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGA
GCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTTCGCCCTCTGCAACTACAAAT
AGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAA
TCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTGTTTCTGTTCAGGATCAC
CAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCAACAAGAAGTCTTATTTACATGC
CACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGC
TCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCTTACACTTGGTGGA
ATAAGAAACTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAG
TAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCCTTT
TTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGT
CCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA
GCATTCCTTCCTGTGTCCATTAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCCA
GGAAAGAAATATATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAG
AGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTA
TTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATAATAATAAATGTA
AATACTGTGAAAAA

FIGURE 602

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCCLVLLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAI LNGMIFSKDCKEL
KRCVCERRAGMVKPESLHVPPETLGED

FIGURE 603

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCCAACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCTTAAACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTAAGGGATTGTGAATAAA
CTTGATACACCA

FIGURE 604

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLLGGALSGWAASDDPIEKVIEGINRGLSNAEREVVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHG VNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 605

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATGG**
TCCCCGGCGCCGCGGGCTGGTGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCACG
GCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACATCT
TCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATTCACC
TTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCAGGACC
AGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCCAGGAGC
ACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTACGTGGAGA
TGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGGCCGAGACG
GCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTCCATCCCAG
TCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTCTGG**TAGAAGA**
GTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCCAGGAATTTTGC
TACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGAAAAGGGTTTGGG
CGTTGCTAGGCTGAAAGGGAAGCCACCACTGGCCTTCCCTTCCCCAGGGCCCCCAAGGGTG
TCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAA
AGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACTCACCTGGCTCCAGCC
TCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGGAGTGGTTTAAAGAGCT
GGTGTTTGGGGACTCAATAAACCTCACTGACTTTTTAGCAATAAAGCTTCTCATCAGGGTTG
CAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 606

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQI
HLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIIISDNAVDNDSFYV
EMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

FIGURE 607

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCCATGTGGCTGC
 CCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGTCTGTGA
 GAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGGAGACCTACA
 TTAAGTGGTGGTGGCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTGAAACCAGAGGGT
 CGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGAAAGACCGCACGTTCA
 CTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTTACTGGTGTGGGATTGAAAGAA
 GAGGACCTGACCTTGGGACTCAAGTGAAAGTGATCGTTGACCCAGAGGGAGCGGCTTCCACAA
 CAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTTCATCGGCTCCACAAAGAGGAACCACT
 ACATGCTCCTGGTATTTGTGAAGGTGCCCATCTTGCTCATCTTGGTCACTGCCATCCTCTGGT
 TGAAGGGGTCTCAGAGGGTCCCTGAGGAGCCAGGGGAACAGCCTATCTACATGAACTTCTCCG
 AACCTCTGACTAAAGACATGGCCACTTAGAGAGATGGATCTGCAGAGCCTTCTGCCCCTGGCC
 ACGTTTCCAGAAGAGACTCGGGCTGTGGAAGGAACATCTACGAGTCTCGGGATGCAGTGACT
 GAGATAGGGGCCCTGGGCCTCCGCCCTGGCCTTGGAGCTGGTGGGCACCTCCCTGTTCTGCAC
 AGCTCAGGGACTTAGCCAGGTCTCTCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTG
 TTCTCTTGGTCAGGAGCTGTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTG
 GAATAACTCGGGCACAGAGCATGGGACCAAAGTACAGAAAGAGGTTGGGGGAGACCCCCCAG
 CCCTAGACTTCCATCATTCCGGAGACCAACTCAACACCGTCTTTGCCCTGAGAACCTGATATATCC
 GTGTTTTTAAATTTTTTTTTTTCTAGCAAAGTTGGGTTTTAATGACTTATGTTTCATAGGAAAC
 CTCTCTGATCCACACACAAGGAGGGTGATTCTGGGATGAGTTCCTGGTTCCTAGGGCATGAGG
 GGCTGGATGGACCCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCAAT
 GGGAACTCCCTGGCCCCGGCCGGTGCTTGTCTCCCCCTCCACCTCTTCTCCTCCTAGCT
 CCCCCAAGCTCCCTGCCTATTCCCCCACCTCCGAGGGGCTGCAGCTTGGGAGCCTCCTCAGCAT
 GACAGCTTGGGTCTCCTCCCCAAAAGAGCCTGTGAGGCCTCAAGAACCACCTCCAGGTGGGGA
 GGGCAGTAACGAAAACCATCGCAGGAAATGGCACCTCCCTTTTCGGTGATGTTGAAATCATG
 TTACTAATGAAAAGTGTCTAGGGAAGTGGTCTGTCTCCTCACAGGCTTCACCCACGGCGAT
 GAGGCCCTTGAATGTGGTCACTTTGTGCTGTATGGTTGAGGGACCCTCACACCAAAGGGACCT
 TCCCATGTGAGATGTGCTCCCGCCCCCACCTGCCCACAAGCAAACACACCACACATGTTCCGC
 ATGTTGCCCTTTGAACACCCATGAGGACGCCTCCAACCTGCTCTTGGTTCCTAATAGGGAGTAC
 TGAAGTGTGAGCAGTGGATAAAGGAGAGGGGACCCTCTGGTCCCTAGCATGGCACCCAGAGCCT
 CCCCTCTTCTTGTCTTCTCAGCCAAAGAGAACTTTCTCTGACTTTGAACTGAATTTAGGTCTC
 TGGCCAATGATGGGCCTGAAAATTCATAATGGCCAGAGAGGAGAGTTTCGAGCCCGGCTAAGA
 TCCCCCTGAGTCATTCTGTGAGGGACCAAGACCCACAGTCCACCAGCCCCAGGGCCCTACCTCC
 TGGAAATGCTTTCTTGGATCCAGCTTCCCGAAGATCCGACCAGACCCAGGGAGGACGGCACCGC
 TCCGCGGGAGGGAAAGCCAAAGCATGGTGTCTTACCAGCTGGACTCAGGGGCGAGGGGACATG
 GGCGCTTGTCAACGTGATGTCACTTTTCCACCGTTTCTTCTGTTGATATTCAATGAATC
 CGTCAATCTCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 608

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105849
><subunit 1 of 1, 201 aa, 1 stop
><MW: 22689, pI: 7.41, NX(S/T): 1
MWLPPALLLLSLSGCFSIQGPESVRAPEQGSLTVQCHYKQGWETYIKWWCRGVRWDTCKI
LIETRGSEQGEKSDRVSIKDNQKDRTFTVTMEGLRRDDADVWCGIERRGPDLTQVKVI
VDPEGAASTTASSPTNSNMAVFIGSHKRNHYMLLVFVKVPILLILVTAILWLKGSQRVPE
EPGEQPIYMNFSEPLTKDMAT
```

Important features of the protein:

Signal peptide:

Amino acids 1-17

Transmembrane domain:

Amino acids 151-170

N-glycosylation site:

Amino acids 190-194

Tyrosine kinase phosphorylation site:

Amino acids 95-103

N-myristoylation sites:

Amino acids 66-72;125-131

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 5-16

FIGURE 609

GATGGCGCAGCCACAGCTTCTGTGAGATTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT
ACAGTAAAAAAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCTAGGGGGGTTATTTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

FIGURE 610

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPMSFSIYSLQVPAVPG LTCWALTAEPGWGQNKGATTCATNSHSDSEL
RPEIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVI
ATNLQEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVF
KNYQTPDHYTLRKISSLANSLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQ
AAVVKALGELDILLQWMEETE
```

Important features of the protein:

Signal peptide:

Amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 192-196;225-229

N-myristoylation sites:

Amino acids 42-48;46-52;136-142

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FIELD OF THE INVENTION

[0001] The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

BACKGROUND OF THE INVENTION

[0002] Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of action in the extracellular environment.

[0003] Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Pat. No. 5,536,637].

[0004] Membrane-bound proteins and receptors can play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and nerve growth factor receptor.

[0005] Membrane-bound proteins and receptor molecules have various industrial applications, including as pharma-

ceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

[0006] Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

SUMMARY OF THE INVENTION

[0007] In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

[0008] In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

[0009] In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

[0010] In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

[0011] Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

[0012] Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide

probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

[0013] In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

[0014] In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93%

amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

[0015] In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

[0016] In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

[0017] Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

[0018] In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as

defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

[0019] In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

[0020] In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

[0021] Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

[0022] In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

[0023] In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

[0024] In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

[0025] In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

[0026] In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

BRIEF DESCRIPTION OF THE DRAWINGS

[0027] FIG. 1 shows a nucleotide sequence (SEQ ID NO: 1) of a native sequence PRO276 cDNA, wherein SEQ ID NO: 1 is a clone designated herein as "DNA16435-1208".

[0028] FIG. 2 shows the amino acid sequence (SEQ ID NO: 2) derived from the coding sequence of SEQ ID NO: 1 shown in FIG. 1.

[0029] FIG. 3 shows a nucleotide sequence (SEQ ID NO: 3) of a native sequence PRO284 cDNA, wherein SEQ ID NO: 3 is a clone designated herein as "DNA23318-1211".

[0030] FIG. 4 shows the amino acid sequence (SEQ ID NO: 4) derived from the coding sequence of SEQ ID NO: 3 shown in FIG. 3.

[0031] FIG. 5 shows a nucleotide sequence (SEQ ID NO: 5) of a native sequence PRO193 cDNA, wherein SEQ ID NO: 5 is a clone designated herein as "DNA23322-1393".

[0032] FIG. 6 shows the amino acid sequence (SEQ ID NO: 6) derived from the coding sequence of SEQ ID NO: 5 shown in FIG. 5.

[0033] FIG. 7 shows a nucleotide sequence (SEQ ID NO: 7) of a native sequence PRO190 cDNA, wherein SEQ ID NO: 7 is a clone designated herein as "DNA23334-1392".

[0034] FIG. 8 shows the amino acid sequence (SEQ ID NO: 8) derived from the coding sequence of SEQ ID NO: 7 shown in FIG. 7.

[0035] FIG. 9 shows a nucleotide sequence (SEQ ID NO: 9) of a native sequence PRO180 cDNA, wherein SEQ ID NO: 9 is a clone designated herein as "DNA26843-1389".

[0036] FIG. 10 shows the amino acid sequence (SEQ ID NO: 10) derived from the coding sequence of SEQ ID NO: 9 shown in FIG. 9.

[0037] FIG. 11 shows a nucleotide sequence (SEQ ID NO: 11) of a native sequence PRO194 cDNA, wherein SEQ ID NO: 11 is a clone designated herein as "DNA26844-1394".

[0038] FIG. 12 shows the amino acid sequence (SEQ ID NO: 12) derived from the coding sequence of SEQ ID NO: 11 shown in FIG. 11.

[0039] FIG. 13 shows a nucleotide sequence (SEQ ID NO: 13) of a native sequence PRO218 cDNA, wherein SEQ ID NO: 13 is a clone designated herein as "DNA30867-1335".

[0040] FIG. 14 shows the amino acid sequence (SEQ ID NO: 14) derived from the coding sequence of SEQ ID NO: 13 shown in FIG. 13.

[0041] FIG. 15 shows a nucleotide sequence (SEQ ID NO: 15) of a native sequence PRO260 cDNA, wherein SEQ ID NO: 15 is a clone designated herein as "DNA33470-1175".

[0042] FIG. 16 shows the amino acid sequence (SEQ ID NO: 16) derived from the coding sequence of SEQ ID NO: 15 shown in FIG. 15.

[0043] FIG. 17 shows a nucleotide sequence (SEQ ID NO: 17) of a native sequence PRO233 cDNA, wherein SEQ ID NO: 17 is a clone designated herein as "DNA34436-1238".

[0044] FIG. 18 shows the amino acid sequence (SEQ ID NO: 18) derived from the coding sequence of SEQ ID NO: 17 shown in FIG. 17.

[0045] FIG. 19 shows a nucleotide sequence (SEQ ID NO: 19) of a native sequence PRO234 cDNA, wherein SEQ ID NO: 19 is a clone designated herein as "DNA35557-1137".

[0046] FIG. 20 shows the amino acid sequence (SEQ ID NO: 20) derived from the coding sequence of SEQ ID NO: 19 shown in FIG. 19.

[0047] FIG. 21 shows a nucleotide sequence (SEQ ID NO: 21) of a native sequence PRO236 cDNA, wherein SEQ ID NO: 21 is a clone designated herein as "DNA35599-1168".

[0048] FIG. 22 shows the amino acid sequence (SEQ ID NO: 22) derived from the coding sequence of SEQ ID NO: 21 shown in FIG. 21.

[0049] FIG. 23 shows a nucleotide sequence (SEQ ID NO: 23) of a native sequence PRO244 cDNA, wherein SEQ ID NO: 23 is a clone designated herein as "DNA35668-1171".

[0050] FIG. 24 shows the amino acid sequence (SEQ ID NO: 24) derived from the coding sequence of SEQ ID NO: 23 shown in FIG. 23.

[0051] FIG. 25 shows a nucleotide sequence (SEQ ID NO: 25) of a native sequence PRO262 cDNA, wherein SEQ ID NO: 25 is a clone designated herein as "DNA36992-1168".

[0052] FIG. 26 shows the amino acid sequence (SEQ ID NO: 26) derived from the coding sequence of SEQ ID NO: 25 shown in FIG. 25.

[0053] FIG. 27 shows a nucleotide sequence (SEQ ID NO: 27) of a native sequence PRO271 cDNA, wherein SEQ ID NO: 27 is a clone designated herein as "DNA39423-1182".

[0054] FIG. 28 shows the amino acid sequence (SEQ ID NO: 28) derived from the coding sequence of SEQ ID NO: 27 shown in FIG. 27.

[0055] FIG. 29 shows a nucleotide sequence (SEQ ID NO: 29) of a native sequence PRO268 cDNA, wherein SEQ ID NO: 29 is a clone designated herein as "DNA39427-1179".

[0056] FIG. 30 shows the amino acid sequence (SEQ ID NO: 30) derived from the coding sequence of SEQ ID NO: 29 shown in FIG. 29.

[0057] FIG. 31 shows a nucleotide sequence (SEQ ID NO: 31) of a native sequence PRO270 cDNA, wherein SEQ ID NO: 31 is a clone designated herein as "DNA39510-1181".

[0058] FIG. 32 shows the amino acid sequence (SEQ ID NO: 32) derived from the coding sequence of SEQ ID NO: 31 shown in FIG. 31.

[0059] FIG. 33 shows a nucleotide sequence (SEQ ID NO: 33) of a native sequence PRO355 cDNA, wherein SEQ ID NO: 33 is a clone designated herein as "DNA39518-1247".

[0060] FIG. 34 shows the amino acid sequence (SEQ ID NO: 34) derived from the coding sequence of SEQ ID NO: 33 shown in FIG. 33.

[0061] FIG. 35 shows a nucleotide sequence (SEQ ID NO: 35) of a native sequence PRO298 cDNA, wherein SEQ ID NO: 35 is a clone designated herein as "DNA39975-1210".

[0062] FIG. 36 shows the amino acid sequence (SEQ ID NO: 36) derived from the coding sequence of SEQ ID NO: 35 shown in FIG. 35.

[0063] FIG. 37 shows a nucleotide sequence (SEQ ID NO: 37) of a native sequence PRO299 cDNA, wherein SEQ ID NO: 37 is a clone designated herein as "DNA39976-1215".

[0064] FIG. 38 shows the amino acid sequence (SEQ ID NO: 38) derived from the coding sequence of SEQ ID NO: 37 shown in FIG. 37.

[0065] FIG. 39 shows a nucleotide sequence (SEQ ID NO: 39) of a native sequence PRO296 cDNA, wherein SEQ ID NO: 39 is a clone designated herein as "DNA39979-1213".

[0066] FIG. 40 shows the amino acid sequence (SEQ ID NO: 40) derived from the coding sequence of SEQ ID NO: 39 shown in FIG. 39.

[0067] FIG. 41 shows a nucleotide sequence (SEQ ID NO: 41) of a native sequence PRO329 cDNA, wherein SEQ ID NO: 41 is a clone designated herein as "DNA40594-1233".

[0068] FIG. 42 shows the amino acid sequence (SEQ ID NO: 42) derived from the coding sequence of SEQ ID NO: 41 shown in FIG. 41.

[0069] FIG. 43 shows a nucleotide sequence (SEQ ID NO: 43) of a native sequence PRO330 cDNA, wherein SEQ ID NO: 43 is a clone designated herein as "DNA40603-1232".

[0070] FIG. 44 shows the amino acid sequence (SEQ ID NO: 44) derived from the coding sequence of SEQ ID NO: 43 shown in FIG. 43.

[0071] FIG. 45 shows a nucleotide sequence (SEQ ID NO: 45) of a native sequence PRO294 cDNA, wherein SEQ ID NO: 45 is a clone designated herein as "DNA40604-1187".

[0072] FIG. 46 shows the amino acid sequence (SEQ ID NO: 46) derived from the coding sequence of SEQ ID NO: 45 shown in FIG. 45.

[0073] FIG. 47 shows a nucleotide sequence (SEQ ID NO: 47) of a native sequence PRO300 cDNA, wherein SEQ ID NO: 47 is a clone designated herein as "DNA40625-1189".

[0074] FIG. 48 shows the amino acid sequence (SEQ ID NO: 48) derived from the coding sequence of SEQ ID NO: 47 shown in FIG. 47.

[0075] FIG. 49 shows a nucleotide sequence (SEQ ID NO: 49) of a native sequence PRO307 cDNA, wherein SEQ ID NO: 49 is a clone designated herein as "DNA41225-1217".

[0076] FIG. 50 shows the amino acid sequence (SEQ ID NO: 50) derived from the coding sequence of SEQ ID NO: 49 shown in FIG. 49.

[0077] FIG. 51 shows a nucleotide sequence (SEQ ID NO: 51) of a native sequence PRO334 cDNA, wherein SEQ ID NO: 51 is a clone designated herein as "DNA41379-1236".

[0078] FIG. 52 shows the amino acid sequence (SEQ ID NO: 52) derived from the coding sequence of SEQ ID NO: 51 shown in FIG. 51.

[0079] FIG. 53 shows a nucleotide sequence (SEQ ID NO: 53) of a native sequence PRO352 cDNA, wherein SEQ ID NO: 53 is a clone designated herein as "DNA41386-1316".

[0080] FIG. 54 shows the amino acid sequence (SEQ ID NO: 54) derived from the coding sequence of SEQ ID NO: 53 shown in FIG. 53.

[0081] FIG. 55 shows a nucleotide sequence (SEQ ID NO: 55) of a native sequence PRO710 cDNA, wherein SEQ ID NO: 55 is a clone designated herein as "DNA44161-1434".

[0082] FIG. 56 shows the amino acid sequence (SEQ ID NO: 56) derived from the coding sequence of SEQ ID NO: 55 shown in FIG. 55.

[0083] FIG. 57 shows a nucleotide sequence (SEQ ID NO: 57) of a native sequence PRO873 cDNA, wherein SEQ ID NO: 57 is a clone designated herein as "DNA44179-1362".

[0084] FIG. 58 shows the amino acid sequence (SEQ ID NO: 58) derived from the coding sequence of SEQ ID NO: 57 shown in FIG. 57.

[0085] FIG. 59 shows a nucleotide sequence (SEQ ID NO: 59) of a native sequence PRO354 cDNA, wherein SEQ ID NO: 59 is a clone designated herein as "DNA44192-1246".

[0086] FIG. 60 shows the amino acid sequence (SEQ ID NO: 60) derived from the coding sequence of SEQ ID NO: 59 shown in FIG. 59.

[0087] FIG. 61 shows a nucleotide sequence (SEQ ID NO: 61) of a native sequence PRO1151 cDNA, wherein SEQ ID NO: 61 is a clone designated herein as "DNA44694-1500".

[0088] FIG. 62 shows the amino acid sequence (SEQ ID NO: 62) derived from the coding sequence of SEQ ID NO: 61 shown in FIG. 61.

[0089] FIG. 63 shows a nucleotide sequence (SEQ ID NO: 63) of a native sequence PRO382 cDNA, wherein SEQ ID NO: 63 is a clone designated herein as "DNA45234-1277".

[0090] FIG. 64 shows the amino acid sequence (SEQ ID NO: 64) derived from the coding sequence of SEQ ID NO: 63 shown in FIG. 63.

[0091] FIG. 65 shows a nucleotide sequence (SEQ ID NO: 65) of a native sequence PRO1864 cDNA, wherein SEQ ID NO: 65 is a clone designated herein as "DNA45409-2511".

[0092] FIG. 66 shows the amino acid sequence (SEQ ID NO: 66) derived from the coding sequence of SEQ ID NO: 65 shown in FIG. 65.

[0093] FIG. 67 shows a nucleotide sequence (SEQ ID NO: 67) of a native sequence PRO386 cDNA, wherein SEQ ID NO: 67 is a clone designated herein as "DNA45415-1318".

[0094] **FIG. 68** shows the amino acid sequence (SEQ ID NO: 68) derived from the coding sequence of SEQ ID NO: 67 shown in **FIG. 67**.

[0095] **FIG. 69** shows a nucleotide sequence (SEQ ID NO: 69) of a native sequence PRO541 cDNA, wherein SEQ ID NO: 69 is a clone designated herein as "DNA45417-1432".

[0096] **FIG. 70** shows the amino acid sequence (SEQ ID NO: 70) derived from the coding sequence of SEQ ID NO: 69 shown in **FIG. 69**.

[0097] **FIG. 71** shows a nucleotide sequence (SEQ ID NO: 71) of a native sequence PRO852 cDNA, wherein SEQ ID NO: 71 is a clone designated herein as "DNA45493-1349".

[0098] **FIG. 72** shows the amino acid sequence (SEQ ID NO: 72) derived from the coding sequence of SEQ ID NO: 71 shown in **FIG. 71**.

[0099] **FIG. 73** shows a nucleotide sequence (SEQ ID NO: 73) of a native sequence PRO700 cDNA, wherein SEQ ID NO: 73 is a clone designated herein as "DNA46776-1284".

[0100] **FIG. 74** shows the amino acid sequence (SEQ ID NO: 74) derived from the coding sequence of SEQ ID NO: 73 shown in **FIG. 73**.

[0101] **FIGS. 75A-75B** show a nucleotide sequence (SEQ ID NO: 75) of a native sequence PRO708 cDNA, wherein SEQ ID NO: 75 is a clone designated herein as "DNA48296-1292".

[0102] **FIG. 76** shows the amino acid sequence (SEQ ID NO: 76) derived from the coding sequence of SEQ ID NO: 75 shown in **FIGS. 75A-75B**.

[0103] **FIG. 77** shows a nucleotide sequence (SEQ ID NO: 77) of a native sequence PRO707 cDNA, wherein SEQ ID NO: 77 is a clone designated herein as "DNA48306-1291".

[0104] **FIG. 78** shows the amino acid sequence (SEQ ID NO: 78) derived from the coding sequence of SEQ ID NO: 77 shown in **FIG. 77**.

[0105] **FIG. 79** shows a nucleotide sequence (SEQ ID NO: 79) of a native sequence PRO864 cDNA, wherein SEQ ID NO: 79 is a clone designated herein as "DNA48328-1355".

[0106] **FIG. 80** shows the amino acid sequence (SEQ ID NO: 80) derived from the coding sequence of SEQ ID NO: 79 shown in **FIG. 79**.

[0107] **FIG. 81** shows a nucleotide sequence (SEQ ID NO: 81) of a native sequence PRO706 cDNA, wherein SEQ ID NO: 81 is a clone designated herein as "DNA48329-1290".

[0108] **FIG. 82** shows the amino acid sequence (SEQ ID NO: 82) derived from the coding sequence of SEQ ID NO: 81 shown in **FIG. 81**.

[0109] **FIG. 83** shows a nucleotide sequence (SEQ ID NO: 83) of a native sequence PRO732 cDNA, wherein SEQ ID NO: 83 is a clone designated herein as "DNA48334-1435".

[0110] **FIG. 84** shows the amino acid sequence (SEQ ID NO: 84) derived from the coding sequence of SEQ ID NO: 83 shown in **FIG. 83**.

[0111] **FIG. 85** shows a nucleotide sequence (SEQ ID NO: 85) of a native sequence PRO537 cDNA, wherein SEQ ID NO: 85 is a clone designated herein as "DNA49141-1431".

[0112] **FIG. 86** shows the amino acid sequence (SEQ ID NO: 86) derived from the coding sequence of SEQ ID NO: 85 shown in **FIG. 85**.

[0113] **FIG. 87** shows a nucleotide sequence (SEQ ID NO: 87) of a native sequence PRO545 cDNA, wherein SEQ ID NO: 87 is a clone designated herein as "DNA49624-1279".

[0114] **FIG. 88** shows the amino acid sequence (SEQ ID NO: 88) derived from the coding sequence of SEQ ID NO: 87 shown in **FIG. 87**.

[0115] **FIG. 89** shows a nucleotide sequence (SEQ ID NO: 89) of a native sequence PRO718 cDNA, wherein SEQ ID NO: 89 is a clone designated herein as "DNA49647-1398".

[0116] **FIG. 90** shows the amino acid sequence (SEQ ID NO: 90) derived from the coding sequence of SEQ ID NO: 89 shown in **FIG. 89**.

[0117] **FIG. 91** shows a nucleotide sequence (SEQ ID NO: 91) of a native sequence PRO872 cDNA, wherein SEQ ID NO: 91 is a clone designated herein as "DNA49819-1439".

[0118] **FIG. 92** shows the amino acid sequence (SEQ ID NO: 92) derived from the coding sequence of SEQ ID NO: 91 shown in **FIG. 91**.

[0119] **FIG. 93** shows a nucleotide sequence (SEQ ID NO: 93) of a native sequence PRO704 cDNA, wherein SEQ ID NO: 93 is a clone designated herein as "DNA50911-1288".

[0120] **FIG. 94** shows the amino acid sequence (SEQ ID NO: 94) derived from the coding sequence of SEQ ID NO: 93 shown in **FIG. 93**.

[0121] **FIG. 95** shows a nucleotide sequence (SEQ ID NO: 95) of a native sequence PRO705 cDNA, wherein SEQ ID NO: 95 is a clone designated herein as "DNA50914-1289".

[0122] **FIG. 96** shows the amino acid sequence (SEQ ID NO: 96) derived from the coding sequence of SEQ ID NO: 95 shown in **FIG. 95**.

[0123] **FIG. 97** shows a nucleotide sequence (SEQ ID NO: 97) of a native sequence PRO871 cDNA, wherein SEQ ID NO: 97 is a clone designated herein as "DNA50919-1361".

[0124] **FIG. 98** shows the amino acid sequence (SEQ ID NO: 98) derived from the coding sequence of SEQ ID NO: 97 shown in **FIG. 97**.

[0125] **FIG. 99** shows a nucleotide sequence (SEQ ID NO: 99) of a native sequence PRO702 cDNA, wherein SEQ ID NO: 99 is a clone designated herein as "DNA50980-1286".

[0126] **FIG. 100** shows the amino acid sequence (SEQ ID NO: 100) derived from the coding sequence of SEQ ID NO: 99 shown in **FIG. 99**.

[0127] **FIG. 101** shows a nucleotide sequence (SEQ ID NO: 101) of a native sequence PRO944 cDNA, wherein SEQ ID NO: 101 is a clone designated herein as "DNA52185-1370".

[0128] **FIG. 102** shows the amino acid sequence (SEQ ID NO: 102) derived from the coding sequence of SEQ ID NO: 101 shown in **FIG. 101**.

[0129] **FIG. 103** shows a nucleotide sequence (SEQ ID NO: 103) of a native sequence PRO739 cDNA, wherein SEQ ID NO: 103 is a clone designated herein as "DNA52756".

[0130] **FIG. 104** shows the amino acid sequence (SEQ ID NO: 104) derived from the coding sequence of SEQ ID NO: 103 shown in **FIG. 103**.

[0131] **FIG. 105** shows a nucleotide sequence (SEQ ID NO: 105) of a native sequence PRO941 cDNA, wherein SEQ ID NO: 105 is a clone designated herein as "DNA53906-1368".

[0132] **FIG. 106** shows the amino acid sequence (SEQ ID NO: 106) derived from the coding sequence of SEQ ID NO: 105 shown in **FIG. 105**.

[0133] **FIG. 107** shows a nucleotide sequence (SEQ ID NO: 107) of a native sequence PRO1082 cDNA, wherein SEQ ID NO: 107 is a clone designated herein as "DNA53912-1457".

[0134] **FIG. 108** shows the amino acid sequence (SEQ ID NO: 108) derived from the coding sequence of SEQ ID NO: 107 shown in **FIG. 107**.

[0135] **FIG. 109** shows a nucleotide sequence (SEQ ID NO: 109) of a native sequence PRO1133 cDNA, wherein SEQ ID NO: 109 is a clone designated herein as "DNA53913-1490".

[0136] **FIG. 110** shows the amino acid sequence (SEQ ID NO: 110) derived from the coding sequence of SEQ ID NO: 109 shown in **FIG. 109**.

[0137] **FIG. 111** shows a nucleotide sequence (SEQ ID NO: 111) of a native sequence PRO983 cDNA, wherein SEQ ID NO: 111 is a clone designated herein as "DNA53977-1371".

[0138] **FIG. 112** shows the amino acid sequence (SEQ ID NO: 112) derived from the coding sequence of SEQ ID NO: 111 shown in **FIG. 111**.

[0139] **FIG. 113** shows a nucleotide sequence (SEQ ID NO: 113) of a native sequence PRO784 cDNA, wherein SEQ ID NO: 113 is a clone designated herein as "DNA53978-1443".

[0140] **FIG. 114** shows the amino acid sequence (SEQ ID NO: 114) derived from the coding sequence of SEQ ID NO: 113 shown in **FIG. 113**.

[0141] **FIG. 115** shows a nucleotide sequence (SEQ ID NO: 115) of a native sequence PRO783 cDNA, wherein SEQ ID NO: 115 is a clone designated herein as "DNA53996-1442".

[0142] **FIG. 116** shows the amino acid sequence (SEQ ID NO: 116) derived from the coding sequence of SEQ ID NO: 115 shown in **FIG. 115**.

[0143] **FIG. 117** shows a nucleotide sequence (SEQ ID NO: 117) of a native sequence PRO940 cDNA, wherein SEQ ID NO: 117 is a clone designated herein as "DNA54002-1367".

[0144] **FIG. 118** shows the amino acid sequence (SEQ ID NO: 118) derived from the coding sequence of SEQ ID NO: 117 shown in **FIG. 117**.

[0145] **FIG. 119** shows a nucleotide sequence (SEQ ID NO: 119) of a native sequence PRO768 cDNA, wherein SEQ ID NO: 119 is a clone designated herein as "DNA55737-1345".

[0146] **FIG. 120** shows the amino acid sequence (SEQ ID NO: 120) derived from the coding sequence of SEQ ID NO: 119 shown in **FIG. 119**.

[0147] **FIG. 121** shows a nucleotide sequence (SEQ ID NO: 121) of a native sequence PRO1079 cDNA, wherein SEQ ID NO: 121 is a clone designated herein as "DNA56050-1455".

[0148] **FIG. 122** shows the amino acid sequence (SEQ ID NO: 122) derived from the coding sequence of SEQ ID NO: 121 shown in **FIG. 121**.

[0149] **FIG. 123** shows a nucleotide sequence (SEQ ID NO: 123) of a native sequence PRO1078 cDNA, wherein SEQ ID NO: 123 is a clone designated herein as "DNA56052-1454".

[0150] **FIG. 124** shows the amino acid sequence (SEQ ID NO: 124) derived from the coding sequence of SEQ ID NO: 123 shown in **FIG. 123**.

[0151] **FIG. 125** shows a nucleotide sequence (SEQ ID NO: 125) of a native sequence PRO118 cDNA, wherein SEQ ID NO: 125 is a clone designated herein as "DNA56107-1415".

[0152] **FIG. 126** shows the amino acid sequence (SEQ ID NO: 126) derived from the coding sequence of SEQ ID NO: 125 shown in **FIG. 125**.

[0153] **FIG. 127** shows a nucleotide sequence (SEQ ID NO: 127) of a native sequence PRO793 cDNA, wherein SEQ ID NO: 127 is a clone designated herein as "DNA56110-1437".

[0154] **FIG. 128** shows the amino acid sequence (SEQ ID NO: 128) derived from the coding sequence of SEQ ID NO: 127 shown in **FIG. 127**.

[0155] **FIG. 129** shows a nucleotide sequence (SEQ ID NO: 129) of a native sequence PRO1773 cDNA, wherein SEQ ID NO: 129 is a clone designated herein as "DNA56406-1704".

[0156] **FIG. 130** shows the amino acid sequence (SEQ ID NO: 130) derived from the coding sequence of SEQ ID NO: 129 shown in **FIG. 129**.

[0157] **FIG. 131** shows a nucleotide sequence (SEQ ID NO: 131) of a native sequence PRO1014 cDNA, wherein SEQ ID NO: 131 is a clone designated herein as "DNA56409-1377".

[0158] **FIG. 132** shows the amino acid sequence (SEQ ID NO: 132) derived from the coding sequence of SEQ ID NO: 131 shown in **FIG. 131**.

[0159] **FIG. 133** shows a nucleotide sequence (SEQ ID NO: 133) of a native sequence PRO1013 cDNA, wherein SEQ ID NO: 133 is a clone designated herein as "DNA56410-1414".

[0160] **FIG. 134** shows the amino acid sequence (SEQ ID NO: 134) derived from the coding sequence of SEQ ID NO: 133 shown in **FIG. 133**.

[0161] **FIG. 135** shows a nucleotide sequence (SEQ ID NO: 135) of a native sequence PRO937 cDNA, wherein SEQ ID NO: 135 is a clone designated herein as "DNA56436-1448".

[0162] **FIG. 136** shows the amino acid sequence (SEQ ID NO: 136) derived from the coding sequence of SEQ ID NO: 135 shown in **FIG. 135**.

[0163] **FIG. 137** shows a nucleotide sequence (SEQ ID NO: 137) of a native sequence PRO1477 cDNA, wherein SEQ ID NO: 137 is a clone designated herein as "DNA56529-1647".

[0164] **FIG. 138** shows the amino acid sequence (SEQ ID NO: 138) derived from the coding sequence of SEQ ID NO: 137 shown in **FIG. 137**.

[0165] **FIG. 139** shows a nucleotide sequence (SEQ ID NO: 139) of a native sequence PRO842 cDNA, wherein SEQ ID NO: 139 is a clone designated herein as "DNA56855-1447".

[0166] **FIG. 140** shows the amino acid sequence (SEQ ID NO: 140) derived from the coding sequence of SEQ ID NO: 139 shown in **FIG. 139**.

[0167] **FIG. 141** shows a nucleotide sequence (SEQ ID NO: 141) of a native sequence PRO839 cDNA, wherein SEQ ID NO: 141 is a clone designated herein as "DNA56859-1445".

[0168] **FIG. 142** shows the amino acid sequence (SEQ ID NO: 142) derived from the coding sequence of SEQ ID NO: 141 shown in **FIG. 141**.

[0169] **FIG. 143** shows a nucleotide sequence (SEQ ID NO: 143) of a native sequence PRO1180 cDNA, wherein SEQ ID NO: 143 is a clone designated herein as "DNA56860-1510".

[0170] **FIG. 144** shows the amino acid sequence (SEQ ID NO: 144) derived from the coding sequence of SEQ ID NO: 143 shown in **FIG. 143**.

[0171] **FIG. 145** shows a nucleotide sequence (SEQ ID NO: 145) of a native sequence PRO1134 cDNA, wherein SEQ ID NO: 145 is a clone designated herein as "DNA56865-1491".

[0172] **FIG. 146** shows the amino acid sequence (SEQ ID NO: 146) derived from the coding sequence of SEQ ID NO: 145 shown in **FIG. 145**.

[0173] **FIG. 147** shows a nucleotide sequence (SEQ ID NO: 147) of a native sequence PRO1115 cDNA, wherein SEQ ID NO: 147 is a clone designated herein as "DNA56868-1478".

[0174] **FIG. 148** shows the amino acid sequence (SEQ ID NO: 148) derived from the coding sequence of SEQ ID NO: 147 shown in **FIG. 147**.

[0175] **FIG. 149** shows a nucleotide sequence (SEQ ID NO: 149) of a native sequence PRO1277 cDNA, wherein SEQ ID NO: 149 is a clone designated herein as "DNA56869-1545".

[0176] **FIG. 150** shows the amino acid sequence (SEQ ID NO: 150) derived from the coding sequence of SEQ ID NO: 149 shown in **FIG. 149**.

[0177] **FIG. 151** shows a nucleotide sequence (SEQ ID NO: 151) of a native sequence PRO1135 cDNA, wherein SEQ ID NO: 151 is a clone designated herein as "DNA56870-1492".

[0178] **FIG. 152** shows the amino acid sequence (SEQ ID NO: 152) derived from the coding sequence of SEQ ID NO: 151 shown in **FIG. 151**.

[0179] **FIG. 153** shows a nucleotide sequence (SEQ ID NO: 153) of a native sequence PRO827 cDNA, wherein SEQ ID NO: 153 is a clone designated herein as "DNA57039-1402".

[0180] **FIG. 154** shows the amino acid sequence (SEQ ID NO: 154) derived from the coding sequence of SEQ ID NO: 153 shown in **FIG. 153**.

[0181] **FIG. 155** shows a nucleotide sequence (SEQ ID NO: 155) of a native sequence PRO1057 cDNA, wherein SEQ ID NO: 155 is a clone designated herein as "DNA57253-1382".

[0182] **FIG. 156** shows the amino acid sequence (SEQ ID NO: 156) derived from the coding sequence of SEQ ID NO: 155 shown in **FIG. 155**.

[0183] **FIG. 157** shows a nucleotide sequence (SEQ ID NO: 157) of a native sequence PRO1113 cDNA, wherein SEQ ID NO: 157 is a clone designated herein as "DNA57254-1477".

[0184] **FIG. 158** shows the amino acid sequence (SEQ ID NO: 158) derived from the coding sequence of SEQ ID NO: 157 shown in **FIG. 157**.

[0185] **FIG. 159** shows a nucleotide sequence (SEQ ID NO: 159) of a native sequence PRO1006 cDNA, wherein SEQ ID NO: 159 is a clone designated herein as "DNA57699-1412".

[0186] **FIG. 160** shows the amino acid sequence (SEQ ID NO: 160) derived from the coding sequence of SEQ ID NO: 159 shown in **FIG. 159**.

[0187] **FIG. 161** shows a nucleotide sequence (SEQ ID NO: 161) of a native sequence PRO1074 cDNA, wherein SEQ ID NO: 161 is a clone designated herein as "DNA57704-1452".

[0188] **FIG. 162** shows the amino acid sequence (SEQ ID NO: 162) derived from the coding sequence of SEQ ID NO: 161 shown in **FIG. 161**.

[0189] **FIG. 163** shows a nucleotide sequence (SEQ ID NO: 163) of a native sequence PRO1073 cDNA, wherein SEQ ID NO: 163 is a clone designated herein as "DNA57710-1451".

[0190] **FIG. 164** shows the amino acid sequence (SEQ ID NO: 164) derived from the coding sequence of SEQ ID NO: 163 shown in **FIG. 163**.

[0191] **FIG. 165** shows a nucleotide sequence (SEQ ID NO: 165) of a native sequence PRO1136 cDNA, wherein SEQ ID NO: 165 is a clone designated herein as "DNA57827-1493".

[0192] **FIG. 166** shows the amino acid sequence (SEQ ID NO: 166) derived from the coding sequence of SEQ ID NO: 165 shown in **FIG. 165**.

[0193] **FIG. 167** shows a nucleotide sequence (SEQ ID NO: 167) of a native sequence PRO1004 cDNA, wherein SEQ ID NO: 167 is a clone designated herein as "DNA57844-1410".

[0194] **FIG. 168** shows the amino acid sequence (SEQ ID NO: 168) derived from the coding sequence of SEQ ID NO: 167 shown in **FIG. 167**.

[0195] **FIG. 169** shows a nucleotide sequence (SEQ ID NO: 169) of a native sequence PRO1344 cDNA, wherein SEQ ID NO: 169 is a clone designated herein as "DNA58723-1588".

[0196] **FIG. 170** shows the amino acid sequence (SEQ ID NO: 170) derived from the coding sequence of SEQ ID NO: 169 shown in **FIG. 169**.

[0197] **FIG. 171** shows a nucleotide sequence (SEQ ID NO: 171) of a native sequence PRO1110 cDNA, wherein SEQ ID NO: 171 is a clone designated herein as "DNA58727-1474".

[0198] **FIG. 172** shows the amino acid sequence (SEQ ID NO: 172) derived from the coding sequence of SEQ ID NO: 171 shown in **FIG. 171**.

[0199] **FIG. 173** shows a nucleotide sequence (SEQ ID NO: 173) of a native sequence PRO1378 cDNA, wherein SEQ ID NO: 173 is a clone designated herein as "DNA58730-1607".

[0200] **FIG. 174** shows the amino acid sequence (SEQ ID NO: 174) derived from the coding sequence of SEQ ID NO: 173 shown in **FIG. 173**.

[0201] **FIG. 175** shows a nucleotide sequence (SEQ ID NO: 175) of a native sequence PRO1481 cDNA, wherein SEQ ID NO: 175 is a clone designated herein as "DNA58732-1650".

[0202] **FIG. 176** shows the amino acid sequence (SEQ ID NO: 176) derived from the coding sequence of SEQ ID NO: 175 shown in **FIG. 175**.

[0203] **FIG. 177** shows a nucleotide sequence (SEQ ID NO: 177) of a native sequence PRO1109 cDNA, wherein SEQ ID NO: 177 is a clone designated herein as "DNA58737-1473".

[0204] **FIG. 178** shows the amino acid sequence (SEQ ID NO: 178) derived from the coding sequence of SEQ ID NO: 177 shown in **FIG. 177**.

[0205] **FIG. 179** shows a nucleotide sequence (SEQ ID NO: 179) of a native sequence PRO1383 cDNA, wherein SEQ ID NO: 179 is a clone designated herein as "DNA58743-1609".

[0206] **FIG. 180** shows the amino acid sequence (SEQ ID NO: 180) derived from the coding sequence of SEQ ID NO: 179 shown in **FIG. 179**.

[0207] **FIG. 181** shows a nucleotide sequence (SEQ ID NO: 181) of a native sequence PRO1072 cDNA, wherein SEQ ID NO: 181 is a clone designated herein as "DNA58747-1384".

[0208] **FIG. 182** shows the amino acid sequence (SEQ ID NO: 182) derived from the coding sequence of SEQ ID NO: 181 shown in **FIG. 181**.

[0209] **FIG. 183** shows a nucleotide sequence (SEQ ID NO: 183) of a native sequence PRO1189 cDNA, wherein SEQ ID NO: 183 is a clone designated herein as "DNA58828-1519".

[0210] **FIG. 184** shows the amino acid sequence (SEQ ID NO: 184) derived from the coding sequence of SEQ ID NO: 183 shown in **FIG. 183**.

[0211] **FIG. 185** shows a nucleotide sequence (SEQ ID NO: 185) of a native sequence PRO1003 cDNA, wherein SEQ ID NO: 185 is a clone designated herein as "DNA58846-1409".

[0212] **FIG. 186** shows the amino acid sequence (SEQ ID NO: 186) derived from the coding sequence of SEQ ID NO: 185 shown in **FIG. 185**.

[0213] **FIG. 187** shows a nucleotide sequence (SEQ ID NO: 187) of a native sequence PRO1108 cDNA, wherein SEQ ID NO: 187 is a clone designated herein as "DNA58848-1472".

[0214] **FIG. 188** shows the amino acid sequence (SEQ ID NO: 188) derived from the coding sequence of SEQ ID NO: 187 shown in **FIG. 187**.

[0215] **FIG. 189** shows a nucleotide sequence (SEQ ID NO: 189) of a native sequence PRO1137 cDNA, wherein SEQ ID NO: 189 is a clone designated herein as "DNA58849-1494".

[0216] **FIG. 190** shows the amino acid sequence (SEQ ID NO: 190) derived from the coding sequence of SEQ ID NO: 189 shown in **FIG. 189**.

[0217] **FIG. 191** shows a nucleotide sequence (SEQ ID NO: 191) of a native sequence PRO1138 cDNA, wherein SEQ ID NO: 191 is a clone designated herein as "DNA58850-1495".

[0218] **FIG. 192** shows the amino acid sequence (SEQ ID NO: 192) derived from the coding sequence of SEQ ID NO: 191 shown in **FIG. 191**.

[0219] **FIG. 193** shows a nucleotide sequence (SEQ ID NO: 193) of a native sequence PRO1415 cDNA, wherein SEQ ID NO: 193 is a clone designated herein as "DNA58852-1637".

[0220] **FIG. 194** shows the amino acid sequence (SEQ ID NO: 194) derived from the coding sequence of SEQ ID NO: 193 shown in **FIG. 193**.

[0221] **FIG. 195** shows a nucleotide sequence (SEQ ID NO: 195) of a native sequence PRO1054 cDNA, wherein SEQ ID NO: 195 is a clone designated herein as "DNA58853-1423".

[0222] **FIG. 196** shows the amino acid sequence (SEQ ID NO: 196) derived from the coding sequence of SEQ ID NO: 195 shown in **FIG. 195**.

[0223] **FIG. 197** shows a nucleotide sequence (SEQ ID NO: 197) of a native sequence PRO994 cDNA, wherein SEQ ID NO: 197 is a clone designated herein as "DNA58855-1422".

[0224] **FIG. 198** shows the amino acid sequence (SEQ ID NO: 198) derived from the coding sequence of SEQ ID NO: 197 shown in **FIG. 197**.

[0225] **FIG. 199** shows a nucleotide sequence (SEQ ID NO: 199) of a native sequence PRO1069 cDNA, wherein SEQ ID NO: 199 is a clone designated herein as "DNA59211-1450".

[0226] **FIG. 200** shows the amino acid sequence (SEQ ID NO: 200) derived from the coding sequence of SEQ ID NO: 199 shown in **FIG. 199**.

[0227] **FIG. 201** shows a nucleotide sequence (SEQ ID NO: 201) of a native sequence PRO1411 cDNA, wherein SEQ ID NO: 201 is a clone designated herein as "DNA59212-1627".

[0228] **FIG. 202** shows the amino acid sequence (SEQ ID NO: 202) derived from the coding sequence of SEQ ID NO: 201 shown in **FIG. 201**.

[0229] **FIG. 203** shows a nucleotide sequence (SEQ ID NO: 203) of a native sequence PRO1129 cDNA, wherein SEQ ID NO: 203 is a clone designated herein as "DNA59213-1487".

[0230] **FIG. 204** shows the amino acid sequence (SEQ ID NO: 204) derived from the coding sequence of SEQ ID NO: 203 shown in **FIG. 203**.

[0231] **FIG. 205** shows a nucleotide sequence (SEQ ID NO: 205) of a native sequence PRO1359 cDNA, wherein SEQ ID NO: 205 is a clone designated herein as "DNA59219-1613".

[0232] **FIG. 206** shows the amino acid sequence (SEQ ID NO: 206) derived from the coding sequence of SEQ ID NO: 205 shown in **FIG. 205**.

[0233] **FIG. 207** shows a nucleotide sequence (SEQ ID NO: 207) of a native sequence PRO1139 cDNA, wherein SEQ ID NO: 207 is a clone designated herein as "DNA59497-1496".

[0234] **FIG. 208** shows the amino acid sequence (SEQ ID NO: 208) derived from the coding sequence of SEQ ID NO: 207 shown in **FIG. 207**.

[0235] **FIG. 209** shows a nucleotide sequence (SEQ ID NO: 209) of a native sequence PRO1065 cDNA, wherein SEQ ID NO: 209 is a clone designated herein as "DNA59602-1436".

[0236] **FIG. 210** shows the amino acid sequence (SEQ ID NO: 210) derived from the coding sequence of SEQ ID NO: 209 shown in **FIG. 209**.

[0237] **FIG. 211** shows a nucleotide sequence (SEQ ID NO: 211) of a native sequence PRO1028 cDNA, wherein SEQ ID NO: 211 is a clone designated herein as "DNA59603-1419".

[0238] **FIG. 212** shows the amino acid sequence (SEQ ID NO: 212) derived from the coding sequence of SEQ ID NO: 211 shown in **FIG. 211**.

[0239] **FIG. 213** shows a nucleotide sequence (SEQ ID NO: 213) of a native sequence PRO1027 cDNA, wherein SEQ ID NO: 213 is a clone designated herein as "DNA59605-1418".

[0240] **FIG. 214** shows the amino acid sequence (SEQ ID NO: 214) derived from the coding sequence of SEQ ID NO: 213 shown in **FIG. 213**.

[0241] **FIG. 215** shows a nucleotide sequence (SEQ ID NO: 215) of a native sequence PRO1140 cDNA, wherein SEQ ID NO: 215 is a clone designated herein as "DNA59607-1497".

[0242] **FIG. 216** shows the amino acid sequence (SEQ ID NO: 216) derived from the coding sequence of SEQ ID NO: 215 shown in **FIG. 215**.

[0243] **FIG. 217** shows a nucleotide sequence (SEQ ID NO: 217) of a native sequence PRO1291 cDNA, wherein SEQ ID NO: 217 is a clone designated herein as "DNA59610-1556".

[0244] **FIG. 218** shows the amino acid sequence (SEQ ID NO: 218) derived from the coding sequence of SEQ ID NO: 217 shown in **FIG. 217**.

[0245] **FIG. 219** shows a nucleotide sequence (SEQ ID NO: 219) of a native sequence PRO1105 cDNA, wherein SEQ ID NO: 219 is a clone designated herein as "DNA59612-1466".

[0246] **FIG. 220** shows the amino acid sequence (SEQ ID NO: 220) derived from the coding sequence of SEQ ID NO: 219 shown in **FIG. 219**.

[0247] **FIG. 221** shows a nucleotide sequence (SEQ ID NO: 221) of a native sequence PRO1026 cDNA, wherein SEQ ID NO: 221 is a clone designated herein as "DNA59613-1417".

[0248] **FIG. 222** shows the amino acid sequence (SEQ ID NO: 222) derived from the coding sequence of SEQ ID NO: 221 shown in **FIG. 221**.

[0249] **FIG. 223** shows a nucleotide sequence (SEQ ID NO: 223) of a native sequence PRO1104 cDNA, wherein SEQ ID NO: 223 is a clone designated herein as "DNA59616-1465".

[0250] **FIG. 224** shows the amino acid sequence (SEQ ID NO: 224) derived from the coding sequence of SEQ ID NO: 223 shown in **FIG. 223**.

[0251] **FIG. 225** shows a nucleotide sequence (SEQ ID NO: 225) of a native sequence PRO1100 cDNA, wherein SEQ ID NO: 225 is a clone designated herein as "DNA59619-1464".

[0252] **FIG. 226** shows the amino acid sequence (SEQ ID NO: 226) derived from the coding sequence of SEQ ID NO: 225 shown in **FIG. 225**.

[0253] **FIG. 227** shows a nucleotide sequence (SEQ ID NO: 227) of a native sequence PRO1141 cDNA, wherein SEQ ID NO: 227 is a clone designated herein as "DNA59625-1498".

[0254] FIG. 228 shows the amino acid sequence (SEQ ID NO: 228) derived from the coding sequence of SEQ ID NO: 227 shown in FIG. 227.

[0255] FIG. 229 shows a nucleotide sequence (SEQ ID NO: 229) of a native sequence PRO1772 cDNA, wherein SEQ ID NO: 229 is a clone designated herein as "DNA59817-1703".

[0256] FIG. 230 shows the amino acid sequence (SEQ ID NO: 230) derived from the coding sequence of SEQ ID NO: 229 shown in FIG. 229.

[0257] FIG. 231 shows a nucleotide sequence (SEQ ID NO: 231) of a native sequence PRO1064 cDNA, wherein SEQ ID NO: 231 is a clone designated herein as "DNA59827-1426".

[0258] FIG. 232 shows the amino acid sequence (SEQ ID NO: 232) derived from the coding sequence of SEQ ID NO: 231 shown in FIG. 231.

[0259] FIG. 233 shows a nucleotide sequence (SEQ ID NO: 233) of a native sequence PRO1379 cDNA, wherein SEQ ID NO: 233 is a clone designated herein as "DNA59828-1608".

[0260] FIG. 234 shows the amino acid sequence (SEQ ID NO: 234) derived from the coding sequence of SEQ ID NO: 233 shown in FIG. 233.

[0261] FIG. 235 shows a nucleotide sequence (SEQ ID NO: 235) of a native sequence PRO3573 cDNA, wherein SEQ ID NO: 235 is a clone designated herein as "DNA59837-2545".

[0262] FIG. 236 shows the amino acid sequence (SEQ ID NO: 236) derived from the coding sequence of SEQ ID NO: 235 shown in FIG. 235.

[0263] FIG. 237 shows a nucleotide sequence (SEQ ID NO: 237) of a native sequence PRO3566 cDNA, wherein SEQ ID NO: 237 is a clone designated herein as "DNA59844-2542".

[0264] FIG. 238 shows the amino acid sequence (SEQ ID NO: 238) derived from the coding sequence of SEQ ID NO: 237 shown in FIG. 237.

[0265] FIG. 239 shows a nucleotide sequence (SEQ ID NO: 239) of a native sequence PRO1156 cDNA, wherein SEQ ID NO: 239 is a clone designated herein as "DNA59853-1505".

[0266] FIG. 240 shows the amino acid sequence (SEQ ID NO: 240) derived from the coding sequence of SEQ ID NO: 239 shown in FIG. 239.

[0267] FIG. 241 shows a nucleotide sequence (SEQ ID NO: 241) of a native sequence PRO1098 cDNA, wherein SEQ ID NO: 241 is a clone designated herein as "DNA59854-1459".

[0268] FIG. 242 shows the amino acid sequence (SEQ ID NO: 242) derived from the coding sequence of SEQ ID NO: 241 shown in FIG. 241.

[0269] FIG. 243 shows a nucleotide sequence (SEQ ID NO: 243) of a native sequence PRO1128 cDNA, wherein SEQ ID NO: 243 is a clone designated herein as "DNA59855-1485".

[0270] FIG. 244 shows the amino acid sequence (SEQ ID NO: 244) derived from the coding sequence of SEQ ID NO: 243 shown in FIG. 243.

[0271] FIG. 245 shows a nucleotide sequence (SEQ ID NO: 245) of a native sequence PRO1248 cDNA, wherein SEQ ID NO: 245 is a clone designated herein as "DNA60278-1530".

[0272] FIG. 246 shows the amino acid sequence (SEQ ID NO: 246) derived from the coding sequence of SEQ ID NO: 245 shown in FIG. 245.

[0273] FIG. 247 shows a nucleotide sequence (SEQ ID NO: 247) of a native sequence PRO1127 cDNA, wherein SEQ ID NO: 247 is a clone designated herein as "DNA60283-1484".

[0274] FIG. 248 shows the amino acid sequence (SEQ ID NO: 248) derived from the coding sequence of SEQ ID NO: 247 shown in FIG. 247.

[0275] FIG. 249 shows a nucleotide sequence (SEQ ID NO: 249) of a native sequence PRO1316 cDNA, wherein SEQ ID NO: 249 is a clone designated herein as "DNA60608-1577".

[0276] FIG. 250 shows the amino acid sequence (SEQ ID NO: 250) derived from the coding sequence of SEQ ID NO: 249 shown in FIG. 249.

[0277] FIG. 251 shows a nucleotide sequence (SEQ ID NO: 251) of a native sequence PRO1197 cDNA, wherein SEQ ID NO: 251 is a clone designated herein as "DNA60611-1524".

[0278] FIG. 252 shows the amino acid sequence (SEQ ID NO: 252) derived from the coding sequence of SEQ ID NO: 251 shown in FIG. 251.

[0279] FIG. 253 shows a nucleotide sequence (SEQ ID NO: 253) of a native sequence PRO1125 cDNA, wherein SEQ ID NO: 253 is a clone designated herein as "DNA60619-1482".

[0280] FIG. 254 shows the amino acid sequence (SEQ ID NO: 254) derived from the coding sequence of SEQ ID NO: 253 shown in FIG. 253.

[0281] FIG. 255 shows a nucleotide sequence (SEQ ID NO: 255) of a native sequence PRO1158 cDNA, wherein SEQ ID NO: 255 is a clone designated herein as "DNA60625-1507".

[0282] FIG. 256 shows the amino acid sequence (SEQ ID NO: 256) derived from the coding sequence of SEQ ID NO: 255 shown in FIG. 255.

[0283] FIG. 257 shows a nucleotide sequence (SEQ ID NO: 257) of a native sequence PRO1124 cDNA, wherein SEQ ID NO: 257 is a clone designated herein as "DNA60629-1481".

[0284] FIG. 258 shows the amino acid sequence (SEQ ID NO: 258) derived from the coding sequence of SEQ ID NO: 257 shown in FIG. 257.

[0285] FIG. 259 shows a nucleotide sequence (SEQ ID NO: 259) of a native sequence PRO1380 cDNA, wherein SEQ ID NO: 259 is a clone designated herein as "DNA60740-1615".

[0286] **FIG. 260** shows the amino acid sequence (SEQ ID NO: 260) derived from the coding sequence of SEQ ID NO: 259 shown in **FIG. 259**.

[0287] **FIG. 261** shows a nucleotide sequence (SEQ ID NO: 261) of a native sequence PRO1377 cDNA, wherein SEQ ID NO: 261 is a clone designated herein as "DNA61608-1606".

[0288] **FIG. 262** shows the amino acid sequence (SEQ ID NO: 262) derived from the coding sequence of SEQ ID NO: 261 shown in **FIG. 261**.

[0289] **FIG. 263** shows a nucleotide sequence (SEQ ID NO: 263) of a native sequence PRO1287 cDNA, wherein SEQ ID NO: 263 is a clone designated herein as "DNA61755-1554".

[0290] **FIG. 264** shows the amino acid sequence (SEQ ID NO: 264) derived from the coding sequence of SEQ ID NO: 263 shown in **FIG. 263**.

[0291] **FIG. 265** shows a nucleotide sequence (SEQ ID NO: 265) of a native sequence PRO1249 cDNA, wherein SEQ ID NO: 265 is a clone designated herein as "DNA62809-1531".

[0292] **FIG. 266** shows the amino acid sequence (SEQ ID NO: 266) derived from the coding sequence of SEQ ID NO: 265 shown in **FIG. 265**.

[0293] **FIG. 267** shows a nucleotide sequence (SEQ ID NO: 267) of a native sequence PRO1335 cDNA, wherein SEQ ID NO: 267 is a clone designated herein as "DNA62812-1594".

[0294] **FIG. 268** shows the amino acid sequence (SEQ ID NO: 268) derived from the coding sequence of SEQ ID NO: 267 shown in **FIG. 267**.

[0295] **FIG. 269** shows a nucleotide sequence (SEQ ID NO: 269) of a native sequence PRO3572 cDNA, wherein SEQ ID NO: 269 is a clone designated herein as "DNA62813-2544".

[0296] **FIG. 270** shows the amino acid sequence (SEQ ID NO: 270) derived from the coding sequence of SEQ ID NO: 269 shown in **FIG. 269**.

[0297] **FIG. 271** shows a nucleotide sequence (SEQ ID NO: 271) of a native sequence PRO1599 cDNA, wherein SEQ ID NO: 271 is a clone designated herein as "DNA62845-1684".

[0298] **FIG. 272** shows the amino acid sequence (SEQ ID NO: 272) derived from the coding sequence of SEQ ID NO: 271 shown in **FIG. 271**.

[0299] **FIG. 273** shows a nucleotide sequence (SEQ ID NO: 273) of a native sequence PRO1374 cDNA, wherein SEQ ID NO: 273 is a clone designated herein as "DNA64849-1604".

[0300] **FIG. 274** shows the amino acid sequence (SEQ ID NO: 274) derived from the coding sequence of SEQ ID NO: 273 shown in **FIG. 273**.

[0301] **FIG. 275** shows a nucleotide sequence (SEQ ID NO: 275) of a native sequence PRO1345 cDNA, wherein SEQ ID NO: 275 is a clone designated herein as "DNA64852-1589".

[0302] **FIG. 276** shows the amino acid sequence (SEQ ID NO: 276) derived from the coding sequence of SEQ ID NO: 275 shown in **FIG. 275**.

[0303] **FIG. 277** shows a nucleotide sequence (SEQ ID NO: 277) of a native sequence PRO1311 cDNA, wherein SEQ ID NO: 277 is a clone designated herein as "DNA64863-1573".

[0304] **FIG. 278** shows the amino acid sequence (SEQ ID NO: 278) derived from the coding sequence of SEQ ID NO: 277 shown in **FIG. 277**.

[0305] **FIG. 279** shows a nucleotide sequence (SEQ ID NO: 279) of a native sequence PRO1357 cDNA, wherein SEQ ID NO: 279 is a clone designated herein as "DNA64881-1602".

[0306] **FIG. 280** shows the amino acid sequence (SEQ ID NO: 280) derived from the coding sequence of SEQ ID NO: 279 shown in **FIG. 279**.

[0307] **FIG. 281** shows a nucleotide sequence (SEQ ID NO: 281) of a native sequence PRO1557 cDNA, wherein SEQ ID NO: 281 is a clone designated herein as "DNA64902-1667".

[0308] **FIG. 282** shows the amino acid sequence (SEQ ID NO: 282) derived from the coding sequence of SEQ ID NO: 281 shown in **FIG. 281**.

[0309] **FIG. 283** shows a nucleotide sequence (SEQ ID NO: 283) of a native sequence PRO1305 cDNA, wherein SEQ ID NO: 283 is a clone designated herein as "DNA64952-1568".

[0310] **FIG. 284** shows the amino acid sequence (SEQ ID NO: 284) derived from the coding sequence of SEQ ID NO: 283 shown in **FIG. 283**.

[0311] **FIG. 285** shows a nucleotide sequence (SEQ ID NO: 285) of a native sequence PRO1302 cDNA, wherein SEQ ID NO: 285 is a clone designated herein as "DNA65403-1565".

[0312] **FIG. 286** shows the amino acid sequence (SEQ ID NO: 286) derived from the coding sequence of SEQ ID NO: 285 shown in **FIG. 285**.

[0313] **FIG. 287** shows a nucleotide sequence (SEQ ID NO: 287) of a native sequence PRO1266 cDNA, wherein SEQ ID NO: 287 is a clone designated herein as "DNA65413-1534".

[0314] **FIG. 288** shows the amino acid sequence (SEQ ID NO: 288) derived from the coding sequence of SEQ ID NO: 287 shown in **FIG. 287**.

[0315] **FIGS. 289A-289B** show a nucleotide sequence (SEQ ID NO: 289) of a native sequence PRO1336 cDNA, wherein SEQ ID NO: 289 is a clone designated herein as "DNA65423-1595".

[0316] **FIG. 290** shows the amino acid sequence (SEQ ID NO: 290) derived from the coding sequence of SEQ ID NO: 289 shown in **FIGS. 289A-289B**.

[0317] **FIG. 291** shows a nucleotide sequence (SEQ ID NO: 291) of a native sequence PRO1278 cDNA, wherein SEQ ID NO: 291 is a clone designated herein as "DNA66304-1546".

[0318] **FIG. 292** shows the amino acid sequence (SEQ ID NO: 292) derived from the coding sequence of SEQ ID NO: 291 shown in **FIG. 291**.

[0319] **FIG. 293** shows a nucleotide sequence (SEQ ID NO: 293) of a native sequence PRO1270 cDNA, wherein SEQ ID NO: 293 is a clone designated herein as "DNA66308-1537".

[0320] **FIG. 294** shows the amino acid sequence (SEQ ID NO: 294) derived from the coding sequence of SEQ ID NO: 293 shown in **FIG. 293**.

[0321] **FIG. 295** shows a nucleotide sequence (SEQ ID NO: 295) of a native sequence PRO1298 cDNA, wherein SEQ ID NO: 295 is a clone designated herein as "DNA66511-1563".

[0322] **FIG. 296** shows the amino acid sequence (SEQ ID NO: 296) derived from the coding sequence of SEQ ID NO: 295 shown in **FIG. 295**.

[0323] **FIG. 297** shows a nucleotide sequence (SEQ ID NO: 297) of a native sequence PRO1301 cDNA, wherein SEQ ID NO: 297 is a clone designated herein as "DNA66512-1564".

[0324] **FIG. 298** shows the amino acid sequence (SEQ ID NO: 298) derived from the coding sequence of SEQ ID NO: 297 shown in **FIG. 297**.

[0325] **FIG. 299** shows a nucleotide sequence (SEQ ID NO: 299) of a native sequence PRO1268 cDNA, wherein SEQ ID NO: 299 is a clone designated herein as "DNA66519-1535".

[0326] **FIG. 300** shows the amino acid sequence (SEQ ID NO: 300) derived from the coding sequence of SEQ ID NO: 299 shown in **FIG. 299**.

[0327] **FIG. 301** shows a nucleotide sequence (SEQ ID NO: 301) of a native sequence PRO1327 cDNA, wherein SEQ ID NO: 301 is a clone designated herein as "DNA66521-1583".

[0328] **FIG. 302** shows the amino acid sequence (SEQ ID NO: 302) derived from the coding sequence of SEQ ID NO: 301 shown in **FIG. 301**.

[0329] **FIG. 303** shows a nucleotide sequence (SEQ ID NO: 303) of a native sequence PRO1328 cDNA, wherein SEQ ID NO: 303 is a clone designated herein as "DNA66658-1584".

[0330] **FIG. 304** shows the amino acid sequence (SEQ ID NO: 304) derived from the coding sequence of SEQ ID NO: 303 shown in **FIG. 303**.

[0331] **FIG. 305** shows a nucleotide sequence (SEQ ID NO: 305) of a native sequence PRO1329 cDNA, wherein SEQ ID NO: 305 is a clone designated herein as "DNA66660-1585".

[0332] **FIG. 306** shows the amino acid sequence (SEQ ID NO: 306) derived from the coding sequence of SEQ ID NO: 305 shown in **FIG. 305**.

[0333] **FIG. 307** shows a nucleotide sequence (SEQ ID NO: 307) of a native sequence PRO1339 cDNA, wherein SEQ ID NO: 307 is a clone designated herein as "DNA66669-1597".

[0334] **FIG. 308** shows the amino acid sequence (SEQ ID NO: 308) derived from the coding sequence of SEQ ID NO: 307 shown in **FIG. 307**.

[0335] **FIG. 309** shows a nucleotide sequence (SEQ ID NO: 309) of a native sequence PRO1342 cDNA, wherein SEQ ID NO: 309 is a clone designated herein as "DNA66674-1599".

[0336] **FIG. 310** shows the amino acid sequence (SEQ ID NO: 310) derived from the coding sequence of SEQ ID NO: 309 shown in **FIG. 309**.

[0337] **FIGS. 311A-311B** show a nucleotide sequence (SEQ ID NO: 311) of a native sequence PRO1487 cDNA, wherein SEQ ID NO: 311 is a clone designated herein as "DNA68836-1656".

[0338] **FIG. 312** shows the amino acid sequence (SEQ ID NO: 312) derived from the coding sequence of SEQ ID NO: 311 shown in **FIGS. 311A-311B**.

[0339] **FIG. 313** shows a nucleotide sequence (SEQ ID NO: 313) of a native sequence PRO3579 cDNA, wherein SEQ ID NO: 313 is a clone designated herein as "DNA68862-2546".

[0340] **FIG. 314** shows the amino acid sequence (SEQ ID NO: 314) derived from the coding sequence of SEQ ID NO: 313 shown in **FIG. 313**.

[0341] **FIG. 315** shows a nucleotide sequence (SEQ ID NO: 315) of a native sequence PRO1472 cDNA, wherein SEQ ID NO: 315 is a clone designated herein as "DNA68866-1644".

[0342] **FIG. 316** shows the amino acid sequence (SEQ ID NO: 316) derived from the coding sequence of SEQ ID NO: 315 shown in **FIG. 315**.

[0343] **FIG. 317** shows a nucleotide sequence (SEQ ID NO: 317) of a native sequence PRO1385 cDNA, wherein SEQ ID NO: 317 is a clone designated herein as "DNA68869-1610".

[0344] **FIG. 318** shows the amino acid sequence (SEQ ID NO: 318) derived from the coding sequence of SEQ ID NO: 317 shown in **FIG. 317**.

[0345] **FIG. 319** shows a nucleotide sequence (SEQ ID NO: 319) of a native sequence PRO1461 cDNA, wherein SEQ ID NO: 319 is a clone designated herein as "DNA68871-1638".

[0346] **FIG. 320** shows the amino acid sequence (SEQ ID NO: 320) derived from the coding sequence of SEQ ID NO: 319 shown in **FIG. 319**.

[0347] **FIG. 321** shows a nucleotide sequence (SEQ ID NO: 321) of a native sequence PRO1429 cDNA, wherein SEQ ID NO: 321 is a clone designated herein as "DNA68879-1631".

[0348] **FIG. 322** shows the amino acid sequence (SEQ ID NO: 322) derived from the coding sequence of SEQ ID NO: 321 shown in **FIG. 321**.

[0349] **FIG. 323** shows a nucleotide sequence (SEQ ID NO: 323) of a native sequence PRO1568 cDNA, wherein SEQ ID NO: 323 is a clone designated herein as "DNA68880-1676".

[0350] **FIG. 324** shows the amino acid sequence (SEQ ID NO: 324) derived from the coding sequence of SEQ ID NO: 323 shown in **FIG. 323**.

[0351] **FIG. 325** shows a nucleotide sequence (SEQ ID NO: 325) of a native sequence PRO1569 cDNA, wherein SEQ ID NO: 325 is a clone designated herein as "DNA68882-1677".

[0352] **FIG. 326** shows the amino acid sequence (SEQ ID NO: 326) derived from the coding sequence of SEQ ID NO: 325 shown in **FIG. 325**.

[0353] **FIG. 327** shows a nucleotide sequence (SEQ ID NO: 327) of a native sequence PRO1753 cDNA, wherein SEQ ID NO: 327 is a clone designated herein as "DNA68883-1691".

[0354] **FIG. 328** shows the amino acid sequence (SEQ ID NO: 328) derived from the coding sequence of SEQ ID NO: 327 shown in **FIG. 327**.

[0355] **FIG. 329** shows a nucleotide sequence (SEQ ID NO: 329) of a native sequence PRO1570 cDNA, wherein SEQ ID NO: 329 is a clone designated herein as "DNA68885-1678".

[0356] **FIG. 330** shows the amino acid sequence (SEQ ID NO: 330) derived from the coding sequence of SEQ ID NO: 329 shown in **FIG. 329**.

[0357] **FIG. 331** shows a nucleotide sequence (SEQ ID NO: 331) of a native sequence PRO1559 cDNA, wherein SEQ ID NO: 331 is a clone designated herein as "DNA68886".

[0358] **FIG. 332** shows the amino acid sequence (SEQ ID NO: 332) derived from the coding sequence of SEQ ID NO: 331 shown in **FIG. 331**.

[0359] **FIG. 333** shows a nucleotide sequence (SEQ ID NO: 333) of a native sequence PRO1486 cDNA, wherein SEQ ID NO: 333 is a clone designated herein as "DNA71180-1655".

[0360] **FIG. 334** shows the amino acid sequence (SEQ ID NO: 334) derived from the coding sequence of SEQ ID NO: 333 shown in **FIG. 333**.

[0361] **FIG. 335** shows a nucleotide sequence (SEQ ID NO: 335) of a native sequence PRO1433 cDNA, wherein SEQ ID NO: 335 is a clone designated herein as "DNA71184-1634".

[0362] **FIG. 336** shows the amino acid sequence (SEQ ID NO: 336) derived from the coding sequence of SEQ ID NO: 335 shown in **FIG. 335**.

[0363] **FIG. 337** shows a nucleotide sequence (SEQ ID NO: 337) of a native sequence PRO1490 cDNA, wherein SEQ ID NO: 337 is a clone designated herein as "DNA71213-1659".

[0364] **FIG. 338** shows the amino acid sequence (SEQ ID NO: 338) derived from the coding sequence of SEQ ID NO: 337 shown in **FIG. 337**.

[0365] **FIG. 339** shows a nucleotide sequence (SEQ ID NO: 339) of a native sequence PRO1482 cDNA, wherein SEQ ID NO: 339 is a clone designated herein as "DNA71234-1651".

[0366] **FIG. 340** shows the amino acid sequence (SEQ ID NO: 340) derived from the coding sequence of SEQ ID NO: 339 shown in **FIG. 339**.

[0367] **FIG. 341** shows a nucleotide sequence (SEQ ID NO: 341) of a native sequence PRO1409 cDNA, wherein SEQ ID NO: 341 is a clone designated herein as "DNA71269-1621".

[0368] **FIG. 342** shows the amino acid sequence (SEQ ID NO: 342) derived from the coding sequence of SEQ ID NO: 341 shown in **FIG. 341**.

[0369] **FIG. 343** shows a nucleotide sequence (SEQ ID NO: 343) of a native sequence PRO1446 cDNA, wherein SEQ ID NO: 343 is a clone designated herein as "DNA71277-1636".

[0370] **FIG. 344** shows the amino acid sequence (SEQ ID NO: 344) derived from the coding sequence of SEQ ID NO: 343 shown in **FIG. 343**.

[0371] **FIG. 345** shows a nucleotide sequence (SEQ ID NO: 345) of a native sequence PRO1604 cDNA, wherein SEQ ID NO: 345 is a clone designated herein as "DNA71286-1687".

[0372] **FIG. 346** shows the amino acid sequence (SEQ ID NO: 346) derived from the coding sequence of SEQ ID NO: 345 shown in **FIG. 345**.

[0373] **FIG. 347** shows a nucleotide sequence (SEQ ID NO: 347) of a native sequence PRO1491 cDNA, wherein SEQ ID NO: 347 is a clone designated herein as "DNA71883-1660".

[0374] **FIG. 348** shows the amino acid sequence (SEQ ID NO: 348) derived from the coding sequence of SEQ ID NO: 347 shown in **FIG. 347**.

[0375] **FIG. 349** shows a nucleotide sequence (SEQ ID NO: 349) of a native sequence PRO1431 cDNA, wherein SEQ ID NO: 349 is a clone designated herein as "DNA73401-1633".

[0376] **FIG. 350** shows the amino acid sequence (SEQ ID NO: 350) derived from the coding sequence of SEQ ID NO: 349 shown in **FIG. 349**.

[0377] **FIGS. 351A-351B** show a nucleotide sequence (SEQ ID NO: 351) of a native sequence PRO1563 cDNA, wherein SEQ ID NO: 351 is a clone designated herein as "DNA73492-1671".

[0378] **FIG. 352** shows the amino acid sequence (SEQ ID NO: 352) derived from the coding sequence of SEQ ID NO: 351 shown in **FIGS. 351A-351B**.

[0379] **FIG. 353** shows a nucleotide sequence (SEQ ID NO: 353) of a native sequence PRO1571 cDNA, wherein SEQ ID NO: 353 is a clone designated herein as "DNA73730-1679".

[0380] **FIG. 354** shows the amino acid sequence (SEQ ID NO: 354) derived from the coding sequence of SEQ ID NO: 353 shown in **FIG. 353**.

[0381] **FIG. 355** shows a nucleotide sequence (SEQ ID NO: 355) of a native sequence PRO1572 cDNA, wherein SEQ ID NO: 355 is a clone designated herein as "DNA73734-1680".

[0382] **FIG. 356** shows the amino acid sequence (SEQ ID NO: 356) derived from the coding sequence of SEQ ID NO: 355 shown in **FIG. 355**.

[0383] **FIG. 357** shows a nucleotide sequence (SEQ ID NO: 357) of a native sequence PRO1573 cDNA, wherein SEQ ID NO: 357 is a clone designated herein as "DNA73735-1681".

[0384] **FIG. 358** shows the amino acid sequence (SEQ ID NO: 358) derived from the coding sequence of SEQ ID NO: 357 shown in **FIG. 357**.

[0385] **FIG. 359** shows a nucleotide sequence (SEQ ID NO: 359) of a native sequence PRO1508 cDNA, wherein SEQ ID NO: 359 is a clone designated herein as "DNA73742-1662".

[0386] **FIG. 360** shows the amino acid sequence (SEQ ID NO: 360) derived from the coding sequence of SEQ ID NO: 359 shown in **FIG. 359**.

[0387] **FIG. 361** shows a nucleotide sequence (SEQ ID NO: 361) of a native sequence PRO1485 cDNA, wherein SEQ ID NO: 361 is a clone designated herein as "DNA73746-1654".

[0388] **FIG. 362** shows the amino acid sequence (SEQ ID NO: 362) derived from the coding sequence of SEQ ID NO: 361 shown in **FIG. 361**.

[0389] **FIG. 363** shows a nucleotide sequence (SEQ ID NO: 363) of a native sequence PRO1564 cDNA, wherein SEQ ID NO: 363 is a clone designated herein as "DNA73760-1672".

[0390] **FIG. 364** shows the amino acid sequence (SEQ ID NO: 364) derived from the coding sequence of SEQ ID NO: 363 shown in **FIG. 363**.

[0391] **FIG. 365** shows a nucleotide sequence (SEQ ID NO: 365) of a native sequence PRO1550 cDNA, wherein SEQ ID NO: 365 is a clone designated herein as "DNA76393-1664".

[0392] **FIG. 366** shows the amino acid sequence (SEQ ID NO: 366) derived from the coding sequence of SEQ ID NO: 365 shown in **FIG. 365**.

[0393] **FIG. 367** shows a nucleotide sequence (SEQ ID NO: 367) of a native sequence PRO1757 cDNA, wherein SEQ ID NO: 367 is a clone designated herein as "DNA76398-1699".

[0394] **FIG. 368** shows the amino acid sequence (SEQ ID NO: 368) derived from the coding sequence of SEQ ID NO: 367 shown in **FIG. 367**.

[0395] **FIG. 369** shows a nucleotide sequence (SEQ ID NO: 369) of a native sequence PRO1758 cDNA, wherein SEQ ID NO: 369 is a clone designated herein as "DNA76399-1700".

[0396] **FIG. 370** shows the amino acid sequence (SEQ ID NO: 370) derived from the coding sequence of SEQ ID NO: 369 shown in **FIG. 369**.

[0397] **FIG. 371** shows a nucleotide sequence (SEQ ID NO: 371) of a native sequence PRO1781 cDNA, wherein SEQ ID NO: 371 is a clone designated herein as "DNA76522-2500".

[0398] **FIG. 372** shows the amino acid sequence (SEQ ID NO: 372) derived from the coding sequence of SEQ ID NO: 371 shown in **FIG. 371**.

[0399] **FIG. 373** shows a nucleotide sequence (SEQ ID NO: 373) of a native sequence PRO1606 cDNA, wherein SEQ ID NO: 373 is a clone designated herein as "DNA76533-1689".

[0400] **FIG. 374** shows the amino acid sequence (SEQ ID NO: 374) derived from the coding sequence of SEQ ID NO: 373 shown in **FIG. 373**.

[0401] **FIG. 375** shows a nucleotide sequence (SEQ ID NO: 375) of a native sequence PRO1784 cDNA, wherein SEQ ID NO: 375 is a clone designated herein as "DNA77303-2502".

[0402] **FIG. 376** shows the amino acid sequence (SEQ ID NO: 376) derived from the coding sequence of SEQ ID NO: 375 shown in **FIG. 375**.

[0403] **FIG. 377** shows a nucleotide sequence (SEQ ID NO: 377) of a native sequence PRO1774 cDNA, wherein SEQ ID NO: 377 is a clone designated herein as "DNA77626-1705".

[0404] **FIG. 378** shows the amino acid sequence (SEQ ID NO: 378) derived from the coding sequence of SEQ ID NO: 377 shown in **FIG. 377**.

[0405] **FIG. 379** shows a nucleotide sequence (SEQ ID NO: 379) of a native sequence PRO1605 cDNA, wherein SEQ ID NO: 379 is a clone designated herein as "DNA77648-1688".

[0406] **FIG. 380** shows the amino acid sequence (SEQ ID NO: 380) derived from the coding sequence of SEQ ID NO: 379 shown in **FIG. 379**.

[0407] **FIG. 381** shows a nucleotide sequence (SEQ ID NO: 381) of a native sequence PRO1928 cDNA, wherein SEQ ID NO: 381 is a clone designated herein as "DNA81754-2532".

[0408] **FIG. 382** shows the amino acid sequence (SEQ ID NO: 382) derived from the coding sequence of SEQ ID NO: 381 shown in **FIG. 381**.

[0409] **FIG. 383** shows a nucleotide sequence (SEQ ID NO: 383) of a native sequence PRO1865 cDNA, wherein SEQ ID NO: 383 is a clone designated herein as "DNA81757-2512".

[0410] **FIG. 384** shows the amino acid sequence (SEQ ID NO: 384) derived from the coding sequence of SEQ ID NO: 383 shown in **FIG. 383**.

[0411] **FIG. 385** shows a nucleotide sequence (SEQ ID NO: 385) of a native sequence PRO1925 cDNA, wherein SEQ ID NO: 385 is a clone designated herein as "DNA82302-2529".

[0412] **FIG. 386** shows the amino acid sequence (SEQ ID NO: 386) derived from the coding sequence of SEQ ID NO: 385 shown in **FIG. 385**.

[0413] **FIG. 387** shows a nucleotide sequence (SEQ ID NO: 387) of a native sequence PRO1926 cDNA, wherein SEQ ID NO: 387 is a clone designated herein as "DNA82340-2530".

[0414] **FIG. 388** shows the amino acid sequence (SEQ ID NO: 388) derived from the coding sequence of SEQ ID NO: 387 shown in **FIG. 387**.

[0415] **FIG. 389** shows a nucleotide sequence (SEQ ID NO: 389) of a native sequence PRO2630 cDNA, wherein SEQ ID NO: 389 is a clone designated herein as "DNA83551".

[0416] **FIG. 390** shows the amino acid sequence (SEQ ID NO: 390) derived from the coding sequence of SEQ ID NO: 389 shown in **FIG. 389**.

[0417] **FIG. 391** shows a nucleotide sequence (SEQ ID NO: 391) of a native sequence PRO3443 cDNA, wherein SEQ ID NO: 391 is a clone designated herein as "DNA87991-2540".

[0418] **FIG. 392** shows the amino acid sequence (SEQ ID NO: 392) derived from the coding sequence of SEQ ID NO: 391 shown in **FIG. 391**.

[0419] **FIG. 393** shows a nucleotide sequence (SEQ ID NO: 393) of a native sequence PRO3301 cDNA, wherein SEQ ID NO: 393 is a clone designated herein as "DNA88002".

[0420] **FIG. 394** shows the amino acid sequence (SEQ ID NO: 394) derived from the coding sequence of SEQ ID NO: 393 shown in **FIG. 393**.

[0421] **FIG. 395** shows a nucleotide sequence (SEQ ID NO: 395) of a native sequence PRO3442 cDNA, wherein SEQ ID NO: 395 is a clone designated herein as "DNA92238-2539".

[0422] **FIG. 396** shows the amino acid sequence (SEQ ID NO: 396) derived from the coding sequence of SEQ ID NO: 395 shown in **FIG. 395**.

[0423] **FIG. 397** shows a nucleotide sequence (SEQ ID NO: 397) of a native sequence PRO4978 cDNA, wherein SEQ ID NO: 397 is a clone designated herein as "DNA95930".

[0424] **FIG. 398** shows the amino acid sequence (SEQ ID NO: 398) derived from the coding sequence of SEQ ID NO: 397 shown in **FIG. 397**.

[0425] **FIG. 399** shows a nucleotide sequence (SEQ ID NO: 399) of a native sequence PRO5801 cDNA, wherein SEQ ID NO: 399 is a clone designated herein as "DNA115291-2681".

[0426] **FIG. 400** shows the amino acid sequence (SEQ ID NO: 400) derived from the coding sequence of SEQ ID NO: 399 shown in **FIG. 399**.

[0427] **FIG. 401** shows a nucleotide sequence (SEQ ID NO: 401) of a native sequence PRO19630 cDNA, wherein SEQ ID NO: 401 is a clone designated herein as "DNA23336-2861".

[0428] **FIG. 402** shows the amino acid sequence (SEQ ID NO: 402) derived from the coding sequence of SEQ ID NO: 401 shown in **FIG. 401**.

[0429] **FIG. 403** shows a nucleotide sequence (SEQ ID NO: 403) of a native sequence PRO203 cDNA, wherein SEQ ID NO: 403 is a clone designated herein as "DNA30862-1396".

[0430] **FIG. 404** shows the amino acid sequence (SEQ ID NO: 404) derived from the coding sequence of SEQ ID NO: 403 shown in **FIG. 403**.

[0431] **FIG. 405** shows a nucleotide sequence (SEQ ID NO: 405) of a native sequence PRO204 cDNA, wherein SEQ ID NO: 405 is a clone designated herein as "DNA30871-1157".

[0432] **FIG. 406** shows the amino acid sequence (SEQ ID NO: 406) derived from the coding sequence of SEQ ID NO: 405 shown in **FIG. 405**.

[0433] **FIG. 407** shows a nucleotide sequence (SEQ ID NO: 407) of a native sequence PRO210 cDNA, wherein SEQ ID NO: 407 is a clone designated herein as "DNA32279-1131".

[0434] **FIG. 408** shows the amino acid sequence (SEQ ID NO: 408) derived from the coding sequence of SEQ ID NO: 407 shown in **FIG. 407**.

[0435] **FIG. 409** shows a nucleotide sequence (SEQ ID NO: 409) of a native sequence PRO223 cDNA, wherein SEQ ID NO: 409 is a clone designated herein as "DNA33206-1165".

[0436] **FIG. 410** shows the amino acid sequence (SEQ ID NO: 410) derived from the coding sequence of SEQ ID NO: 409 shown in **FIG. 409**.

[0437] **FIG. 411** shows a nucleotide sequence (SEQ ID NO: 411) of a native sequence PRO247 cDNA, wherein SEQ ID NO: 411 is a clone designated herein as "DNA35673-1201".

[0438] **FIG. 412** shows the amino acid sequence (SEQ ID NO: 412) derived from the coding sequence of SEQ ID NO: 411 shown in **FIG. 411**.

[0439] **FIG. 413** shows a nucleotide sequence (SEQ ID NO: 413) of a native sequence PRO358 cDNA, wherein SEQ ID NO: 413 is a clone designated herein as "DNA47361-1154-2".

[0440] **FIG. 414** shows the amino acid sequence (SEQ ID NO: 414) derived from the coding sequence of SEQ ID NO: 413 shown in **FIG. 413**.

[0441] **FIG. 415** shows a nucleotide sequence (SEQ ID NO: 415) of a native sequence PRO724 cDNA, wherein SEQ ID NO: 415 is a clone designated herein as "DNA49631-1328".

[0442] **FIG. 416** shows the amino acid sequence (SEQ ID NO: 416) derived from the coding sequence of SEQ ID NO: 415 shown in **FIG. 415**.

[0443] **FIG. 417** shows a nucleotide sequence (SEQ ID NO: 417) of a native sequence PRO868 cDNA, wherein SEQ ID NO: 417 is a clone designated herein as "DNA52594-1270".

[0444] **FIG. 418** shows the amino acid sequence (SEQ ID NO: 418) derived from the coding sequence of SEQ ID NO: 417 shown in **FIG. 417**.

[0445] **FIG. 419** shows a nucleotide sequence (SEQ ID NO: 419) of a native sequence PRO740 cDNA, wherein SEQ ID NO: 419 is a clone designated herein as "DNA55800-1263".

[0446] FIG. 420 shows the amino acid sequence (SEQ ID NO: 420) derived from the coding sequence of SEQ ID NO: 419 shown in FIG. 419.

[0447] FIG. 421 shows a nucleotide sequence (SEQ ID NO: 421) of a native sequence PRO1478 cDNA, wherein SEQ ID NO: 421 is a clone designated herein as "DNA56531-1648".

[0448] FIG. 422 shows the amino acid sequence (SEQ ID NO: 422) derived from the coding sequence of SEQ ID NO: 421 shown in FIG. 421.

[0449] FIG. 423 shows a nucleotide sequence (SEQ ID NO: 423) of a native sequence PRO162 cDNA, wherein SEQ ID NO: 423 is a clone designated herein as "DNA56965-1356".

[0450] FIG. 424 shows the amino acid sequence (SEQ ID NO: 424) derived from the coding sequence of SEQ ID NO: 423 shown in FIG. 423.

[0451] FIG. 425 shows a nucleotide sequence (SEQ ID NO: 425) of a native sequence PRO828 cDNA, wherein SEQ ID NO: 425 is a clone designated herein as "DNA57037-1444".

[0452] FIG. 426 shows the amino acid sequence (SEQ ID NO: 426) derived from the coding sequence of SEQ ID NO: 425 shown in FIG. 425.

[0453] FIG. 427 shows a nucleotide sequence (SEQ ID NO: 427) of a native sequence PRO819 cDNA, wherein SEQ ID NO: 427 is a clone designated herein as "DNA57695-1340".

[0454] FIG. 428 shows the amino acid sequence (SEQ ID NO: 428) derived from the coding sequence of SEQ ID NO: 427 shown in FIG. 427.

[0455] FIG. 429 shows a nucleotide sequence (SEQ ID NO: 429) of a native sequence PRO813 cDNA, wherein SEQ ID NO: 429 is a clone designated herein as "DNA57834-1339".

[0456] FIG. 430 shows the amino acid sequence (SEQ ID NO: 430) derived from the coding sequence of SEQ ID NO: 429 shown in FIG. 429.

[0457] FIG. 431 shows a nucleotide sequence (SEQ ID NO: 431) of a native sequence PRO1194 cDNA, wherein SEQ ID NO: 431 is a clone designated herein as "DNA57841-1522".

[0458] FIG. 432 shows the amino acid sequence (SEQ ID NO: 432) derived from the coding sequence of SEQ ID NO: 431 shown in FIG. 431.

[0459] FIG. 433 shows a nucleotide sequence (SEQ ID NO: 433) of a native sequence PRO887 cDNA, wherein SEQ ID NO: 433 is a clone designated herein as "DNA58130".

[0460] FIG. 434 shows the amino acid sequence (SEQ ID NO: 434) derived from the coding sequence of SEQ ID NO: 433 shown in FIG. 433.

[0461] FIG. 435 shows a nucleotide sequence (SEQ ID NO: 435) of a native sequence PRO1071 cDNA, wherein SEQ ID NO: 435 is a clone designated herein as "DNA58847-1383".

[0462] FIG. 436 shows the amino acid sequence (SEQ ID NO: 436) derived from the coding sequence of SEQ ID NO: 435 shown in FIG. 435.

[0463] FIG. 437 shows a nucleotide sequence (SEQ ID NO: 437) of a native sequence PRO1029 cDNA, wherein SEQ ID NO: 437 is a clone designated herein as "DNA59493-1420".

[0464] FIG. 438 shows the amino acid sequence (SEQ ID NO: 438) derived from the coding sequence of SEQ ID NO: 437 shown in FIG. 437.

[0465] FIG. 439 shows a nucleotide sequence (SEQ ID NO: 439) of a native sequence PRO1190 cDNA, wherein SEQ ID NO: 439 is a clone designated herein as "DNA59586-1520".

[0466] FIG. 440 shows the amino acid sequence (SEQ ID NO: 440) derived from the coding sequence of SEQ ID NO: 439 shown in FIG. 439.

[0467] FIG. 441 shows a nucleotide sequence (SEQ ID NO: 441) of a native sequence PRO4334 cDNA, wherein SEQ ID NO: 441 is a clone designated herein as "DNA59608-2577".

[0468] FIG. 442 shows the amino acid sequence (SEQ ID NO: 442) derived from the coding sequence of SEQ ID NO: 441 shown in FIG. 441.

[0469] FIG. 443 shows a nucleotide sequence (SEQ ID NO: 443) of a native sequence PRO1155 cDNA, wherein SEQ ID NO: 443 is a clone designated herein as "DNA59849-1504".

[0470] FIG. 444 shows the amino acid sequence (SEQ ID NO: 444) derived from the coding sequence of SEQ ID NO: 443 shown in FIG. 443.

[0471] FIG. 445 shows a nucleotide sequence (SEQ ID NO: 445) of a native sequence PRO1157 cDNA, wherein SEQ ID NO: 445 is a clone designated herein as "DNA60292-1506".

[0472] FIG. 446 shows the amino acid sequence (SEQ ID NO: 446) derived from the coding sequence of SEQ ID NO: 445 shown in FIG. 445.

[0473] FIG. 447 shows a nucleotide sequence (SEQ ID NO: 447) of a native sequence PRO1122 cDNA, wherein SEQ ID NO: 447 is a clone designated herein as "DNA62377-1381-1".

[0474] FIG. 448 shows the amino acid sequence (SEQ ID NO: 448) derived from the coding sequence of SEQ ID NO: 447 shown in FIG. 447.

[0475] FIG. 449 shows a nucleotide sequence (SEQ ID NO: 449) of a native sequence PRO1183 cDNA, wherein SEQ ID NO: 449 is a clone designated herein as "DNA62880-1513".

[0476] FIG. 450 shows the amino acid sequence (SEQ ID NO: 450) derived from the coding sequence of SEQ ID NO: 449 shown in FIG. 449.

[0477] FIG. 451 shows a nucleotide sequence (SEQ ID NO: 451) of a native sequence PRO1337 cDNA, wherein SEQ ID NO: 451 is a clone designated herein as "DNA66672-1586".

[0478] **FIG. 452** shows the amino acid sequence (SEQ ID NO: 452) derived from the coding sequence of SEQ ID NO: 451 shown in **FIG. 451**.

[0479] **FIG. 453** shows a nucleotide sequence (SEQ ID NO: 453) of a native sequence PRO1480 cDNA, wherein SEQ ID NO: 453 is a clone designated herein as "DNA67962-1649".

[0480] **FIG. 454** shows the amino acid sequence (SEQ ID NO: 454) derived from the coding sequence of SEQ ID NO: 453 shown in **FIG. 453**.

[0481] **FIG. 455** shows a nucleotide sequence (SEQ ID NO: 455) of a native sequence PRO19645 cDNA, wherein SEQ ID NO: 455 is a clone designated herein as "DNA69555-2867".

[0482] **FIG. 456** shows the amino acid sequence (SEQ ID NO: 456) derived from the coding sequence of SEQ ID NO: 455 shown in **FIG. 455**.

[0483] **FIG. 457** shows a nucleotide sequence (SEQ ID NO: 457) of a native sequence PRO9782 cDNA, wherein SEQ ID NO: 457 is a clone designated herein as "DNA71162-2764".

[0484] **FIG. 458** shows the amino acid sequence (SEQ ID NO: 458) derived from the coding sequence of SEQ ID NO: 457 shown in **FIG. 457**.

[0485] **FIG. 459** shows a nucleotide sequence (SEQ ID NO: 459) of a native sequence PRO1419 cDNA, wherein SEQ ID NO: 459 is a clone designated herein as "DNA71290-1630".

[0486] **FIG. 460** shows the amino acid sequence (SEQ ID NO: 460) derived from the coding sequence of SEQ ID NO: 459 shown in **FIG. 459**.

[0487] **FIG. 461** shows a nucleotide sequence (SEQ ID NO: 461) of a native sequence PRO1575 cDNA, wherein SEQ ID NO: 461 is a clone designated herein as "DNA76401-1683".

[0488] **FIG. 462** shows the amino acid sequence (SEQ ID NO: 462) derived from the coding sequence of SEQ ID NO: 461 shown in **FIG. 461**.

[0489] **FIG. 463** shows a nucleotide sequence (SEQ ID NO: 463) of a native sequence PRO1567 cDNA, wherein SEQ ID NO: 463 is a clone designated herein as "DNA76541-1675".

[0490] **FIG. 464** shows the amino acid sequence (SEQ ID NO: 464) derived from the coding sequence of SEQ ID NO: 463 shown in **FIG. 463**.

[0491] **FIG. 465** shows a nucleotide sequence (SEQ ID NO: 465) of a native sequence PRO1891 cDNA, wherein SEQ ID NO: 465 is a clone designated herein as "DNA76788-2526".

[0492] **FIG. 466** shows the amino acid sequence (SEQ ID NO: 466) derived from the coding sequence of SEQ ID NO: 465 shown in **FIG. 465**.

[0493] **FIG. 467** shows a nucleotide sequence (SEQ ID NO: 467) of a native sequence PRO1889 cDNA, wherein SEQ ID NO: 467 is a clone designated herein as "DNA77623-2524".

[0494] **FIG. 468** shows the amino acid sequence (SEQ ID NO: 468) derived from the coding sequence of SEQ ID NO: 467 shown in **FIG. 467**.

[0495] **FIG. 469** shows a nucleotide sequence (SEQ ID NO: 469) of a native sequence PRO1785 cDNA, wherein SEQ ID NO: 469 is a clone designated herein as "DNA80136-2503".

[0496] **FIG. 470** shows the amino acid sequence (SEQ ID NO: 470) derived from the coding sequence of SEQ ID NO: 469 shown in **FIG. 469**.

[0497] **FIG. 471** shows a nucleotide sequence (SEQ ID NO: 471) of a native sequence PRO6003 cDNA, wherein SEQ ID NO: 471 is a clone designated herein as "DNA83568-2692".

[0498] **FIG. 472** shows the amino acid sequence (SEQ ID NO: 472) derived from the coding sequence of SEQ ID NO: 471 shown in **FIG. 471**.

[0499] **FIG. 473** shows a nucleotide sequence (SEQ ID NO: 473) of a native sequence PRO4333 cDNA, wherein SEQ ID NO: 473 is a clone designated herein as "DNA84210-2576".

[0500] **FIG. 474** shows the amino acid sequence (SEQ ID NO: 474) derived from the coding sequence of SEQ ID NO: 473 shown in **FIG. 473**.

[0501] **FIG. 475** shows a nucleotide sequence (SEQ ID NO: 475) of a native sequence PRO4356 cDNA, wherein SEQ ID NO: 475 is a clone designated herein as "DNA86576-2595".

[0502] **FIG. 476** shows the amino acid sequence (SEQ ID NO: 476) derived from the coding sequence of SEQ ID NO: 475 shown in **FIG. 475**.

[0503] **FIG. 477** shows a nucleotide sequence (SEQ ID NO: 477) of a native sequence PRO4352 cDNA, wherein SEQ ID NO: 477 is a clone designated herein as "DNA87976-2593".

[0504] **FIG. 478** shows the amino acid sequence (SEQ ID NO: 478) derived from the coding sequence of SEQ ID NO: 477 shown in **FIG. 477**.

[0505] **FIG. 479** shows a nucleotide sequence (SEQ ID NO: 479) of a native sequence PRO4354 cDNA, wherein SEQ ID NO: 479 is a clone designated herein as "DNA92256-2596".

[0506] **FIG. 480** shows the amino acid sequence (SEQ ID NO: 480) derived from the coding sequence of SEQ ID NO: 479 shown in **FIG. 479**.

[0507] **FIG. 481** shows a nucleotide sequence (SEQ ID NO: 481) of a native sequence PRO4369 cDNA, wherein SEQ ID NO: 481 is a clone designated herein as "DNA92289-2598".

[0508] **FIG. 482** shows the amino acid sequence (SEQ ID NO: 482) derived from the coding sequence of SEQ ID NO: 481 shown in **FIG. 481**.

[0509] **FIG. 483** shows a nucleotide sequence (SEQ ID NO: 483) of a native sequence PRO6030 cDNA, wherein SEQ ID NO: 483 is a clone designated herein as "DNA96850-2705".

[0510] **FIG. 484** shows the amino acid sequence (SEQ ID NO: 484) derived from the coding sequence of SEQ ID NO: 483 shown in **FIG. 483**.

[0511] **FIG. 485** shows a nucleotide sequence (SEQ ID NO: 485) of a native sequence PRO4433 cDNA, wherein SEQ ID NO: 485 is a clone designated herein as "DNA96855-2629".

[0512] **FIG. 486** shows the amino acid sequence (SEQ ID NO: 486) derived from the coding sequence of SEQ ID NO: 485 shown in **FIG. 485**.

[0513] **FIG. 487** shows a nucleotide sequence (SEQ ID NO: 487) of a native sequence PRO4424 cDNA, wherein SEQ ID NO: 487 is a clone designated herein as "DNA96857-2636".

[0514] **FIG. 488** shows the amino acid sequence (SEQ ID NO: 488) derived from the coding sequence of SEQ ID NO: 487 shown in **FIG. 487**.

[0515] **FIG. 489** shows a nucleotide sequence (SEQ ID NO: 489) of a native sequence PRO6017 cDNA, wherein SEQ ID NO: 489 is a clone designated herein as "DNA96860-2700".

[0516] **FIG. 490** shows the amino acid sequence (SEQ ID NO: 490) derived from the coding sequence of SEQ ID NO: 489 shown in **FIG. 489**.

[0517] **FIG. 491** shows a nucleotide sequence (SEQ ID NO: 491) of a native sequence PRO19563 cDNA, wherein SEQ ID NO: 491 is a clone designated herein as "DNA96861-2844".

[0518] **FIG. 492** shows the amino acid sequence (SEQ ID NO: 492) derived from the coding sequence of SEQ ID NO: 491 shown in **FIG. 491**.

[0519] **FIG. 493** shows a nucleotide sequence (SEQ ID NO: 493) of a native sequence PRO6015 cDNA, wherein SEQ ID NO: 493 is a clone designated herein as "DNA96866-2698".

[0520] **FIG. 494** shows the amino acid sequence (SEQ ID NO: 494) derived from the coding sequence of SEQ ID NO: 493 shown in **FIG. 493**.

[0521] **FIG. 495** shows a nucleotide sequence (SEQ ID NO: 495) of a native sequence PRO5779 cDNA, wherein SEQ ID NO: 495 is a clone designated herein as "DNA96870-2676".

[0522] **FIG. 496** shows the amino acid sequence (SEQ ID NO: 496) derived from the coding sequence of SEQ ID NO: 495 shown in **FIG. 495**.

[0523] **FIG. 497** shows a nucleotide sequence (SEQ ID NO: 497) of a native sequence PRO5776 cDNA, wherein SEQ ID NO: 497 is a clone designated herein as "DNA96872-2674".

[0524] **FIG. 498** shows the amino acid sequence (SEQ ID NO: 498) derived from the coding sequence of SEQ ID NO: 497 shown in **FIG. 497**.

[0525] **FIG. 499** shows a nucleotide sequence (SEQ ID NO: 499) of a native sequence PRO4430 cDNA, wherein SEQ ID NO: 499 is a clone designated herein as "DNA96878-2626".

[0526] **FIG. 500** shows the amino acid sequence (SEQ ID NO: 500) derived from the coding sequence of SEQ ID NO: 499 shown in **FIG. 499**.

[0527] **FIG. 501** shows a nucleotide sequence (SEQ ID NO: 501) of a native sequence PRO4421 cDNA, wherein SEQ ID NO: 501 is a clone designated herein as "DNA96879-2619".

[0528] **FIG. 502** shows the amino acid sequence (SEQ ID NO: 502) derived from the coding sequence of SEQ ID NO: 501 shown in **FIG. 501**.

[0529] **FIG. 503** shows a nucleotide sequence (SEQ ID NO: 503) of a native sequence PRO4499 cDNA, wherein SEQ ID NO: 503 is a clone designated herein as "DNA96889-2641".

[0530] **FIG. 504** shows the amino acid sequence (SEQ ID NO: 504) derived from the coding sequence of SEQ ID NO: 503 shown in **FIG. 503**.

[0531] **FIG. 505** shows a nucleotide sequence (SEQ ID NO: 505) of a native sequence PRO4423 cDNA, wherein SEQ ID NO: 505 is a clone designated herein as "DNA96893-2621".

[0532] **FIG. 506** shows the amino acid sequence (SEQ ID NO: 506) derived from the coding sequence of SEQ ID NO: 505 shown in **FIG. 505**.

[0533] **FIG. 507** shows a nucleotide sequence (SEQ ID NO: 507) of a native sequence PRO5998 cDNA, wherein SEQ ID NO: 507 is a clone designated herein as "DNA96897-2688".

[0534] **FIG. 508** shows the amino acid sequence (SEQ ID NO: 508) derived from the coding sequence of SEQ ID NO: 507 shown in **FIG. 507**.

[0535] **FIG. 509** shows a nucleotide sequence (SEQ ID NO: 509) of a native sequence PRO4501 cDNA, wherein SEQ ID NO: 509 is a clone designated herein as "DNA98564-2643".

[0536] **FIG. 510** shows the amino acid sequence (SEQ ID NO: 510) derived from the coding sequence of SEQ ID NO: 509 shown in **FIG. 509**.

[0537] **FIG. 511** shows a nucleotide sequence (SEQ ID NO: 511) of a native sequence PRO6240 cDNA, wherein SEQ ID NO: 511 is a clone designated herein as "DNA107443-2718".

[0538] **FIG. 512** shows the amino acid sequence (SEQ ID NO: 512) derived from the coding sequence of SEQ ID NO: 511 shown in **FIG. 511**.

[0539] **FIG. 513** shows a nucleotide sequence (SEQ ID NO: 513) of a native sequence PRO6245 cDNA, wherein SEQ ID NO: 513 is a clone designated herein as "DNA107786-2723".

[0540] **FIG. 514** shows the amino acid sequence (SEQ ID NO: 514) derived from the coding sequence of SEQ ID NO: 513 shown in **FIG. 513**.

[0541] **FIG. 515** shows a nucleotide sequence (SEQ ID NO: 515) of a native sequence PRO6175 cDNA, wherein SEQ ID NO: 515 is a clone designated herein as "DNA108682-2712".

[0542] **FIG. 516** shows the amino acid sequence (SEQ ID NO: 516) derived from the coding sequence of SEQ ID NO: 515 shown in **FIG. 515**.

[0543] **FIG. 517** shows a nucleotide sequence (SEQ ID NO: 517) of a native sequence PRO9742 cDNA, wherein SEQ ID NO: 517 is a clone designated herein as "DNA108684-2761".

[0544] **FIG. 518** shows the amino acid sequence (SEQ ID NO: 518) derived from the coding sequence of SEQ ID NO: 517 shown in **FIG. 517**.

[0545] **FIG. 519** shows a nucleotide sequence (SEQ ID NO: 519) of a native sequence PRO7179 cDNA, wherein SEQ ID NO: 519 is a clone designated herein as "DNA108701-2749".

[0546] **FIG. 520** shows the amino acid sequence (SEQ ID NO: 520) derived from the coding sequence of SEQ ID NO: 519 shown in **FIG. 519**.

[0547] **FIG. 521** shows a nucleotide sequence (SEQ ID NO: 521) of a native sequence PRO6239 cDNA, wherein SEQ ID NO: 521 is a clone designated herein as "DNA108720-2717".

[0548] **FIG. 522** shows the amino acid sequence (SEQ ID NO: 522) derived from the coding sequence of SEQ ID NO: 521 shown in **FIG. 521**.

[0549] **FIG. 523** shows a nucleotide sequence (SEQ ID NO: 523) of a native sequence PRO6493 cDNA, wherein SEQ ID NO: 523 is a clone designated herein as "DNA108726-2729".

[0550] **FIG. 524** shows the amino acid sequence (SEQ ID NO: 524) derived from the coding sequence of SEQ ID NO: 523 shown in **FIG. 523**.

[0551] **FIGS. 525A-525B** show a nucleotide sequence (SEQ ID NO: 525) of a native sequence PRO9741 cDNA, wherein SEQ ID NO: 525 is a clone designated herein as "DNA108728-2760".

[0552] **FIG. 526** shows the amino acid sequence (SEQ ID NO: 526) derived from the coding sequence of SEQ ID NO: 525 shown in **FIGS. 525A-525B**.

[0553] **FIG. 527** shows a nucleotide sequence (SEQ ID NO: 527) of a native sequence PRO9822 cDNA, wherein SEQ ID NO: 527 is a clone designated herein as "DNA108738-2767".

[0554] **FIG. 528** shows the amino acid sequence (SEQ ID NO: 528) derived from the coding sequence of SEQ ID NO: 527 shown in **FIG. 527**.

[0555] **FIG. 529** shows a nucleotide sequence (SEQ ID NO: 529) of a native sequence PRO6244 cDNA, wherein SEQ ID NO: 529 is a clone designated herein as "DNA108743-2722".

[0556] **FIG. 530** shows the amino acid sequence (SEQ ID NO: 530) derived from the coding sequence of SEQ ID NO: 529 shown in **FIG. 529**.

[0557] **FIG. 531** shows a nucleotide sequence (SEQ ID NO: 531) of a native sequence PRO9740 cDNA, wherein SEQ ID NO: 531 is a clone designated herein as "DNA108758-2759".

[0558] **FIG. 532** shows the amino acid sequence (SEQ ID NO: 532) derived from the coding sequence of SEQ ID NO: 531 shown in **FIG. 531**.

[0559] **FIG. 533** shows a nucleotide sequence (SEQ ID NO: 533) of a native sequence PRO9739 cDNA, wherein SEQ ID NO: 533 is a clone designated herein as "DNA108765-2758".

[0560] **FIG. 534** shows the amino acid sequence (SEQ ID NO: 534) derived from the coding sequence of SEQ ID NO: 533 shown in **FIG. 533**.

[0561] **FIG. 535** shows a nucleotide sequence (SEQ ID NO: 535) of a native sequence PRO7177 cDNA, wherein SEQ ID NO: 535 is a clone designated herein as "DNA108783-2747".

[0562] **FIG. 536** shows the amino acid sequence (SEQ ID NO: 536) derived from the coding sequence of SEQ ID NO: 535 shown in **FIG. 535**.

[0563] **FIG. 537** shows a nucleotide sequence (SEQ ID NO: 537) of a native sequence PRO7178 cDNA, wherein SEQ ID NO: 537 is a clone designated herein as "DNA108789-2748".

[0564] **FIG. 538** shows the amino acid sequence (SEQ ID NO: 538) derived from the coding sequence of SEQ ID NO: 537 shown in **FIG. 537**.

[0565] **FIG. 539** shows a nucleotide sequence (SEQ ID NO: 539) of a native sequence PRO6246 cDNA, wherein SEQ ID NO: 539 is a clone designated herein as "DNA108806-2724".

[0566] **FIG. 540** shows the amino acid sequence (SEQ ID NO: 540) derived from the coding sequence of SEQ ID NO: 539 shown in **FIG. 539**.

[0567] **FIG. 541** shows a nucleotide sequence (SEQ ID NO: 541) of a native sequence PRO6241 cDNA, wherein SEQ ID NO: 541 is a clone designated herein as "DNA108936-2719".

[0568] **FIG. 542** shows the amino acid sequence (SEQ ID NO: 542) derived from the coding sequence of SEQ ID NO: 541 shown in **FIG. 541**.

[0569] **FIG. 543** shows a nucleotide sequence (SEQ ID NO: 543) of a native sequence PRO9835 cDNA, wherein SEQ ID NO: 543 is a clone designated herein as "DNA119510-2771".

[0570] **FIG. 544** shows the amino acid sequence (SEQ ID NO: 544) derived from the coding sequence of SEQ ID NO: 543 shown in **FIG. 543**.

[0571] **FIG. 545** shows a nucleotide sequence (SEQ ID NO: 545) of a native sequence PRO9857 cDNA, wherein SEQ ID NO: 545 is a clone designated herein as "DNA119517-2778".

[0572] **FIG. 546** shows the amino acid sequence (SEQ ID NO: 546) derived from the coding sequence of SEQ ID NO: 545 shown in **FIG. 545**.

[0573] **FIG. 547** shows a nucleotide sequence (SEQ ID NO: 547) of a native sequence PRO7436 cDNA, wherein SEQ ID NO: 547 is a clone designated herein as "DNA119535-2756".

[0574] **FIG. 548** shows the amino acid sequence (SEQ ID NO: 548) derived from the coding sequence of SEQ ID NO: 547 shown in **FIG. 547**.

[0575] **FIG. 549** shows a nucleotide sequence (SEQ ID NO: 549) of a native sequence PRO9856 cDNA, wherein SEQ ID NO: 549 is a clone designated herein as "DNA119537-2777".

[0576] **FIG. 550** shows the amino acid sequence (SEQ ID NO: 550) derived from the coding sequence of SEQ ID NO: 549 shown in **FIG. 549**.

[0577] **FIG. 551** shows a nucleotide sequence (SEQ ID NO: 551) of a native sequence PRO19605 cDNA, wherein SEQ ID NO: 551 is a clone designated herein as "DNA19714-2851".

[0578] **FIG. 552** shows the amino acid sequence (SEQ ID NO: 552) derived from the coding sequence of SEQ ID NO: 551 shown in **FIG. 551**.

[0579] **FIG. 553** shows a nucleotide sequence (SEQ ID NO: 553) of a native sequence PRO9859 cDNA, wherein SEQ ID NO: 553 is a clone designated herein as "DNA125170-2780".

[0580] **FIG. 554** shows the amino acid sequence (SEQ ID NO: 554) derived from the coding sequence of SEQ ID NO: 553 shown in **FIG. 553**.

[0581] **FIG. 555** shows a nucleotide sequence (SEQ ID NO: 555) of a native sequence PRO12970 cDNA, wherein SEQ ID NO: 555 is a clone designated herein as "DNA129594-2841".

[0582] **FIG. 556** shows the amino acid sequence (SEQ ID NO: 556) derived from the coding sequence of SEQ ID NO: 555 shown in **FIG. 555**.

[0583] **FIG. 557** shows a nucleotide sequence (SEQ ID NO: 557) of a native sequence PRO19626 cDNA, wherein SEQ ID NO: 557 is a clone designated herein as "DNA129793-2857".

[0584] **FIG. 558** shows the amino acid sequence (SEQ ID NO: 558) derived from the coding sequence of SEQ ID NO: 557 shown in **FIG. 557**.

[0585] **FIG. 559** shows a nucleotide sequence (SEQ ID NO: 559) of a native sequence PRO9833 cDNA, wherein SEQ ID NO: 559 is a clone designated herein as "DNA130809-2769".

[0586] **FIG. 560** shows the amino acid sequence (SEQ ID NO: 560) derived from the coding sequence of SEQ ID NO: 559 shown in **FIG. 559**.

[0587] **FIG. 561** shows a nucleotide sequence (SEQ ID NO: 561) of a native sequence PRO19670 cDNA, wherein SEQ ID NO: 561 is a clone designated herein as "DNA131639-2874".

[0588] **FIG. 562** shows the amino acid sequence (SEQ ID NO: 562) derived from the coding sequence of SEQ ID NO: 561 shown in **FIG. 561**.

[0589] **FIG. 563** shows a nucleotide sequence (SEQ ID NO: 563) of a native sequence PRO19624 cDNA, wherein SEQ ID NO: 563 is a clone designated herein as "DNA131649-2855".

[0590] **FIG. 564** shows the amino acid sequence (SEQ ID NO: 564) derived from the coding sequence of SEQ ID NO: 563 shown in **FIG. 563**.

[0591] **FIG. 565** shows a nucleotide sequence (SEQ ID NO: 565) of a native sequence PRO19680 cDNA, wherein SEQ ID NO: 565 is a clone designated herein as "DNA131652-2876".

[0592] **FIG. 566** shows the amino acid sequence (SEQ ID NO: 566) derived from the coding sequence of SEQ ID NO: 565 shown in **FIG. 565**.

[0593] **FIG. 567** shows a nucleotide sequence (SEQ ID NO: 567) of a native sequence PRO19675 cDNA, wherein SEQ ID NO: 567 is a clone designated herein as "DNA131658-2875".

[0594] **FIG. 568** shows the amino acid sequence (SEQ ID NO: 568) derived from the coding sequence of SEQ ID NO: 567 shown in **FIG. 567**.

[0595] **FIG. 569** shows a nucleotide sequence (SEQ ID NO: 569) of a native sequence PRO9834 cDNA, wherein SEQ ID NO: 569 is a clone designated herein as "DNA132162-2770".

[0596] **FIG. 570** shows the amino acid sequence (SEQ ID NO: 570) derived from the coding sequence of SEQ ID NO: 569 shown in **FIG. 569**.

[0597] **FIG. 571** shows a nucleotide sequence (SEQ ID NO: 571) of a native sequence PRO9744 cDNA, wherein SEQ ID NO: 571 is a clone designated herein as "DNA136110-2763".

[0598] **FIG. 572** shows the amino acid sequence (SEQ ID NO: 572) derived from the coding sequence of SEQ ID NO: 571 shown in **FIG. 571**.

[0599] **FIG. 573** shows a nucleotide sequence (SEQ ID NO: 573) of a native sequence PRO19644 cDNA, wherein SEQ ID NO: 573 is a clone designated herein as "DNA139592-2866".

[0600] **FIG. 574** shows the amino acid sequence (SEQ ID NO: 574) derived from the coding sequence of SEQ ID NO: 573 shown in **FIG. 573**.

[0601] **FIG. 575** shows a nucleotide sequence (SEQ ID NO: 575) of a native sequence PRO19625 cDNA, wherein SEQ ID NO: 575 is a clone designated herein as "DNA139608-2856".

[0602] **FIG. 576** shows the amino acid sequence (SEQ ID NO: 576) derived from the coding sequence of SEQ ID NO: 575 shown in **FIG. 575**.

[0603] **FIG. 577** shows a nucleotide sequence (SEQ ID NO: 577) of a native sequence PRO19597 cDNA, wherein SEQ ID NO: 577 is a clone designated herein as "DNA143292-2848".

[0604] **FIG. 578** shows the amino acid sequence (SEQ ID NO: 578) derived from the coding sequence of SEQ ID NO: 577 shown in **FIG. 577**.

[0605] **FIG. 579** shows a nucleotide sequence (SEQ ID NO: 579) of a native sequence PRO16090 cDNA, wherein SEQ ID NO: 579 is a clone designated herein as "DNA144844-2843".

[0606] **FIG. 580** shows the amino acid sequence (SEQ ID NO: 580) derived from the coding sequence of SEQ ID NO: 579 shown in **FIG. 579**.

[0607] **FIG. 581** shows a nucleotide sequence (SEQ ID NO: 581) of a native sequence PRO19576 cDNA, wherein SEQ ID NO: 581 is a clone designated herein as "DNA144857-2845".

[0608] **FIG. 582** shows the amino acid sequence (SEQ ID NO: 582) derived from the coding sequence of SEQ ID NO: 581 shown in **FIG. 581**.

[0609] **FIG. 583** shows a nucleotide sequence (SEQ ID NO: 583) of a native sequence PRO19646 cDNA, wherein SEQ ID NO: 583 is a clone designated herein as "DNA145841-2868".

[0610] **FIG. 584** shows the amino acid sequence (SEQ ID NO: 584) derived from the coding sequence of SEQ ID NO: 583 shown in **FIG. 583**.

[0611] **FIG. 585** shows a nucleotide sequence (SEQ ID NO: 585) of a native sequence PRO19814 cDNA, wherein SEQ ID NO: 585 is a clone designated herein as "DNA148004-2882".

[0612] **FIG. 586** shows the amino acid sequence (SEQ ID NO: 586) derived from the coding sequence of SEQ ID NO: 585 shown in **FIG. 585**.

[0613] **FIG. 587** shows a nucleotide sequence (SEQ ID NO: 587) of a native sequence PRO19669 cDNA, wherein SEQ ID NO: 587 is a clone designated herein as "DNA149893-2873".

[0614] **FIG. 588** shows the amino acid sequence (SEQ ID NO: 588) derived from the coding sequence of SEQ ID NO: 587 shown in **FIG. 587**.

[0615] **FIG. 589** shows a nucleotide sequence (SEQ ID NO: 589) of a native sequence PRO19818 cDNA, wherein SEQ ID NO: 589 is a clone designated herein as "DNA149930-2884".

[0616] **FIG. 590** shows the amino acid sequence (SEQ ID NO: 590) derived from the coding sequence of SEQ ID NO: 589 shown in **FIG. 589**.

[0617] **FIG. 591** shows a nucleotide sequence (SEQ ID NO: 591) of a native sequence PRO20088 cDNA, wherein SEQ ID NO: 591 is a clone designated herein as "DNA150157-2898".

[0618] **FIG. 592** shows the amino acid sequence (SEQ ID NO: 592) derived from the coding sequence of SEQ ID NO: 591 shown in **FIG. 591**.

[0619] **FIG. 593** shows a nucleotide sequence (SEQ ID NO: 593) of a native sequence PRO16089 cDNA, wherein SEQ ID NO: 593 is a clone designated herein as "DNA150163-2842".

[0620] **FIG. 594** shows the amino acid sequence (SEQ ID NO: 594) derived from the coding sequence of SEQ ID NO: 593 shown in **FIG. 593**.

[0621] **FIG. 595** shows a nucleotide sequence (SEQ ID NO: 595) of a native sequence PRO20025 cDNA, wherein SEQ ID NO: 595 is a clone designated herein as "DNA153579-2894".

[0622] **FIG. 596** shows the amino acid sequence (SEQ ID NO: 596) derived from the coding sequence of SEQ ID NO: 595 shown in **FIG. 595**.

[0623] **FIG. 597** shows a nucleotide sequence (SEQ ID NO: 597) of a native sequence PRO20040 cDNA, wherein SEQ ID NO: 597 is a clone designated herein as "DNA164625-2890".

[0624] **FIG. 598** shows the amino acid sequence (SEQ ID NO: 598) derived from the coding sequence of SEQ ID NO: 597 shown in **FIG. 597**.

[0625] **FIG. 599** shows a nucleotide sequence (SEQ ID NO: 599) of a native sequence PRO791 cDNA, wherein SEQ ID NO: 599 is a clone designated herein as "DNA57838-1337".

[0626] **FIG. 600** shows the amino acid sequence (SEQ ID NO: 600) derived from the coding sequence of SEQ ID NO: 599 shown in **FIG. 599**.

[0627] **FIG. 601** shows a nucleotide sequence (SEQ ID NO: 601) of a native sequence PRO1131 cDNA, wherein SEQ ID NO: 601 is a clone designated herein as "DNA59777-1480".

[0628] **FIG. 602** shows the amino acid sequence (SEQ ID NO: 602) derived from the coding sequence of SEQ ID NO: 601 shown in **FIG. 601**.

[0629] **FIG. 603** shows a nucleotide sequence (SEQ ID NO: 603) of a native sequence PRO1343 cDNA, wherein SEQ ID NO: 603 is a clone designated herein as "DNA66675-1587".

[0630] **FIG. 604** shows the amino acid sequence (SEQ ID NO: 604) derived from the coding sequence of SEQ ID NO: 603 shown in **FIG. 603**.

[0631] **FIG. 605** shows a nucleotide sequence (SEQ ID NO: 605) of a native sequence PRO1760 cDNA, wherein SEQ ID NO: 605 is a clone designated herein as "DNA76532-1702".

[0632] **FIG. 606** shows the amino acid sequence (SEQ ID NO: 606) derived from the coding sequence of SEQ ID NO: 605 shown in **FIG. 605**.

[0633] **FIG. 607** shows a nucleotide sequence (SEQ ID NO: 607) of a native sequence PRO6029 cDNA, wherein SEQ ID NO: 607 is a clone designated herein as "DNA105849-2704".

[0634] **FIG. 608** shows the amino acid sequence (SEQ ID NO: 608) derived from the coding sequence of SEQ ID NO: 607 shown in **FIG. 607**.

[0635] **FIG. 609** shows a nucleotide sequence (SEQ ID NO: 609) of a native sequence PRO1801 cDNA, wherein SEQ ID NO: 609 is a clone designated herein as "DNA83500-2506".

[0636] **FIG. 610** shows the amino acid sequence (SEQ ID NO: 610) derived from the coding sequence of SEQ ID NO: 609 shown in **FIG. 609**.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

[0637] I. Definitions

[0638] The terms “PRO polypeptide” and “PRO” as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms “PRO/number polypeptide” and “PRO/number” wherein the term “number” is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term “PRO polypeptide” refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the “PRO polypeptide” refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term “PRO polypeptide” also includes variants of the PRO/number polypeptides disclosed herein.

[0639] A “native sequence PRO polypeptide” comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term “native sequence PRO polypeptide” specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (e.g., an extracellular domain sequence), naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

[0640] The PRO polypeptide “extracellular domain” or “ECD” refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino

acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

[0641] The approximate location of the “signal peptides” of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., *Prot. Eng.* 10:1-6 (1997) and von Heinje et al., *Nucl. Acids. Res.* 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

[0642] “PRO polypeptide variant” means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids

in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

[0643] "Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif. or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

[0644] In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

[0645] where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the

amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X," "Y" and "Z" each represent different hypothetical amino acid residues.

[0646] Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11, and scoring matrix=BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

[0647] Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, Md. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask=yes, strand=all, expected occurrences=10, minimum low complexity length=15/5, multi-pass e-value=0.01, constant for multi-pass=25, dropoff for final gapped alignment=25 and scoring matrix=BLOSUM62.

[0648] In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

[0649] where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

[0650] “PRO variant polynucleotide” or “PRO variant nucleic acid sequence” means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

[0651] Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

[0652] “Percent (%) nucleic acid sequence identity” with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, %

nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif. or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

[0653] In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

[0654] where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated “Comparison DNA” to the nucleic acid sequence designated “PRO-DNA”, wherein “PRO-DNA” represents a hypothetical PRO-encoding nucleic acid sequence of interest, “Comparison DNA” represents the nucleotide sequence of a nucleic acid molecule against which the “PRO-DNA” nucleic acid molecule of interest is being compared, and “N”, “L” and “V” each represent different hypothetical nucleotides.

[0655] Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11, and scoring matrix=BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the

PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement “an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B”, the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

[0656] Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, Md. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask=yes, strand=all, expected occurrences=10, minimum low complexity length=15/5, multi-pass e-value=0.01, constant for multi-pass=25, dropoff for final gapped alignment=25 and scoring matrix=BLOSUM62.

[0657] In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

[0658] where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

[0659] In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

[0660] “Isolated,” when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide in situ within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

[0661] An “isolated” PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic

acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

[0662] The term “control sequences” refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

[0663] Nucleic acid is “operably linked” when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, “operably linked” means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

[0664] The term “antibody” is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypeptidic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term “monoclonal antibody” as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

[0665] “Stringency” of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., *Current Protocols in Molecular Biology*, Wiley Interscience Publishers, (1995).

[0666] "Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50° C.; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42° C.; or (3) employ 50% formamide, 5×SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5×Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42° C., with washes at 42° C. in 0.2×SSC (sodium chloride/sodium citrate) and 50% formamide at 55° C., followed by a high-stringency wash consisting of 0.1×SSC containing EDTA at 55° C.

[0667] "Moderately stringent conditions" may be identified as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and % SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37° C. in a solution comprising: 20% formamide, 5×SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5×Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1×SSC at about 37-50° C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

[0668] The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

[0669] As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

[0670] "Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity

refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

[0671] The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

[0672] "Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

[0673] "Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

[0674] "Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

[0675] Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

[0676] "Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are non-toxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

[0677] "Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable

region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (Zapata et al., *Protein Eng.* 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

[0678] Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

[0679] "Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[0680] The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

[0681] The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

[0682] Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

[0683] "Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

[0684] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H-V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Dia-

bodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., *Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993).

[0685] An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[0686] An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

[0687] The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

[0688] By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Pat. No. 4,275,149.

[0689] A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

[0690] A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

[0691] An "effective amount" of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner in relation to the stated purpose.

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Table 1

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define _M      -8      /* value of a match with a stop */

int      _day[26][26] = {
/*      A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */      { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */      { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */      {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
/* D */      { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */      { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */      {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */      { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */      {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
/* I */      {-1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */      { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */      {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */      {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */      {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
/* N */      { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */      {_M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */      { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */      { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */      {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
/* S */      { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */      { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */      { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */      { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */      {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
/* X */      { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */      {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */      { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};

```

Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

#define DMAT        3       /* value of matching bases */
#define DMIS        0       /* penalty for mismatched bases */
#define DINS0       8       /* penalty for a gap */
#define DINS1       1       /* penalty per base */
#define PINS0       8       /* penalty for a gap */
#define PINS1       4       /* penalty per residue */

struct jmp {
    short          n[MAXJMP];    /* size of jmp (neg for dely) */
    unsigned short x[MAXJMP];    /* base no. of jmp in seq x */
};
/* limits seq to 2^16 - 1 */

struct diag {
    int            score;        /* score at last jmp */
    long           offset;       /* offset of prev block */
    short          ijmp;        /* current jmp index */
    struct jmp     jmp;         /* list of jmps */
};

struct path {
    int            spc;          /* number of leading spaces */
    short          n[JMPS];     /* size of jmp (gap) */
    int            x[JMPS];     /* loc of jmp (last elem before gap) */
};

char              *ofile;       /* output file name */
char              *namex[2];    /* seq names: getseqs() */
char              *prog;        /* prog name for err msgs */
char              *seqx[2];     /* seqs: getseqs() */
int               dmax;         /* best diag: nw() */
int               dmax0;        /* final diag */
int               dna;          /* set if dna: main() */
int               endgaps;      /* set if penalizing end gaps */
int               gapx, gapy;    /* total gaps in seqs */
int               len0, len1;    /* seq lens */
int               ngapx, ngapy;  /* total size of gaps */
int               smax;         /* max score: nw() */
int               *xbm;         /* bitmap for matching */
long              offset;       /* current offset in jmp file */
struct            diag          *dx;    /* holds diagonals */
struct            path          pp[2];  /* holds path for seqs */

char              *calloc(), *malloc(), *index(), *strcpy();
char              *getseq(), *g_calloc();

```

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
* where file1 and file2 are two dna or two protein sequences.
* The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
* Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
#include "nw.h"
#include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static _pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
    1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
int ac;
char *av[];
{
    prog = av[0];
    if (ac != 3) {
        fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';', '>' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file 'align.out'\n");
        exit(1);
    }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
    xbm = (dna)? _dbval : _pbval;

    endgaps = 0; /* 1 to penalize endgaps */
    ofile = "align.out"; /* output file */

    nw(); /* fill in the matrix, get the possible jumps */
    readjumps(); /* get the actual jumps */
    print(); /* print stats, alignment */

    cleanup(0); /* unlink any tmp files */
}

```

main

Table 1 (cont')

```

/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw()
{
    char          *px, *py;          /* seqs and ptrs */
    int           *ndely, *dely;      /* keep track of dely */
    int           ndelx, delx;        /* keep track of delx */
    int           *tmp;               /* for swapping row0, row1 */
    int           mis;                /* score for each type */
    int           ins0, ins1;         /* insertion penalties */
    register      id;                 /* diagonal index */
    register      ij;                 /* jmp index */
    register      *col0, *col1;       /* score for curr, last row */
    register      xx, yy;             /* index into seqs */

    dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;

    smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
        }
        col0[0] = 0;          /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

    /* fill in match matrix
     */
    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
         */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
}

```


Table 1 (cont')**...nw**

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++){
    mis = col0[yy-1];
    if (dna)
        mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
    else
        mis += _day[*px-'A'][*py-'A'];

    /* update penalty for del in x seq;
     * favor new del over ongoing del
     * ignore MAXGAP if weighting endgaps
     */
    if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else {
            dely[yy] -= ins1;
            ndely[yy]++;
        }
    } else {
        if (col0[yy] - (ins0+ins1) >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else
            ndely[yy]++;
    }

    /* update penalty for del in y seq;
     * favor new del over ongoing del
     */
    if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else {
            delx -= ins1;
            ndelx++;
        }
    } else {
        if (col1[yy-1] - (ins0+ins1) >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else
            ndelx++;
    }

    /* pick the maximum score; we're favoring
     * mis over any del and delx over dely
     */

```

Table 1 (cont')

...nw

```

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
    coll[yy] = mis;
else if (delx >= dely[yy]) {
    coll[yy] = delx;
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejumps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
    }
    dx[id].jp.n[ij] = ndelx;
    dx[id].jp.x[ij] = xx;
    dx[id].score = delx;
}
else {
    coll[yy] = dely[yy];
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejumps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
    }
    dx[id].jp.n[ij] = -ndely[yy];
    dx[id].jp.x[ij] = xx;
    dx[id].score = dely[yy];
}
if (xx == len0 && yy < len1) {
    /* last col
    */
    if (endgaps)
        coll[yy] -= ins0+ins1*(len1-yy);
    if (coll[yy] > smax) {
        smax = coll[yy];
        dmax = id;
    }
}
}
if (endgaps && xx < len0)
    coll[yy-1] -= ins0+ins1*(len0-xx);
if (coll[yy-1] > smax) {
    smax = coll[yy-1];
    dmax = id;
}
tmp = col0; col0 = coll; coll = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)coll);
}

```

Table 1 (cont')

```

/*
 *
 * print() -- only routine visible outside this module
 *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

#include "nw.h"

#define SPC      3
#define P_LINE   256      /* maximum output line */
#define P_SPC    3        /* space between name or num and seq */

extern  _day[26][26];
int     olen;             /* set output line length */
FILE    *fx;             /* output file */

print()
{
    int     lx, ly, firstgap, lastgap;      /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
        fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
    olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) {          /* leading gap in x */
        pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) {     /* leading gap in y */
        pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) {         /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) {    /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

```

print

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)                                getmat
{
    int      lx, ly;                      /* "core" (minus endgaps) */
    int      firstgap, lastgap;           /* leading trailing overlap */

    int      nm, i0, i1, siz0, siz1;
    char     outx[32];
    double    pct;
    register  n0, n1;
    register char *p0, *p1;

    /* get total matches, score
     */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
        if (siz0) {
            p1++;
            n1++;
            siz0--;
        }
        else if (siz1) {
            p0++;
            n0++;
            siz1--;
        }
        else {
            if (xbm[*p0-'A'] & xbm[*p1-'A'])
                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
            if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
            p0++;
            p1++;
        }
    }

    /* pct homology:
     * if penalizing endgaps, base is the shorter seq
     * else, knock off overhangs and take shorter core
     */
    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
    pct = 100.*(double)nm/(double)lx;
    fprintf(fx, "\n");
    fprintf(fx, "<%d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);

```

Table 1 (cont')

```

fprintf(fx, "<gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, " (%d %s%s)",
        ngapx, (dna)? "base":"residue", (ngapx == 1)? "" : "s");
    fprintf(fx, "%s", outx);

    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, " (%d %s%s)",
            ngapy, (dna)? "base":"residue", (ngapy == 1)? "" : "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
    else
        fprintf(fx,
            "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINS0, PINS1);
    if (endgaps)
        fprintf(fx,
            "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
            lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
    else
        fprintf(fx, "<endgaps not penalized\n");
}

static      nm;          /* matches in core -- for checking */
static      lmax;        /* lengths of stripped file names */
static      ij[2];       /* jmp index for a path */
static      nc[2];       /* number at start of current line */
static      ni[2];       /* current elem number -- for gapping */
static      siz[2];
static char *ps[2];      /* ptr to current element */
static char *po[2];      /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;          /* char count */
    int      more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(name[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

...getmat

pr_align

Table 1 (cont')

```

for (nn = nm = 0, more = 1; more; ) {
    for (i = more = 0; i < 2; i++) {
        /*
         * do we have more of this sequence?
         */
        if (!*ps[i])
            continue;

        more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
        }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
        }
        else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
            po[i]++;
            ps[i]++;

            /*
             * are we at next gap for this seq?
             */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                 * we need to merge all gaps
                 * at this location
                 */
                siz[i] = pp[i].n[ij[i]]++;
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i]]++;
            }
            ni[i]++;
        }
    }
    if (++nn == olen || !more && nn) {
        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
    }
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
{
    register i;

    for (i = 0; i < 2; i++)
        *po[i]-- = '\0';
}

```

...pr_align

dumpblock

Table 1 (cont')⁴⁰

```

(void) putc('\n', fx);
for (i = 0; i < 2; i++) {
    if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' '))
        if (i == 0)
            nums(i);
        if (i == 0 && *out[1])
            stars();
        putline(i);
        if (i == 0 && *out[1])
            fprintf(fx, star);
        if (i == 1)
            nums(i);
    }
}

/*
 * put out a number line: dumpblock()
 */
static
nums(ix)
{
    int    ix;        /* index in out[] holding seq line */
    char    nline[P_LINE];
    register i, j;
    register char *pn, *px, *py;

    for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
        *pn = ' ';
    for (i = nc[ix], py = out[ix]; *py; py++, pn++){
        if (*py == ' ' || *py == '-')
            *pn = ' ';
        else {
            if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                j = (i < 0)? -i : i;
                for (px = pn; j /= 10, px--)
                    *px = j%10 + '0';
                if (i < 0)
                    *px = '-';
            }
            else
                *pn = ' ';
            i++;
        }
    }
    *pn = '\0';
    nc[ix] = i;
    for (pn = nline; *pn; pn++)
        (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

/*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static
putline(ix)
    int    ix;
    {

```

...dumpblock**nums****putline**

Table 1 (cont')**...putline**

```

int          i;
register char *px;

for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
    (void) putc(*px, fx);
for (; i < lmax+P_SPC; i++)
    (void) putc(' ', fx);

/* these count from 1:
 * ni[] is current element (from 1)
 * nc[] is number at start of current line
 */
for (px = out[ix]; *px; px++)
    (void) putc(*px&0x7F, fx);
(void) putc('\n', fx);
}

```

```

/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
static
stars()
{

```

stars

```

    int          i;
    register char *p0, *p1, cx, *px;

    if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
        return;
    px = star;
    for (i = lmax+P_SPC; i; i--)
        *px++ = ' ';

    for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++){
        if (isalpha(*p0) && isalpha(*p1)) {

            if (xbm[*p0-'A']&xbm[*p1-'A'])
                cx = '*';
            nm++;
        }
        else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
            cx = '.';
        else
            cx = ' ';

    }
    else
        cx = ' ';
    *px++ = cx;
}
*px++ = '\n';
*px = '\0';
}

```


Table 1 (cont')

```
/*  
 * strip path or prefix from pn, return len: pr_align()  
 */  
static  
stripname(pn)  
{  
    char    *pn;    /* file name (may be path) */  
  
    register char    *px, *py;  
  
    py = 0;  
    for (px = pn; *px; px++)  
        if (*px == '/')  
            py = px + 1;  
    if (py)  
        (void) strcpy(pn, py);  
    return(strlen(pn));  
}
```

stripname

Table 1 (cont')

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
 * readjumps() -- get the good jumps, from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

char    *jname = "/tmp/homgXXXXXX";          /* tmp file for jumps */
FILE    *fj;

int      cleanup();                          /* cleanup tmp file */
long     lseek();

/*
 * remove any tmp file if we blow
 */
cleanup(i)
    int    i;
{
    if (fj)
        (void) unlink(jname);
    exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char    *
getseq(file, len)
    char    *file;    /* file name */
    int     *len;     /* seq len */
{
    char      line[1024], *pseq;
    register char *px, *py;
    int       natgc, tlen;
    FILE      *fp;

    if ((fp = fopen(file, "r")) == 0) {
        fprintf(stderr, "%s: can't read %s\n", prog, file);
        exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
    }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
    pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';

```

cleanup

getseq

Table 1 (cont')

```

py = pseq + 4;
*len = tlen;
rewind(fp);

while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++){
        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU",*(py-1)))
            natgc++;
    }
    *py++ = '\0';
    *py = '\0';
    (void) fclose(fp);
    dna = natgc > (tlen/3);
    return(pseq+4);
}

char *
g_calloc(msg, nx, sz)
char *msg;          /* program, calling routine */
int nx, sz;          /* number and size of elements */
{
    char *px, *calloc();

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
            fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
}

/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjumps()
{
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

    if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
        while (1) {
            for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                ;

```

...getseq

g_calloc

readjumps

Table 1 (cont')**...readjumps**

```

        if (j < 0 && dx[dmax].offset && fj) {
            (void) lseek(fd, dx[dmax].offset, 0);
            (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
            (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
            dx[dmax].ijmp = MAXJMP-1;
        }
        else
            break;
    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) { /* gap in second seq */
            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1 */
            /*
            pp[1].x[i1] = xx - dmax + len1 - 1;
            gapy++;
            ngapy -= siz;
            */
            /* ignore MAXGAP when doing endgaps */
            siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
            i1++;
        }
        else if (siz > 0) { /* gap in first seq */
            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
            i0++;
        }
    }
    else
        break;
}

/* reverse the order of jumps
*/
for (j = 0, i0--; j < i0; j++, i0--) {
    i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
    i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
}
for (j = 0, i1--; j < i1; j++, i1--) {
    i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
    i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
}
if (fd >= 0)
    (void) close(fd);
if (fj) {
    (void) unlink(jname);
    fj = 0;
    offset = 0;
}
    
```

Table 1⁴⁶
(cont')

```
/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejumps(ix)
{
    int ix;
    char *mktemp();

    if (!fj) {
        if (mktemp(jname) < 0) {
            fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
            cleanup(1);
        }
        if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
    }
    (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
    (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
}
```

writejumps

TABLE 2

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity = (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 15 = 33.3%

[0692]

TABLE 3

PRO	XXXXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity = (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 10 = 50%

[0693]

TABLE 4

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity = (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 6 divided by 14 = 42.9%

[0694]

TABLE 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

% nucleic acid sequence identity = (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 4 divided by 12 = 33.3%

[0695] II. Compositions and Methods of the Invention

[0696] A. Full-length PRO Polypeptides

[0697] The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

[0698] As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual

nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

[0699] B. PRO Polypeptide Variants

[0700] In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

[0701] Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Pat. No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

[0702] PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

[0703] PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by poly-

merase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

[0704] In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

TABLE 6

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro; ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	leu
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

[0705] Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- [0706] (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- [0707] (2) neutral hydrophilic: cys, ser, thr;
- [0708] (3) acidic: asp, glu;
- [0709] (4) basic: asn, gin, his, lys, arg;
- [0710] (5) residues that influence chain orientation: gly, pro; and
- [0711] (6) aromatic: trp, tyr, phe.

[0712] Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

[0713] The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., *Nucl. Acids Res.*, 13:4331 (1986); Zoller et al., *Nucl. Acids Res.*, 10:6487 (1987)], cassette mutagenesis [Wells et al., *Gene*, 34:315 (1985)], restriction selection mutagenesis [Wells et al., *Philos. Trans. R. Soc. London SerA*, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

[0714] Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, *Science*, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, *The Proteins*, (W. H. Freeman & Co., N.Y.); Chothia, *J. Mol. Biol.*, 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

[0715] C. Modifications of PRO

[0716] Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis-(diazocetyl)-2-phenylethane, glutaraldehyde, N-hydroxy-succinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidyl-propionate), bifunctional maleirides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

[0717] Other modifications include deamidation of glutamyl and asparagyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T. E. Creighton, *Proteins: Structure and Molecular Properties*, W. H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

[0718] Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means),

and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

[0719] Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[0720] Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published Sep. 11, 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

[0721] Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge et al., *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., *Meth. Enzymol.*, 138:350 (1987).

[0722] Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

[0723] The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

[0724] In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., *Mol. Cell. Biol.*, 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., *Molecular and Cellular Biology*, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., *Protein Engineering*, 3(6):547-

553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., *BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., *Science*, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., *J. Biol. Chem.*, 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., *Proc. Natl. Acad. Sci. USA*, 87:6393-6397 (1990)].

[0725] In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also U.S. Pat. No. 5,428,130 issued Jun. 27, 1995.

[0726] D. Preparation of PRO

[0727] The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., *Solid-Phase Peptide Synthesis*, W. H. Freeman Co., San Francisco, Calif. (1969); Merrifield, *J. Am. Chem. Soc.*, 85:2149-2154 (1963)]. In vitro protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, Calif.) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

[0728] 1. Isolation of DNA Encoding PRO

[0729] DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

[0730] Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., *PCR Primer: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 1995)].

[0731] The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ^{32}P -labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

[0732] Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

[0733] Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

[0734] 2. Selection and Transformation of Host Cells

[0735] Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in *Mammalian Cell Biotechnology: a Practical Approach*, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

[0736] Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl_2 , CaPO_4 , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., *Gene*, 23:315 (1983) and WO 89/05859 published Jun. 29, 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, *Virology*, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Pat. No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., *J. Bact.*, 130:946 (1977) and Hsiao et al., *Proc. Natl. Acad. Sci. (USA)*, 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene,

polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., *Methods in Enzymology*, 185:527-537 (1990) and Mansour et al., *Nature*, 336:348-352 (1988).

[0737] Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as Escherichia, e.g., *E. coli*, Enterobacter, Erwinia, Klebsiella, Proteus, Salmonella, e.g., *Salmonella typhimurium*, Serratia, e.g., *Serratia marcescans*, and Shigella, as well as Bacilli such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published Apr. 12, 1989), Pseudomonas such as *P. aeruginosa*, and Streptomyces. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype tonA; *E. coli* W3110 strain 9E4, which has the complete genotype tonA ptr3; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype tonA ptr3phoA E15 (argF-lac)169 degP ompT kan^r; *E. coli* W3110 strain 37D6, which has the complete genotype tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan^r; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant degP deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Pat. No. 4,946,783 issued Aug. 7, 1990. Alternatively, in vitro methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

[0738] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, *Nature*, 290:140 [1981]; EP 139,383 published May 2, 1985); Kluyveromyces hosts (U.S. Pat. No. 4,943,529; Fleer et al., *Bio/Technology*, 9:968-975(1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., *J. Bacteriol.*, 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg et al., *Bio/Technology*, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; yarrowia (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., *J. Basic Microbiol.*, 28:265-278 [1988]); Candida; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., *Proc. Natl. Acad. Sci. USA*, 76:5259-5263 [1979]); Schwanniomycetes such as *Schwanniomycetes occidentalis* (EP 394,538 published Oct. 31, 1990); and filamentous fungi such as, e.g., Neurospora, Penicillium, Tolypocladium (WO 91/00357 published Jan. 10, 1991), and Aspergillus hosts such as *A. nidulans* (Balance et al., *Biochem. Biophys. Res. Commun.*, 112:284-289

[1983]; Tilburn et al., *Gene*, 26:205-221 [1983]; Yelton et al., *Proc. Natl. Acad. Sci. USA*, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, *EMBO J.*, 4:475-479 [1985]). Methylophilic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, *The Biochemistry of Methylophilic Yeasts*, 269 (1982).

[0739] Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., *J. Gen. Virol.*, 36:59 (1977)); Chinese hamster ovary cells/DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, *Biol. Reprod.*, 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

[0740] 3. Selection and Use of a Replicable Vector

[0741] The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

[0742] The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, 12472 pp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Pat. No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published Apr. 4, 1990), or the signal described in WO 90/13646 published Nov. 15, 1990. In mammalian cell expression, mammalian signal sequences

may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

[0743] Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

[0744] Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

[0745] An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., *Nature*, 282:39 (1979); Kingsman et al., *Gene*, 7:141 (1979); Tschemper et al., *Gene*, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, *Genetics*, 85:12 (1977)].

[0746] Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., *Nature*, 275:615 (1978); Goeddel et al., *Nature*, 281:544(1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, *Nucleic Acids Res.*, 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer et al., *Proc. Natl. Acad. Sci. USA*, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

[0747] Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., *J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess et al., *J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

[0748] Other yeast promoters, which are inducible promoters having the additional advantage of transcription

controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

[0749] PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published Jul. 5, 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

[0750] Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

[0751] Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

[0752] Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., *Nature*, 293:620-625 (1981); Mantei et al., *Nature*, 281:40-46 (1979); EP 117,060; and EP 117,058.

[0753] 4. Detecting Gene Amplification/Expression

[0754] Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201-5205 (1980)], dot blotting (DNA analysis), or in situ hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

[0755] Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

[0756] 5. Purification of Polypeptide

[0757] Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

[0758] It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, *Methods in Enzymology*, 182 (1990); Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

[0759] E. Uses for PRO

[0760] Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

[0761] The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases.

Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

[0762] Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

[0763] Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (*Cancer Res.* 48:2659, 1988) and van der Krol et al. (*BioTechniques* 6:958, 1988).

[0764] Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable in vivo (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

[0765] Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increase affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

[0766] Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO_4 -mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either in vivo or ex vivo. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retro-

virus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

[0767] Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

[0768] Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

[0769] Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

[0770] The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

[0771] Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as in situ hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

[0772] When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein

binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

[0773] Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

[0774] Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knock-

out animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

[0775] Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve in vivo synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes in vivo. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik et al, *Proc. Natl. Acad. Sci. USA* 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

[0776] There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells in vitro, or in vivo in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells in vitro include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred in vivo gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau et al., *Trends in Biotechnology* 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., *J. Biol. Chem.* 262, 4429-4432 (1987); and Wagner et al., *Proc. Natl. Acad. Sci. USA* 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson et al., *Science* 256, 808-813 (1992).

[0777] The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

[0778] The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

[0779] The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

[0780] The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEENTM, PLURONICSTM or PEG.

[0781] The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

[0782] Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0783] The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

[0784] Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

[0785] When in vivo administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage

amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 μ g/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

[0786] Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon-(rhIFN-), interleukin-2, and MN rgp120. Johnson et al., *Nat. Med.*, 2:795-799 (1996); Yasuda, *Biomed. Ther.*, 27:1221-1223 (1993); Hora et al., *BioTechnology*, 8:755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in *Vaccine Design: The Subunit and Adjuvant Approach*, Powell and Newman, eds. (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

[0787] The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), *Biodegradable Polymers as Drug Delivery Systems* (Marcel Dekker: New York, 1990), pp. 1-41.

[0788] This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

[0789] The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

[0790] All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

[0791] In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction

mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

[0792] If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, *Nature (London)*, 340:245-246 (1989); Chien et al., *Proc. Natl. Acad. Sci. USA*, 88:9578-9582(1991)) as disclosed by Chevray and Nathans, *Proc. Natl. Acad. Sci. USA*, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-lacZ reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

[0793] Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the

reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

[0794] To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., *Current Protocols in Immun.*, 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

[0795] As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

[0796] In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

[0797] More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain anti-

bodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

[0798] Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix—see Lee et al., *Nucl. Acids Res.*, 6:3073 (1979); Cooney et al., *Science*, 241: 456 (1988); Dervan et al., *Science*, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into the PRO polypeptide (antisense—Okano, *Neurochem.*, 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression* (CRC Press: Boca Raton, Fla., 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed in vivo to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

[0799] Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

[0800] Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, *Current Biology*, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published Sep. 18, 1997).

[0801] Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, supra.

[0802] These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

[0803] Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

[0804] F. Anti-PRO Antibodies

[0805] The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

[0806] 1. Polyclonal Antibodies

[0807] The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

[0808] 2. Monoclonal Antibodies

[0809] The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature* 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro.

[0810] The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine

phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

[0811] Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as RAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, Calif. and the American Type Culture Collection, Manassas, Va. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur et al., *Monoclonal Antibody Production Techniques and Applications*, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

[0812] The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980).

[0813] After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, *supra*]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown in vivo as ascites in a mammal.

[0814] The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

[0815] The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Pat. No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Pat. No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide.

Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

[0816] The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

[0817] In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

[0818] 3. Human and Humanized Antibodies

[0819] The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature* 332:323-329(1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

[0820] Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature* 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human

variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

[0821] Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Pat. Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., *Bio/Technology* 10, 779-783 (1992); Lonberg et al., *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild et al., *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

[0822] The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

[0823] 4. Bispecific Antibodies

[0824] Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

[0825] Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published May 13, 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

[0826] Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain

constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., *Methods in Enzymology*, 121:210 (1986).

[0827] According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

[0828] Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared can be prepared using chemical linkage. Brennan et al., *Science* 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

[0829] Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

[0830] Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the

hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., *J. Immunol.* 152:5368 (1994). Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

[0831] Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI(CD64), FcγRII(CD32) and FcγRIII(CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

[0832] 5. Heteroconjugate Antibodies

[0833] Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Pat. No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Pat. No. 4,676,980.

[0834] 6. Effector Function Engineering

[0835] It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp. Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using

heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

[0836] 7. Immunoconjugates

[0837] The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

[0838] Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcubin, croton, saponaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re . Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimide HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl)hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., *Science* 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionuclide to the antibody. See WO94/11026.

[0839] In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is conjugated to a cytotoxic agent (e.g., a radionuclide).

[0840] 8. Immunoliposomes

[0841] The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., *Proc. Natl. Acad. Sci. USA*, 82: 3688 (1985); Hwang et al., *Proc. Natl. Acad. Sci. USA*, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Pat. No. 5,013,556.

[0842] Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid compo-

sition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al., *J. Biol. Chem.*, 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon et al., *J. National Cancer Inst.*, 81(19): 1484 (1989).

[0843] 9. Pharmaceutical Compositions of Antibodies

[0844] Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

[0845] If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, e.g., Marasco et al., *Proc. Natl. Acad. Sci. USA*, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

[0846] The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nano-capsules) or in macroemulsions. Such techniques are disclosed in Remington's *Pharmaceutical Sciences*, supra.

[0847] The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

[0848] Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™

(injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37° C., resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S—S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

[0849] G. Uses for anti-PRO Antibodies

[0850] The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, e.g., detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, *Monoclonal Antibodies: A Manual of Techniques*, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

[0851] Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such as a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

[0852] The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

[0853] All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

[0854] Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, Va.

Example 1

Extracellular Domain Homology Screening to
Identify Novel Polypeptides and cDNA Encoding
Therefor

[0855] The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g. LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, Calif.). The search was performed using the computer program BLAST or BLAST-2 (Altschul et al., *Methods in Enzymology*, 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Wash.).

[0856] Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

[0857] Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5 kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., *Current Protocols in Molecular Biology*, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

[0858] The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, Calif. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is

a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., *Science*, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

Example 2

Isolation of cDNA Clones by Amylase Screening

[0859] 1. Preparation of Oligo dT Primed cDNA Library

[0860] mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, Calif. (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, Md. (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linker cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

[0861] 2. Preparation of Random Primed cDNA Library

[0862] A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was sized to 500-1000 bp, tinkered with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

[0863] 3. Transformation and Detection

[0864] DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37° C. for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37° C.). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, e.g. CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

[0865] The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

[0866] The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha,

ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL⁺, SUC⁺, GAL⁺. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in sec71, sec72, sec62, with truncated sec71 being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (e.g., SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

[0867] Transformation was performed based on the protocol outlined by Gietz et al., *Nucl. Acid. Res.*, 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30° C. The YEPD broth was prepared as described in Kaiser et al., *Methods in Yeast Genetics*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., p. 207 (1994). The overnight culture was then diluted to about 2×10⁶ cells/ml (approx. OD₆₀₀=0.1) into fresh YEPD broth (500 ml) and regrown to 1×10⁷ cells/ml (approx. OD₆₀₀=0.4-0.5).

[0868] The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li₂OOCCH₃), and resuspended into LiAc/TE (2.5 ml).

[0869] Transformation took place by mixing the prepared cells (100 μ l) with freshly denatured single stranded salmon testes DNA (Lofstrand Labs, Gaithersburg, Md.) and transforming DNA (1 μ g, vol.<10 μ l) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/m (600 μ l, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li₂OOCCH₃, pH 7.5) was added. This mixture was gently mixed and incubated at 30° C. while agitating for 30 minutes. The cells were then heat shocked at 42° C. for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 μ l, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200 μ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

[0870] Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

[0871] The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser et al., *Methods in Yeast Genetics*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., p. 208-210 (1994). Transformants were grown at 30° C. for 2-3 days.

[0872] The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely et al.,

Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

[0873] The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

[0874] 4. Isolation of DNA by PCR Amplification

[0875] When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 μ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 μ l) was used as a template for the PCR reaction in a 25 μ l volume containing: 0.5 μ l KlenTaq (Clontech, Palo Alto, Calif.); 4.0 μ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 μ l Kentaq buffer (Clontech); 0.25 μ l forward oligo 1; 0.25 μ l reverse oligo 2; 12.5 μ l distilled water.

[0876] The sequence of reverse oligonucleotide 1 was:

[0877] 5'-TGTAACGACGGCCAGTTAAATA-GACCTGCAATTATTAATCT-3' (SEQ ID NO: 611)

[0878] The sequence of reverse oligonucleotide 2 was:

[0879] 5'-CAGGAAACAGCTATGACCACCTG-CACACCTGAAATCCAAT-3' (SEQ ID NO: 612)

[0880] PCR was then performed as follows:

a.	Denature	92° C., 5 minutes
b. 3 cycles of	Denature	92° C., 30 seconds
	Anneal	59° C., 30 seconds
	Extend	72° C., 60 seconds
c. 3 cycles of	Denature	92° C., 30 seconds
	Anneal	57° C., 30 seconds
	Extend	72° C., 60 seconds
d. 25 cycles of	Denature	92° C., 30 seconds
	Anneal	55° C., 30 seconds
	Extend	72° C., 60 seconds
e.	Hold	4° C.

[0881] The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

[0882] Following the PCR, an aliquot of the reaction (5 μ l) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook et al, supra. Clones resulting in a single strong PCR product larger than 400 bp

were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, Calif.).

Example 3

Isolation of cDNA Clones Using Signal Algorithm Analysis

[0883] Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, Calif.) upon ESTs as well as clustered and assembled EST fragments from public (e.g., GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, Calif.) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

Example 4

Isolation of cDNA Clones Encoding Human PRO Polypeptides

[0884] Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, Va. 20110-2209, USA (ATCC) as shown in Table 7 below.

TABLE 7

Material	ATCC Dep. No.	Deposit Date
DNA16435-1208	209930	Jun. 2, 1998
DNA23318-1211	209787	Apr. 21, 1998
DNA23322-1393	203400	Oct. 27, 1998
DNA23334-1392	209918	Jun. 2, 1998
DNA26843-1389	203099	Aug. 4, 1998
DNA26844-1394	209926	Jun. 2, 1998
DNA30867-1335	209807	Apr. 28, 1998
DNA33470-1175	209398	Oct. 17, 1997
DNA34436-1238	209523	Dec. 10, 1997
DNA35557-1137	209255	Sep. 16, 1997
DNA35599-1168	209373	Oct. 16, 1997
DNA35668-1171	209371	Oct. 16, 1997
DNA36992-1168	209382	Oct. 16, 1997
DNA39423-1182	209387	Oct. 17, 1997
DNA39427-1179	209395	Oct. 17, 1997
DNA39510-1181	209392	Oct. 17, 1997
DNA39518-1247	209529	Dec. 10, 1997
DNA39975-1210	209783	Apr. 21, 1998
DNA39976-1215	209524	Dec. 10, 1997

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA39979-1213	209789	Apr. 21, 1998
DNA40594-1233	209617	Feb. 5, 1998
DNA40603-1232	209486	Nov. 21, 1997
DNA40604-1187	209394	Oct. 17, 1997
DNA40625-1189	209788	Apr. 21, 1998
DNA41225-1217	209491	Nov. 21, 1997
DNA41379-1236	209488	Nov. 21, 1997
DNA41386-1316	209703	Mar. 26, 1998
DNA44161-1434	209907	May 27, 1998
DNA44179-1362	209851	May 6, 1998
DNA44192-1246	209531	Dec. 10, 1997
DNA44694-1500	203114	Aug. 11, 1998
DNA45234-1277	209654	Mar. 5, 1998
DNA45409-2511	203579	Jan. 12, 1999
DNA45415-1318	209810	Apr. 28, 1998
DNA45417-1432	209910	May 27, 1998
DNA45493-1349	209805	Apr. 28, 1998
DNA46776-1284	209721	Mar. 31, 1998
DNA48296-1292	209668	Mar. 11, 1998
DNA48306-1291	209911	May 27, 1998
DNA48328-1355	209843	May 6, 1998
DNA48329-1290	209785	Apr. 21, 1998
DNA48334-1435	209924	Jun. 2, 1998
DNA49141-1431	203003	Jun. 23, 1998
DNA49624-1279	209655	Mar. 5, 1998
DNA49647-1398	209919	Jun. 2, 1998
DNA49819-1439	209931	Jun. 2, 1998
DNA50911-1288	209714	Mar. 31, 1998
DNA50914-1289	209722	Mar. 31, 1998
DNA50919-1361	209848	May 6, 1998
DNA50980-1286	209717	Mar. 31, 1998
DNA52185-1370	209861	May 14, 1998
DNA53906-1368	209747	Apr. 7, 1998
DNA53912-1457	209870	May 14, 1998
DNA53913-1490	203162	Aug. 25, 1998
DNA53977-1371	209862	May 14, 1998
DNA53978-1443	209983	Jun. 16, 1998
DNA53996-1442	209921	Jun. 2, 1998
DNA54002-1367	209754	Apr. 7, 1998
DNA55737-1345	209753	Apr. 7, 1998
DNA56050-1455	203011	Jun. 23, 1998
DNA56052-1454	203026	Jun. 23, 1998
DNA56107-1415	203405	Oct. 27, 1998
DNA56110-1437	203113	Aug. 11, 1998
DNA56406-1704	203478	Nov. 17, 1998
DNA56409-1377	209882	May 20, 1998
DNA56410-1414	209923	Jun. 2, 1998
DNA56436-1448	209902	May 27, 1998
DNA56529-1647	203293	Sep. 29, 1998
DNA56855-1447	203004	Jun. 23, 1998
DNA56859-1445	203019	Jun. 23, 1998
DNA56860-1510	209952	Jun. 9, 1998
DNA56865-1491	203022	Jun. 23, 1998
DNA56868-1478	203024	Jun. 23, 1998
DNA56869-1545	203161	Aug. 25, 1998
DNA56870-1492	209925	Jun. 2, 1998
DNA57039-1402	209777	Apr. 14, 1998
DNA57253-1382	209867	May 14, 1998
DNA57254-1477	203289	Sep. 29, 1998
DNA57699-1412	203020	Jun. 23, 1998
DNA57704-1452	209953	Jun. 9, 1998
DNA57710-1451	203048	Jul. 1, 1998
DNA57827-1493	203045	Jul. 1, 1998
DNA57844-1410	203010	Jun. 23, 1998
DNA58723-1588	203133	Aug. 18, 1998
DNA58727-1474	203171	Sep. 1, 1998
DNA58730-1607	203221	Sep. 15, 1998
DNA58732-1650	203290	Sep. 29, 1998
DNA58737-1473	203136	Aug. 18, 1998
DNA58743-1609	203154	Aug. 25, 1998
DNA58747-1384	209868	May 14, 1998
DNA58828-1519	203172	Sep. 1, 1998
DNA58846-1409	209957	Jun. 9, 1998
DNA58848-1472	209955	Jun. 9, 1998

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA58849-1494	209958	Jun. 9, 1998
DNA58850-1495	209956	Jun. 9, 1998
DNA58852-1637	203271	Sep. 22, 1998
DNA58853-1423	203016	Jun. 23, 1998
DNA58855-1422	203018	Jun. 23, 1998
DNA59211-1450	209960	Jun. 9, 1998
DNA59212-1627	203245	Sep. 9, 1998
DNA59213-1487	209959	Jun. 9, 1998
DNA59219-1613	203220	Sep. 15, 1998
DNA59497-1496	209941	Jun. 4, 1998
DNA59602-1436	203051	Jul. 1, 1998
DNA59603-1419	209944	Jun. 9, 1998
DNA59605-1418	203005	Jun. 23, 1998
DNA59607-1497	209946	Jun. 9, 1998
DNA59610-1556	209990	Jun. 16, 1998
DNA59612-1466	209947	Jun. 9, 1998
DNA59613-1417	203007	Jun. 23, 1998
DNA59616-1465	209991	Jun. 16, 1998
DNA59619-1464	203041	Jul. 1, 1998
DNA59625-1498	209992	Jun. 16, 1998
DNA59817-1703	203470	Nov. 17, 1998
DNA59827-1426	203089	Aug. 4, 1998
DNA59828-1608	203158	Aug. 25, 1998
DNA59837-2545	203658	Feb. 9, 1999
DNA59844-2542	203650	Feb. 9, 1999
DNA59853-1505	209985	Jun. 16, 1998
DNA59854-1459	209974	Jun. 16, 1998
DNA59855-1485	209987	Jun. 16, 1998
DNA60278-1530	203170	Sep. 1, 1998
DNA60283-1484	203043	Jul. 1, 1998
DNA60608-1577	203126	Aug. 18, 1998
DNA60611-1524	203175	Sep. 1, 1998
DNA60619-1482	209993	Jun. 16, 1998
DNA60625-1507	209975	Jun. 16, 1998
DNA60629-1481	209979	Jun. 16, 1998
DNA60740-1615	203456	Nov. 3, 1998
DNA61608-1606	203239	Sep. 9, 1998
DNA61755-1554	203112	Aug. 11, 1998
DNA62809-1531	203237	Sep. 9, 1998
DNA62812-1594	203248	Sep. 9, 1998
DNA62813-2544	203655	Feb. 9, 1999
DNA62845-1684	203361	Oct. 20, 1998
DNA64849-1604	203468	Nov. 17, 1998
DNA64852-1589	203127	Aug. 18, 1998
DNA64863-1573	203251	Sep. 9, 1998
DNA64881-1602	203240	Sep. 9, 1998
DNA64902-1667	203317	Oct. 6, 1998
DNA64952-1568	203222	Sep. 15, 1998
DNA65403-1565	203230	Sep. 15, 1998
DNA65413-1534	203234	Sep. 15, 1998
DNA65423-1595	203227	Sep. 15, 1998
DNA66304-1546	203321	Oct. 6, 1998
DNA66308-1537	203159	Aug. 25, 1998
DNA66511-1563	203228	Sep. 15, 1998
DNA66512-1564	203218	Sep. 15, 1998
DNA66519-1535	203236	Sep. 15, 1998
DNA66521-1583	203225	Sep. 15, 1998
DNA66558-1584	203229	Sep. 15, 1998
DNA66660-1585	203279	Sep. 22, 1998
DNA66669-1597	203272	Sep. 22, 1998
DNA66674-1599	203281	Sep. 22, 1998
DNA68836-1656	203455	Nov. 3, 1998
DNA68862-2546	203652	Feb. 9, 1999
DNA68866-1644	203283	Sep. 22, 1998
DNA68869-1610	203164	Aug. 25, 1998
DNA68871-1638	203280	Sep. 22, 1998
DNA68879-1631	203274	Sep. 22, 1998
DNA68880-1676	203319	Oct. 6, 1998
DNA68882-1677	203318	Oct. 6, 1998
DNA68883-1691	203535	Dec. 15, 1998
DNA68885-1678	203311	Oct. 6, 1998
DNA71180-1655	203403	Oct. 27, 1998
DNA71184-1634	203266	Sep. 22, 1998
DNA71213-1659	203401	Oct. 27, 1998

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA71234-1651	203402	Oct. 27, 1998
DNA71269-1621	203284	Sep. 22, 1998
DNA71277-1636	203285	Sep. 22, 1998
DNA71286-1687	203357	Oct. 20, 1998
DNA71883-1660	203475	Nov. 17, 1998
DNA73401-1633	203273	Sep. 22, 1998
DNA73492-1671	203324	Oct. 6, 1998
DNA73730-1679	203320	Oct. 6, 1998
DNA73734-1680	203363	Oct. 20, 1998
DNA73735-1681	203356	Oct. 20, 1998
DNA73742-1662	203316	Oct. 6, 1998
DNA73746-1654	203411	Oct. 27, 1998
DNA73760-1672	203314	Oct. 6, 1998
DNA76393-1664	203323	Oct. 6, 1998
DNA76398-1699	203474	Nov. 17, 1998
DNA76399-1700	203472	Nov. 17, 1998
DNA76522-2500	203469	Nov. 17, 1998
DNA76533-1689	203410	Oct. 27, 1998
DNA77303-2502	203479	Nov. 17, 1998
DNA77626-1705	203536	Dec. 15, 1998
DNA77648-1688	203408	Oct. 27, 1998
DNA81754-2532	203542	Dec. 15, 1998
DNA81757-2512	203543	Dec. 15, 1998
DNA82302-2529	203534	Dec. 15, 1998
DNA82340-2530	203547	Dec. 22, 1998
DNA87991-2540	203656	Feb. 9, 1999
DNA92238-2539	203602	Jan. 20, 1999
DNA115291-2681	PTA-202	Jun. 8, 1999
DNA23336-2861	PTA-1673	Apr. 11, 2000
DNA30862-1396	209920	Jun. 2, 1998
DNA30871-1157	209380	Oct. 16, 1997
DNA32279-1131	209259	Sep. 16, 1997
DNA33206-1165	209372	Oct. 16, 1997
DNA35673-1201	209418	Oct. 28, 1997
DNA47361-1154-2	209431	Nov. 7, 1997
DNA49631-1328	209806	Apr. 28, 1998
DNA52594-1270	209679	Mar. 17, 1998
DNA55800-1263	209680	Mar. 17, 1998
DNA56531-1648	203286	Sep. 29, 1998
DNA56965-1356	209842	May 6, 1998
DNA57037-1444	209903	May 27, 1998
DNA57695-1340	203006	Jun. 23, 1998
DNA57834-1339	209954	Jun. 9, 1998
DNA57841-1522	203458	Nov. 3, 1998
DNA58847-1383	209879	May 20, 1998
DNA59493-1420	203050	Jul. 1, 1998
DNA59586-1520	203288	Sep. 29, 1998
DNA59608-2577	203870	Mar. 23, 1999
DNA59849-1504	209986	Jun. 16, 1998
DNA60292-1506	203540	Dec. 15, 1998
DNA62377-1381-1	203552	Dec. 22, 1998
DNA62880-1513	203097	Aug. 4, 1998
DNA66672-1586	203265	Sep. 22, 1998
DNA67962-1649	203291	Sep. 29, 1998
DNA69555-2867	PTA-1632	Apr. 4, 2000
DNA71162-2764	PTA-860	Oct. 19, 1999
DNA71290-1630	203275	Sep. 22, 1998
DNA76401-1683	203360	Oct. 20, 1998
DNA76541-1675	203409	Oct. 27, 1998
DNA76788-2526	203551	Dec. 22, 1998
DNA77623-2524	203546	Dec. 22, 1998
DNA80136-2503	203541	Dec. 15, 1998
DNA83568-2692	PTA-386	Jul. 20, 1999
DNA84210-2576	203818	Mar. 2, 1999
DNA86576-2595	203868	Mar. 23, 1999
DNA87976-2593	203888	Mar. 30, 1999
DNA92256-2596	203891	Mar. 30, 1999
DNA92289-2598	PTA-131	May 25, 1999
DNA96850-2705	PTA-479	Aug. 3, 1999
DNA96855-2629	PTA-18	May 4, 1999
DNA96857-2636	PTA-17	May 4, 1999
DNA96860-2700	PTA-478	Aug. 3, 1999
DNA96861-2844	PTA-1436	Mar. 2, 2000
DNA96866-2698	PTA-491	Aug. 3, 1999

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA96870-2676	PTA-254	Jun. 22, 1999
DNA96872-2674	PTA-550	Aug. 17, 1999
DNA96878-2626	PTA-23	May 4, 1999
DNA96879-2619	203967	Apr. 27, 1999
DNA96889-2641	PTA-119	May 25, 1999
DNA96893-2621	PTA-12	May 4, 1999
DNA96897-2688	PTA-379	Jul. 20, 1999
DNA98564-2643	PTA-125	May 25, 1999
DNA107443-2718	PTA-490	Aug. 3, 1999
DNA107786-2723	PTA-474	Aug. 3, 1999
DNA108682-2712	PTA-486	Aug. 3, 1999
DNA108684-2761	PTA-653	Sep. 14, 1999
DNA108701-2749	PTA-554	Aug. 17, 1999
DNA108720-2717	PTA-511	Aug. 10, 1999
DNA108726-2729	PTA-514	Aug. 10, 1999
DNA108728-2760	PTA-654	Sep. 14, 1999
DNA108738-2767	PTA-862	Oct. 19, 1999
DNA108743-2722	PTA-508	Aug. 10, 1999
DNA108758-2759	PTA-655	Sep. 14, 1999
DNA108765-2758	PTA-657	Sep. 14, 1999
DNA108783-2747	PTA-616	Aug. 31, 1999
DNA108789-2748	PTA-547	Aug. 17, 1999
DNA108806-2724	PTA-610	Aug. 31, 1999
DNA108936-2719	PTA-519	Aug. 10, 1999
DNA119510-2771	PTA-947	Nov. 9, 1999
DNA119517-2778	PTA-951	Nov. 16, 1999
DNA119535-2756	PTA-613	Aug. 31, 1999
DNA119537-2777	PTA-956	Nov. 16, 1999
DNA119714-2851	PTA-1537	Mar. 21, 2000
DNA125170-2780	PTA-953	Nov. 16, 1999
DNA129594-2841	PTA-1481	Mar. 14, 2000
DNA129793-2857	PTA-1733	Apr. 18, 2000
DNA130809-2769	PTA-949	Nov. 9, 1999
DNA131639-2874	PTA-1784	Apr. 25, 2000
DNA131649-2855	PTA-1482	Mar. 14, 2000
DNA131652-2876	PTA-1628	Apr. 4, 2000
DNA131658-2875	PTA-1671	Apr. 11, 2000
DNA132162-2770	PTA-950	Nov. 9, 1999
DNA136110-2763	PTA-652	Sep. 14, 1999
DNA139592-2866	PTA-1587	Mar. 28, 2000
DNA139608-2856	PTA-1581	Mar. 28, 2000
DNA143292-2848	PTA-1778	Apr. 25, 2000
DNA144844-2843	PTA-1536	Mar. 21, 2000
DNA144857-2845	PTA-1589	Mar. 28, 2000
DNA145841-2868	PTA-1678	Apr. 11, 2000
DNA148004-2882	PTA-1779	Apr. 25, 2000
DNA149893-2873	PTA-1672	Apr. 11, 2000
DNA149930-2884	PTA-1668	Apr. 11, 2000
DNA150157-2898	PTA-1777	Apr. 25, 2000
DNA150163-2842	PTA-1533	Mar. 21, 2000
DNA153579-2894	PTA-1729	Apr. 18, 2000
DNA164625-2890	PTA-1535	Mar. 21, 2000
DNA57838-1337	203014	Jun. 23, 1998
DNA59777-1480	203111	Aug. 11, 1998
DNA66675-1587	203282	Sep. 22, 1998
DNA76532-1702	203473	Nov. 17, 1998
DNA105849-2704	PTA-473	Aug. 3, 1999
DNA83500-2506	203391	Oct. 29, 1998

[0885] These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent

application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

[0886] The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

Example 5

Use of PRO as a Hybridization Probe

[0887] The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

[0888] DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

[0889] Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5×SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2×Denhardt's solution, and 10% dextran sulfate at 42° C. for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1×SSC and 0.1% SDS at 42° C.

[0890] DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

Example 6

Expression of PRO in *E. coli*

[0891] This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

[0892] The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

[0893] The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., *supra*. Transformants are identified by their

ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

[0894] Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

[0895] After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

[0896] PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq)). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30° C. with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate•2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30° C. with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

[0897] *E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1 M and 0.02 M, respectively, and the solution is stirred overnight at 4° C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4° C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

[0898] The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM

cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4° C. for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

[0899] Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

[0900] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 7

Expression of PRO in Mammalian Cells

[0901] This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

[0902] The vector, pRK5 (see EP 307,247, published Mar. 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO.

[0903] In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-PRO DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂. To this mixture is added, dropwise, 500 µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄, and a precipitate is allowed to form for 10 minutes at 25° C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37° C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

[0904] Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μ Ci/ml ^{35} S-cysteine and 200 μ Ci/ml ^{35} S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

[0905] In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μ g/ml bovine insulin and 0.1 μ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

[0906] In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as CaPO₄ or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35} S-methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

[0907] Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by Ni²⁺-chelate affinity chromatography.

[0908] PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

[0909] Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

[0910] Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., *Current Protocols of Molecular Biology*, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., *Nucl. Acids Res.* 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

[0911] Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Qiagen), Dosper® or Eugene® (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3 $\times$ 10⁷ cells are frozen in an ampule for further growth and production as described below.

[0912] The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μ m filtered PS20 with 5% 0.2 μ m diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37° C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3 $\times$ 10⁵ cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Pat. No. 5,122,469, issued Jun. 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2 $\times$ 10⁶ cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33° C., and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μ m filter. The filtrate was either stored at 4° C. or immediately loaded onto columns for purification.

[0913] For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 mL Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 mL/min. at 4° C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 mL G25 Superfine (Pharmacia) column and stored at -80° C.

[0914] Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

[0915] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 8

Expression of PRO in Yeast

[0916] The following method describes recombinant expression of PRO in yeast.

[0917] First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

[0918] Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

[0919] Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

[0920] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 9

Expression of PRO in Baculovirus-infected Insect Cells

[0921] The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

[0922] The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the

sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

[0923] Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4-5 days of incubation at 28° C., the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., *Baculovirus expression vectors: A Laboratory Manual*, Oxford: Oxford University Press (1994).

[0924] Expressed poly-his tagged PRO can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., *Nature*, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μ m filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO are pooled and dialyzed against loading buffer.

[0925] Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

[0926] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 10

Preparation of Antibodies that Bind PRO

[0927] This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

[0928] Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

[0929] Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, Mont.) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

[0930] After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

[0931] The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

[0932] The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

Example 11

Purification of PRO Polypeptides Using Specific Antibodies

[0933] Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

[0934] Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotech-

nology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

[0935] Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

[0936] A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (e.g., high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (e.g., a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

Example 12

Drug Screening

[0937] This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

[0938] Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

[0939] Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on Sep. 13, 1984. Briefly stated,

large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

[0940] This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

Example 13

Rational Drug Design

[0941] The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (i.e., a PRO polypeptide) or of small molecules with which they interact, e.g., agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide in vivo (c.f., Hodgson, *Bio/Technology*, 9: 19-21 (1991)).

[0942] In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, *Biochemistry*, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda et al, *J. Biochem.*, 113:742-746 (1993).

[0943] It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

[0944] By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to

perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

Example 14

Identification of PRO Polypeptides That Stimulate TNF- α Release in Human Blood (Assay 128)

[0945] This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF- α in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF- α would be desired and for the therapeutic treatment of conditions wherein enhanced TNF- α release would be beneficial. Specifically, 200 μ l of human blood supplemented with 50 mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300 μ l of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37° C. for 6 hours. The samples are then centrifuged and 50 μ l of plasma is collected from each well and tested for the presence of TNF- α by ELISA assay. A positive in the assay is a higher amount of TNF- α in the PRO polypeptide treated samples as compared to the negative control samples.

[0946] The following PRO polypeptides tested positive in this assay:

[0947] PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567, and PRO4333.

Example 15

Promotion of Chondrocyte Redifferentiation (Assay 129)

[0948] This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

[0949] Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm² in Ham F-12 containing 10% FBS and 4 μ g/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100 μ l of the same media without serum and 100 μ l of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200 μ l/well. After 5 days at 37° C., 22 μ l of media containing 100 μ g/ml Hoechst 33342 and 50 μ g/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37° C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is

obtained when the >50% of the PRO polypeptide treated cells are differentiated (compared to the background obtained by the negative control).

[0950] PRO6029 polypeptide tested positive in this assay.

Example 16

Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors

[0951] Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

[0952] The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on Mar. 31, 2000 and which is herein incorporated by reference.

[0953] In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Two sets of experimental data were generated. In one set, cancerous human colon tumor tissue and matched non-cancerous human colon tumor tissue from the same patient ("matched colon control") were obtained and analyzed for PRO polypeptide expression using the above described microarray technology. In the second set of data, cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the

pooled "universal control" sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

[0954] In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from the tumor tissues listed above were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio was designated as a "cutoff ratio". Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in various human tumor tissues as compared to a non-cancerous human tissue control. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, but also serve as therapeutic targets for the treatment of those tumors.

TABLE 8

Molecule	is overexpressed in:	as compared to:
PRO276	lung tumor	universal normal control
PRO284	colon tumor	universal normal control
PRO284	lung tumor	universal normal control
PRO284	breast tumor	universal normal control
PRO193	colon tumor	universal normal control
PRO193	lung tumor	universal normal control
PRO193	breast tumor	universal normal control
PRO193	prostate tumor	universal normal control
PRO190	colon tumor	universal normal control
PRO190	lung tumor	universal normal control
PRO190	breast tumor	universal normal control
PRO180	colon tumor	universal normal control
PRO180	lung tumor	universal normal control
PRO180	breast tumor	universal normal control
PRO194	colon tumor	universal normal control
PRO194	lung tumor	universal normal control
PRO194	breast tumor	universal normal control
PRO194	cervical tumor	universal normal control
PRO218	colon tumor	universal normal control
PRO218	lung tumor	universal normal control
PRO260	colon tumor	universal normal control
PRO260	lung tumor	universal normal control
PRO260	breast tumor	universal normal control
PRO260	rectal tumor	universal normal control
PRO233	colon tumor	universal normal control
PRO233	lung tumor	universal normal control
PRO233	breast tumor	universal normal control
PRO234	colon tumor	universal normal control
PRO234	lung tumor	universal normal control
PRO234	breast tumor	universal normal control
PRO234	liver tumor	universal normal control
PRO236	colon tumor	universal normal control
PRO236	lung tumor	universal normal control
PRO236	breast tumor	universal normal control
PRO244	colon tumor	universal normal control
PRO244	lung tumor	universal normal control
PRO262	colon tumor	universal normal control
PRO262	lung tumor	universal normal control
PRO262	breast tumor	universal normal control
PRO271	colon tumor	universal normal control
PRO271	lung tumor	universal normal control
PRO268	colon tumor	universal normal control
PRO268	lung tumor	universal normal control
PRO268	breast tumor	universal normal control
PRO270	colon tumor	universal normal control
PRO270	lung tumor	universal normal control
PRO270	breast tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO1137	colon tumor	universal normal control
PRO1137	lung tumor	universal normal control
PRO1137	breast tumor	universal normal control
PRO1138	colon tumor	universal normal control
PRO1138	lung tumor	universal normal control
PRO1138	breast tumor	universal normal control
PRO1415	colon tumor	universal normal control
PRO1415	lung tumor	universal normal control
PRO1415	prostate tumor	universal normal control
PRO1054	lung tumor	universal normal control
PRO1054	breast tumor	universal normal control
PRO0994	colon tumor	universal normal control
PRO0994	lung tumor	universal normal control
PRO0994	rectal tumor	universal normal control
PRO1069	lung tumor	universal normal control
PRO1069	breast tumor	universal normal control
PRO1411	colon tumor	universal normal control
PRO1411	lung tumor	universal normal control
PRO1129	lung tumor	universal normal control
PRO1129	rectal tumor	universal normal control
PRO1359	colon tumor	universal normal control
PRO1359	lung tumor	universal normal control
PRO1359	breast tumor	universal normal control
PRO1359	prostate tumor	universal normal control
PRO1139	lung tumor	universal normal control
PRO1065	lung tumor	universal normal control
PRO1028	colon tumor	universal normal control
PRO1028	lung tumor	universal normal control
PRO1028	breast tumor	universal normal control
PRO1028	cervical tumor	universal normal control
PRO1027	colon tumor	universal normal control
PRO1027	lung tumor	universal normal control
PRO1027	breast tumor	universal normal control
PRO1140	colon tumor	universal normal control
PRO1140	breast tumor	universal normal control
PRO1291	colon tumor	universal normal control
PRO1291	breast tumor	universal normal control
PRO1105	colon tumor	universal normal control
PRO1105	lung tumor	universal normal control
PRO1026	lung tumor	universal normal control
PRO1026	prostate tumor	universal normal control
PRO1104	colon tumor	universal normal control
PRO1104	lung tumor	universal normal control
PRO1104	breast tumor	universal normal control
PRO1100	colon tumor	universal normal control
PRO1100	lung tumor	universal normal control
PRO1100	breast tumor	universal normal control
PRO1100	rectal tumor	universal normal control
PRO1141	lung tumor	universal normal control
PRO1772	colon tumor	universal normal control
PRO1772	lung tumor	universal normal control
PRO1772	breast tumor	universal normal control
PRO1772	cervical tumor	universal normal control
PRO1064	colon tumor	universal normal control
PRO1064	lung tumor	universal normal control
PRO1379	colon tumor	universal normal control
PRO1379	lung tumor	universal normal control
PRO1379	cervical tumor	universal normal control
PRO3573	lung tumor	universal normal control
PRO3573	breast tumor	universal normal control
PRO3566	colon tumor	universal normal control
PRO3566	lung tumor	universal normal control
PRO1156	lung tumor	universal normal control
PRO1156	breast tumor	universal normal control
PRO1156	prostate tumor	universal normal control
PRO1098	colon tumor	universal normal control
PRO1098	lung tumor	universal normal control
PRO1098	rectal tumor	universal normal control
PRO1128	colon tumor	universal normal control
PRO1128	lung tumor	universal normal control
PRO1128	breast tumor	universal normal control
PRO1248	lung tumor	universal normal control
PRO1248	breast tumor	universal normal control
PRO1127	colon tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO1757	lung tumor	universal normal control
PRO1757	breast tumor	universal normal control
PRO1757	prostate tumor	universal normal control
PRO1758	lung tumor	universal normal control
PRO1781	colon tumor	universal normal control
PRO1781	lung tumor	universal normal control
PRO1781	breast tumor	universal normal control
PRO1606	lung tumor	universal normal control
PRO1606	breast tumor	universal normal control
PRO1784	colon tumor	universal normal control
PRO1784	lung tumor	universal normal control
PRO1784	breast tumor	universal normal control
PRO1774	colon tumor	universal normal control
PRO1774	lung tumor	universal normal control
PRO1774	breast tumor	universal normal control
PRO1605	colon tumor	universal normal control
PRO1605	lung tumor	universal normal control
PRO1605	prostate tumor	universal normal control
PRO1928	colon tumor	universal normal control
PRO1928	lung tumor	universal normal control
PRO1928	cervical tumor	universal normal control
PRO1865	lung tumor	universal normal control
PRO1865	liver tumor	universal normal control
PRO1925	lung tumor	universal normal control
PRO1926	liver tumor	universal normal control
PRO2630	colon tumor	universal normal control
PRO2630	lung tumor	universal normal control
PRO2630	breast tumor	universal normal control
PRO2630	liver tumor	universal normal control
PRO3443	colon tumor	universal normal control
PRO3443	lung tumor	universal normal control
PRO3443	breast tumor	universal normal control
PRO3301	colon tumor	universal normal control
PRO3301	lung tumor	universal normal control
PRO3301	breast tumor	universal normal control
PRO3301	rectal tumor	universal normal control
PRO3442	colon tumor	universal normal control
PRO3442	lung tumor	universal normal control
PRO3442	rectal tumor	universal normal control
PRO4978	colon tumor	universal normal control
PRO4978	lung tumor	universal normal control
PRO4978	breast tumor	universal normal control
PRO4978	rectal tumor	universal normal control
PRO5801	colon tumor	universal normal control
PRO5801	breast tumor	universal normal control
PRO19630	colon tumor	universal normal control
PRO203	colon tumor	universal normal control
PRO204	colon tumor	universal normal control
PRO204	lung tumor	universal normal control
PRO204	breast tumor	universal normal control
PRO204	prostate tumor	universal normal control
PRO210	colon tumor	universal normal control
PRO210	lung tumor	universal normal control
PRO223	lung tumor	universal normal control
PRO223	breast tumor	universal normal control
PRO247	colon tumor	universal normal control
PRO247	lung tumor	universal normal control
PRO247	breast	universal normal control
PRO358	lung tumor	universal normal control
PRO358	breast tumor	universal normal control
PRO358	prostate tumor	universal normal control
PRO724	lung tumor	universal normal control
PRO868	colon tumor	universal normal control
PRO868	lung tumor	universal normal control
PRO868	prostate tumor	universal normal control
PRO868	rectal tumor	universal normal control
PRO740	colon tumor	universal normal control
PRO1478	colon tumor	universal normal control
PRO1478	lung tumor	universal normal control
PRO162	colon tumor	universal normal control
PRO162	lung tumor	universal normal control
PRO162	breast tumor	universal normal control
PRO828	colon tumor	universal normal control
PRO828	lung tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO828	breast tumor	universal normal control
PRO828	cervical tumor	universal normal control
PRO828	liver tumor	universal normal control
PRO819	lung tumor	universal normal control
PRO819	breast tumor	universal normal control
PRO819	rectal tumor	universal normal control
PRO813	colon tumor	universal normal control
PRO813	lung tumor	universal normal control
PRO813	breast tumor	universal normal control
PRO813	prostate tumor	universal normal control
PRO1194	colon tumor	universal normal control
PRO1194	lung tumor	universal normal control
PRO1194	breast tumor	universal normal control
PRO887	colon tumor	universal normal control
PRO887	lung tumor	universal normal control
PRO887	rectal tumor	universal normal control
PRO1071	colon tumor	universal normal control
PRO1071	lung tumor	universal normal control
PRO1071	breast tumor	universal normal control
PRO1029	colon tumor	universal normal control
PRO1029	lung tumor	universal normal control
PRO1029	breast tumor	universal normal control
PRO1190	lung tumor	universal normal control
PRO1190	breast tumor	universal normal control
PRO4334	lung tumor	universal normal control
PRO1155	colon tumor	universal normal control
PRO1155	lung tumor	universal normal control
PRO1157	breast tumor	universal normal control
PRO1157	cervical tumor	universal normal control
PRO1122	lung tumor	universal normal control
PRO1122	breast tumor	universal normal control
PRO1183	colon tumor	universal normal control
PRO1183	lung tumor	universal normal control
PRO1183	breast tumor	universal normal control
PRO1337	colon tumor	universal normal control
PRO1337	lung tumor	universal normal control
PRO1337	breast tumor	universal normal control
PRO1480	colon tumor	universal normal control
PRO1480	lung tumor	universal normal control
PRO1480	breast tumor	universal normal control
PRO19645	colon tumor	universal normal control
PRO9782	colon tumor	universal normal control
PRO1419	colon tumor	universal normal control
PRO1575	colon tumor	universal normal control
PRO1575	lung tumor	universal normal control
PRO1567	colon tumor	universal normal control
PRO1567	lung tumor	universal normal control
PRO1567	breast tumor	universal normal control
PRO1891	colon tumor	universal normal control
PRO1889	colon tumor	universal normal control
PRO1889	lung tumor	universal normal control
PRO1785	lung tumor	universal normal control
PRO1785	prostate tumor	universal normal control
PRO6003	colon tumor	universal normal control
PRO4333	colon tumor	universal normal control
PRO4356	colon tumor	universal normal control
PRO4352	colon tumor	universal normal control
PRO4354	colon tumor	universal normal control
PRO4354	lung tumor	universal normal control
PRO4354	prostate tumor	universal normal control
PRO4369	colon tumor	universal normal control
PRO6030	colon tumor	universal normal control
PRO4433	colon tumor	universal normal control
PRO4424	colon tumor	universal normal control
PRO4424	breast tumor	universal normal control
PRO6017	colon tumor	universal normal control
PRO19563	colon tumor	universal normal control
PRO6015	colon tumor	universal normal control
PRO5779	colon tumor	universal normal control
PRO5776	colon tumor	universal normal control
PRO4430	lung tumor	universal normal control
PRO4421	colon tumor	universal normal control
PRO4499	colon tumor	universal normal control
PRO4423	colon tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO5998	colon tumor	universal normal control
PRO5998	lung tumor	universal normal control
PRO4501	colon tumor	universal normal control
PRO6240	colon tumor	universal normal control
PRO6245	colon tumor	universal normal control
PRO6175	colon tumor	universal normal control
PRO9742	colon tumor	universal normal control
PRO7179	colon tumor	universal normal control
PRO6239	colon tumor	universal normal control
PRO6493	colon tumor	universal normal control
PRO9741	colon tumor	universal normal control
PRO9822	colon tumor	universal normal control
PRO6244	colon tumor	universal normal control
PRO9740	colon tumor	universal normal control
PRO9739	colon tumor	universal normal control
PRO7177	colon tumor	universal normal control
PRO7178	colon tumor	universal normal control
PRO6246	colon tumor	universal normal control
PRO6241	colon tumor	universal normal control
PRO9835	colon tumor	universal normal control
PRO9857	colon tumor	universal normal control
PRO7436	colon tumor	universal normal control
PRO9856	colon tumor	universal normal control
PRO19605	colon tumor	universal normal control
PRO9859	colon tumor	universal normal control
PRO12970	colon tumor	universal normal control
PRO19626	colon tumor	universal normal control
PRO9883	colon tumor	universal normal control
PRO19670	colon tumor	universal normal control
PRO19624	colon tumor	universal normal control
PRO19680	colon tumor	universal normal control
PRO19675	colon tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO9834	colon tumor	universal normal control
PRO9744	colon tumor	universal normal control
PRO19644	colon tumor	universal normal control
PRO19625	colon tumor	universal normal control
PRO19597	colon tumor	universal normal control
PRO16090	colon tumor	universal normal control
PRO19576	colon tumor	universal normal control
PRO19646	colon tumor	universal normal control
PRO19814	colon tumor	universal normal control
PRO19669	colon tumor	universal normal control
PRO19818	colon tumor	universal normal control
PRO20088	colon tumor	universal normal control
PRO16089	colon tumor	universal normal control
PRO20025	colon tumor	universal normal control
PRO20040	colon tumor	universal normal control
PRO1760	adrenal tumor	universal normal control
PRO1760	breast tumor	universal normal control
PRO1760	cervical tumor	universal normal control
PRO1760	colon tumor	universal normal control
PRO1760	liver tumor	universal normal control
PRO1760	lung tumor	universal normal control
PRO1760	prostate tumor	universal normal control
PRO1760	rectal tumor	universal normal control
PRO6029	adrenal tumor	universal normal control
PRO6029	colon tumor	universal normal control
PRO6029	prostate tumor	universal normal control
PRO1801	colon tumor	universal normal control
PRO1801	lung tumor	universal normal control

[0955]

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/sequence.html?DocID=20030027262>). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in **FIG. 2** (SEQ ID NO: 2), **FIG. 4** (SEQ ID NO: 4), **FIG. 6** (SEQ ID NO: 6), **FIG. 8** (SEQ ID NO: 8), **FIG. 10** (SEQ ID NO: 10), **FIG. 12** (SEQ ID NO: 12), **FIG. 14** (SEQ ID NO: 14), **FIG. 16** (SEQ ID NO: 16), **FIG. 18** (SEQ ID NO: 18), **FIG. 20** (SEQ ID NO: 20), **FIG. 22** (SEQ ID NO: 22), **FIG. 24** (SEQ ID NO: 24), **FIG. 26** (SEQ ID NO: 26), **FIG. 28** (SEQ ID NO: 28), **FIG. 30** (SEQ ID NO: 30), **FIG. 32** (SEQ ID NO: 32), **FIG. 34** (SEQ ID NO: 34), **FIG. 36** (SEQ ID NO: 36), **FIG. 38** (SEQ ID NO: 38), **FIG. 40** (SEQ ID NO: 40), **FIG. 42** (SEQ ID NO: 42), **FIG. 44** (SEQ ID NO: 44), **FIG. 46** (SEQ ID NO: 46), **FIG. 48** (SEQ ID NO: 48), **FIG. 50** (SEQ ID NO: 50), **FIG. 52** (SEQ ID NO: 52), **FIG. 54** (SEQ ID NO: 54), **FIG. 56** (SEQ ID NO: 56), **FIG. 58** (SEQ ID NO: 58), **FIG. 60** (SEQ ID NO: 60), **FIG. 62** (SEQ ID NO: 62), **FIG. 64** (SEQ

ID NO: 64), **FIG. 66** (SEQ ID NO: 66), **FIG. 68** (SEQ ID NO: 68), **FIG. 70** (SEQ ID NO: 70), **FIG. 72** (SEQ ID NO: 72), **FIG. 74** (SEQ ID NO: 74), **FIG. 76** (SEQ ID NO: 76), **FIG. 78** (SEQ ID NO: 78), **FIG. 80** (SEQ ID NO: 80), **FIG. 82** (SEQ ID NO: 82), **FIG. 84** (SEQ ID NO: 84), **FIG. 86** (SEQ ID NO: 86), **FIG. 88** (SEQ ID NO: 88), **FIG. 90** (SEQ ID NO: 90), **FIG. 92** (SEQ ID NO: 92), **FIG. 94** (SEQ ID NO: 94), **FIG. 96** (SEQ ID NO: 96), **FIG. 98** (SEQ ID NO: 98), **FIG. 100** (SEQ ID NO: 100), **FIG. 102** (SEQ ID NO: 102), **FIG. 104** (SEQ ID NO: 104), **FIG. 106** (SEQ ID NO: 106), **FIG. 108** (SEQ ID NO: 108), **FIG. 110** (SEQ ID NO: 110), **FIG. 112** (SEQ ID NO: 112), **FIG. 114** (SEQ ID NO: 114), **FIG. 116** (SEQ ID NO: 116), **FIG. 118** (SEQ ID NO: 118), **FIG. 120** (SEQ ID NO: 120), **FIG. 122** (SEQ ID NO: 122), **FIG. 124** (SEQ ID NO: 124), **FIG. 126** (SEQ ID NO: 126), **FIG. 128** (SEQ ID NO: 128), **FIG. 130** (SEQ ID NO: 130), **FIG. 132** (SEQ ID NO: 132), **FIG. 134** (SEQ ID NO: 134), **FIG. 136** (SEQ ID NO: 136), **FIG. 138** (SEQ ID NO: 138), **FIG. 140** (SEQ ID NO: 140), **FIG. 142** (SEQ ID NO:

NO: 31), FIG. 33 (SEQ ID NO: 33), FIG. 35 (SEQ ID NO: 35), FIG. 37 (SEQ ID NO: 37), FIG. 39 (SEQ ID NO: 39), FIG. 41 (SEQ ID NO: 41), FIG. 43 (SEQ ID NO: 43), FIG. 45 (SEQ ID NO: 45), FIG. 47 (SEQ ID NO: 47), FIG. 49 (SEQ ID NO: 49), FIG. 51 (SEQ ID NO: 51), FIG. 53 (SEQ ID NO: 53), FIG. 55 (SEQ ID NO: 55), FIG. 57 (SEQ ID NO: 57), FIG. 59 (SEQ ID NO: 59), FIG. 61 (SEQ ID NO: 61), FIG. 63 (SEQ ID NO: 63), FIG. 65 (SEQ ID NO: 65), FIG. 67 (SEQ ID NO: 67), FIG. 69 (SEQ ID NO: 69), FIG. 71 (SEQ ID NO: 71), FIG. 73 (SEQ ID NO: 73), FIGS. 75A-75B (SEQ ID NO: 75), FIG. 77 (SEQ ID NO: 77), FIG. 79 (SEQ ID NO: 79), FIG. 81 (SEQ ID NO: 81), FIG. 83 (SEQ ID NO: 83), FIG. 85 (SEQ ID NO: 85), FIG. 87 (SEQ ID NO: 87), FIG. 89 (SEQ ID NO: 89), FIG. 91 (SEQ ID NO: 91), FIG. 93 (SEQ ID NO: 93), FIG. 95 (SEQ ID NO: 95), FIG. 97 (SEQ ID NO: 97), FIG. 99 (SEQ ID NO: 99), FIG. 101 (SEQ ID NO: 101), FIG. 103 (SEQ ID NO: 103), FIG. 105 (SEQ ID NO: 105), FIG. 107 (SEQ ID NO: 107), FIG. 109 (SEQ ID NO: 109), FIG. 111 (SEQ ID NO: 111), FIG. 113 (SEQ ID NO: 113), FIG. 115 (SEQ ID NO: 115), FIG. 117 (SEQ ID NO: 117), FIG. 119 (SEQ ID NO: 119), FIG. 121 (SEQ ID NO: 121), FIG. 123 (SEQ ID NO: 123), FIG. 125 (SEQ ID NO: 125), FIG. 127 (SEQ ID NO: 127), FIG. 129 (SEQ ID NO: 129), FIG. 131 (SEQ ID NO: 131), FIG. 133 (SEQ ID NO: 133), FIG. 135 (SEQ ID NO: 135), FIG. 137 (SEQ ID NO: 137), FIG. 139 (SEQ ID NO: 139), FIG. 141 (SEQ ID NO: 141), FIG. 143 (SEQ ID NO: 143), FIG. 145 (SEQ ID NO: 145), FIG. 147 (SEQ ID NO: 147), FIG. 149 (SEQ ID NO: 149), FIG. 151 (SEQ ID NO: 151), FIG. 153 (SEQ ID NO: 153), FIG. 155 (SEQ ID NO: 155), FIG. 157 (SEQ ID NO: 157), FIG. 159 (SEQ ID NO: 159), FIG. 161 (SEQ ID NO: 161), FIG. 163 (SEQ ID NO: 163), FIG. 165 (SEQ ID NO: 165), FIG. 167 (SEQ ID NO: 167), FIG. 169 (SEQ ID NO: 169), FIG. 171 (SEQ ID NO: 171), FIG. 173 (SEQ ID NO: 173), FIG. 175 (SEQ ID NO: 175), FIG. 177 (SEQ ID NO: 177), FIG. 179 (SEQ ID NO: 179), FIG. 181 (SEQ ID NO: 181), FIG. 183 (SEQ ID NO: 183), FIG. 185 (SEQ ID NO: 185), FIG. 187 (SEQ ID NO: 187), FIG. 189 (SEQ ID NO: 189), FIG. 191 (SEQ ID NO: 191), FIG. 193 (SEQ ID NO: 193), FIG. 195 (SEQ ID NO: 195), FIG. 197 (SEQ ID NO: 197), FIG. 199 (SEQ ID NO: 199), FIG. 201 (SEQ ID NO: 201), FIG. 203 (SEQ ID NO: 203), FIG. 205 (SEQ ID NO: 205), FIG. 207 (SEQ ID NO: 207), FIG. 209 (SEQ ID NO: 209), FIG. 211 (SEQ ID NO: 211), FIG. 213 (SEQ ID NO: 213), FIG. 215 (SEQ ID NO: 215), FIG. 217 (SEQ ID NO: 217), FIG. 219 (SEQ ID NO: 219), FIG. 221 (SEQ ID NO: 221), FIG. 223 (SEQ ID NO: 223), FIG. 225 (SEQ ID NO: 225), FIG. 227 (SEQ ID NO: 227), FIG. 229 (SEQ ID NO: 229), FIG. 231 (SEQ ID NO: 231), FIG. 233 (SEQ ID NO: 233), FIG. 235 (SEQ ID NO: 235), FIG. 237 (SEQ ID NO: 237), FIG. 239 (SEQ ID NO: 239), FIG. 241 (SEQ ID NO: 241), FIG. 243 (SEQ ID NO: 243), FIG. 245 (SEQ ID NO: 245), FIG. 247 (SEQ ID NO: 247), FIG. 249 (SEQ ID NO: 249), FIG. 251 (SEQ ID NO: 251), FIG. 253 (SEQ ID NO: 253), FIG. 255 (SEQ ID NO: 255), FIG. 257 (SEQ ID NO: 257), FIG. 259 (SEQ ID NO: 259), FIG. 261 (SEQ ID NO: 261), FIG. 263 (SEQ ID NO: 263), FIG. 265 (SEQ ID NO: 265), FIG. 267 (SEQ ID NO: 267), FIG. 269 (SEQ ID NO: 269), FIG. 271 (SEQ ID NO: 271), FIG. 273 (SEQ ID NO: 273), FIG. 275 (SEQ ID NO: 275), FIG. 277 (SEQ ID NO: 277), FIG. 279 (SEQ ID NO: 279), FIG. 281 (SEQ ID NO: 281), FIG. 283 (SEQ ID NO: 283), FIG. 285 (SEQ ID NO: 285), FIG. 287 (SEQ ID NO: 287), FIGS. 289A-289B (SEQ ID NO: 289), FIG. 291 (SEQ

ID NO: 291), FIG. 293 (SEQ ID NO: 293), FIG. 295 (SEQ ID NO: 295), FIG. 297 (SEQ ID NO: 297), FIG. 299 (SEQ ID NO: 299), FIG. 301 (SEQ ID NO: 301), FIG. 303 (SEQ ID NO: 303), FIG. 305 (SEQ ID NO: 305), FIG. 307 (SEQ ID NO: 307), FIG. 309 (SEQ ID NO: 309), FIGS. 311A-311B (SEQ ID NO: 311), FIG. 313 (SEQ ID NO: 313), FIG. 315 (SEQ ID NO: 315), FIG. 317 (SEQ ID NO: 317), FIG. 319 (SEQ ID NO: 319), FIG. 321 (SEQ ID NO: 321), FIG. 323 (SEQ ID NO: 323), FIG. 325 (SEQ ID NO: 325), FIG. 327 (SEQ ID NO: 327), FIG. 329 (SEQ ID NO: 329), FIG. 331 (SEQ ID NO: 331), FIG. 333 (SEQ ID NO: 333), FIG. 335 (SEQ ID NO: 335), FIG. 337 (SEQ ID NO: 337), FIG. 339 (SEQ ID NO: 339), FIG. 341 (SEQ ID NO: 341), FIG. 343 (SEQ ID NO: 343), FIG. 345 (SEQ ID NO: 345), FIG. 347 (SEQ ID NO: 347), FIG. 349 (SEQ ID NO: 349), FIGS. 351A-351B (SEQ ID NO: 351), FIG. 353 (SEQ ID NO: 353), FIG. 355 (SEQ ID NO: 355), FIG. 357 (SEQ ID NO: 357), FIG. 359 (SEQ ID NO: 359), FIG. 361 (SEQ ID NO: 361), FIG. 363 (SEQ ID NO: 363), FIG. 365 (SEQ ID NO: 365), FIG. 367 (SEQ ID NO: 367), FIG. 369 (SEQ ID NO: 369), FIG. 371 (SEQ ID NO: 371), FIG. 373 (SEQ ID NO: 373), FIG. 375 (SEQ ID NO: 375), FIG. 377 (SEQ ID NO: 377), FIG. 379 (SEQ ID NO: 379), FIG. 381 (SEQ ID NO: 381), FIG. 383 (SEQ ID NO: 383), FIG. 385 (SEQ ID NO: 385), FIG. 387 (SEQ ID NO: 387), FIG. 389 (SEQ ID NO: 389), FIG. 391 (SEQ ID NO: 391), FIG. 393 (SEQ ID NO: 393), FIG. 395 (SEQ ID NO: 395), FIG. 397 (SEQ ID NO: 397), FIG. 399 (SEQ ID NO: 399), FIG. 401 (SEQ ID NO: 401), FIG. 403 (SEQ ID NO: 403), FIG. 405 (SEQ ID NO: 405), FIG. 407 (SEQ ID NO: 407), FIG. 409 (SEQ ID NO: 409), FIG. 411 (SEQ ID NO: 411), FIG. 413 (SEQ ID NO: 413), FIG. 415 (SEQ ID NO: 415), FIG. 417 (SEQ ID NO: 417), FIG. 419 (SEQ ID NO: 419), FIG. 421 (SEQ ID NO: 421), FIG. 423 (SEQ ID NO: 423), FIG. 425 (SEQ ID NO: 425), FIG. 427 (SEQ ID NO: 427), FIG. 429 (SEQ ID NO: 429), FIG. 431 (SEQ ID NO: 431), FIG. 433 (SEQ ID NO: 433), FIG. 435 (SEQ ID NO: 435), FIG. 437 (SEQ ID NO: 437), FIG. 439 (SEQ ID NO: 439), FIG. 441 (SEQ ID NO: 441), FIG. 443 (SEQ ID NO: 443), FIG. 445 (SEQ ID NO: 445), FIG. 447 (SEQ ID NO: 447), FIG. 449 (SEQ ID NO: 449), FIG. 451 (SEQ ID NO: 451), FIG. 453 (SEQ ID NO: 453), FIG. 455 (SEQ ID NO: 455), FIG. 457 (SEQ ID NO: 457), FIG. 459 (SEQ ID NO: 459), FIG. 461 (SEQ ID NO: 461), FIG. 463 (SEQ ID NO: 463), FIG. 465 (SEQ ID NO: 465), FIG. 467 (SEQ ID NO: 467), FIG. 469 (SEQ ID NO: 469), FIG. 471 (SEQ ID NO: 471), FIG. 473 (SEQ ID NO: 473), FIG. 475 (SEQ ID NO: 475), FIG. 477 (SEQ ID NO: 477), FIG. 479 (SEQ ID NO: 479), FIG. 481 (SEQ ID NO: 481), FIG. 483 (SEQ ID NO: 483), FIG. 485 (SEQ ID NO: 485), FIG. 487 (SEQ ID NO: 487), FIG. 489 (SEQ ID NO: 489), FIG. 491 (SEQ ID NO: 491), FIG. 493 (SEQ ID NO: 493), FIG. 495 (SEQ ID NO: 495), FIG. 497 (SEQ ID NO: 497), FIG. 499 (SEQ ID NO: 499), FIG. 501 (SEQ ID NO: 501), FIG. 503 (SEQ ID NO: 503), FIG. 505 (SEQ ID NO: 505), FIG. 507 (SEQ ID NO: 507), FIG. 509 (SEQ ID NO: 509), FIG. 511 (SEQ ID NO: 511), FIG. 513 (SEQ ID NO: 513), FIG. 515 (SEQ ID NO: 515), FIG. 517 (SEQ ID NO: 517), FIG. 519 (SEQ ID NO: 519), FIG. 521 (SEQ ID NO: 521), FIG. 523 (SEQ ID NO: 523), FIGS. 525A-525B (SEQ ID NO: 525), FIG. 527 (SEQ ID NO: 527), FIG. 529 (SEQ ID NO: 529), FIG. 531 (SEQ ID NO: 531), FIG. 533 (SEQ ID NO: 533), FIG. 535 (SEQ ID NO: 535), FIG. 537 (SEQ ID NO: 537), FIG. 539 (SEQ ID NO: 539), FIG. 541 (SEQ ID NO: 541), FIG. 543 (SEQ ID NO: 543), FIG. 545 (SEQ

ID NO: 545), **FIG. 547** (SEQ ID NO: 547), **FIG. 549** (SEQ ID NO: 549), **FIG. 551** (SEQ ID NO: 551), **FIG. 553** (SEQ ID NO: 553), **FIG. 555** (SEQ ID NO: 555), **FIG. 557** (SEQ ID NO: 557), **FIG. 559** (SEQ ID NO: 559), **FIG. 561** (SEQ ID NO: 561), **FIG. 563** (SEQ ID NO: 563), **FIG. 565** (SEQ ID NO: 565), **FIG. 567** (SEQ ID NO: 567), **FIG. 569** (SEQ ID NO: 569), **FIG. 571** (SEQ ID NO: 571), **FIG. 573** (SEQ ID NO: 573), **FIG. 575** (SEQ ID NO: 575), **FIG. 577** (SEQ ID NO: 577), **FIG. 579** (SEQ ID NO: 579), **FIG. 581** (SEQ ID NO: 581), **FIG. 583** (SEQ ID NO: 583), **FIG. 585** (SEQ ID NO: 585), **FIG. 587** (SEQ ID NO: 587), **FIG. 589** (SEQ ID NO: 589), **FIG. 591** (SEQ ID NO: 591), **FIG. 593** (SEQ ID NO: 593), **FIG. 595** (SEQ ID NO: 595), **FIG. 597** (SEQ ID NO: 597), **FIG. 599** (SEQ ID NO: 599), **FIG. 601** (SEQ ID NO: 601), **FIG. 603** (SEQ ID NO: 603), **FIG. 605** (SEQ ID NO: 605), **FIG. 607** (SEQ ID NO: 607), and **FIG. 609** (SEQ ID NO: 609).

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in **FIG. 1** (SEQ ID NO: 1), **FIG. 3** (SEQ ID NO: 3), **FIG. 5** (SEQ ID NO: 5), **FIG. 7** (SEQ ID NO: 7), **FIG. 9** (SEQ ID NO: 9), **FIG. 11** (SEQ ID NO: 11), **FIG. 13** (SEQ ID NO: 13), **FIG. 15** (SEQ ID NO: 15), **FIG. 17** (SEQ ID NO: 17), **FIG. 19** (SEQ ID NO: 19), **FIG. 21** (SEQ ID NO: 21), **FIG. 23** (SEQ ID NO: 23), **FIG. 25** (SEQ ID NO: 25), **FIG. 27** (SEQ ID NO: 27), **FIG. 29** (SEQ ID NO: 29), **FIG. 31** (SEQ ID NO: 31), **FIG. 33** (SEQ ID NO: 33), **FIG. 35** (SEQ ID NO: 35), **FIG. 37** (SEQ ID NO: 37), **FIG. 39** (SEQ ID NO: 39), **FIG. 41** (SEQ ID NO: 41), **FIG. 43** (SEQ ID NO: 43), **FIG. 45** (SEQ ID NO: 45), **FIG. 47** (SEQ ID NO: 47), **FIG. 49** (SEQ ID NO: 49), **FIG. 51** (SEQ ID NO: 51), **FIG. 53** (SEQ ID NO: 53), **FIG. 55** (SEQ ID NO: 55), **FIG. 57** (SEQ ID NO: 57), **FIG. 59** (SEQ ID NO: 59), **FIG. 61** (SEQ ID NO: 61), **FIG. 63** (SEQ ID NO: 63), **FIG. 65** (SEQ ID NO: 65), **FIG. 67** (SEQ ID NO: 67), **FIG. 69** (SEQ ID NO: 69), **FIG. 71** (SEQ ID NO: 71), **FIG. 73** (SEQ ID NO: 73), **FIGS. 75A-75B** (SEQ ID NO: 75), **FIG. 77** (SEQ ID NO: 77), **FIG. 79** (SEQ ID NO: 79), **FIG. 81** (SEQ ID NO: 81), **FIG. 83** (SEQ ID NO: 83), **FIG. 85** (SEQ ID NO: 85), **FIG. 87** (SEQ ID NO: 87), **FIG. 89** (SEQ ID NO: 89), **FIG. 91** (SEQ ID NO: 91), **FIG. 93** (SEQ ID NO: 93), **FIG. 95** (SEQ ID NO: 95), **FIG. 97** (SEQ ID NO: 97), **FIG. 99** (SEQ ID NO: 99), **FIG. 101** (SEQ ID NO: 101), **FIG. 103** (SEQ ID NO: 103), **FIG. 105** (SEQ ID NO: 105), **FIG. 107** (SEQ ID NO: 107), **FIG. 109** (SEQ ID NO: 109), **FIG. 111** (SEQ ID NO: 111), **FIG. 113** (SEQ ID NO: 113), **FIG. 115** (SEQ ID NO: 115), **FIG. 117** (SEQ ID NO: 117), **FIG. 119** (SEQ ID NO: 119), **FIG. 121** (SEQ ID NO: 121), **FIG. 123** (SEQ ID NO: 123), **FIG. 125** (SEQ ID NO: 125), **FIG. 127** (SEQ ID NO: 127), **FIG. 129** (SEQ ID NO: 129), **FIG. 131** (SEQ ID NO: 131), **FIG. 133** (SEQ ID NO: 133), **FIG. 135** (SEQ ID NO: 135), **FIG. 137** (SEQ ID NO: 137), **FIG. 139** (SEQ ID NO: 139), **FIG. 141** (SEQ ID NO: 141), **FIG. 143** (SEQ ID NO: 143), **FIG. 145** (SEQ ID NO: 145), **FIG. 147** (SEQ ID NO: 147), **FIG. 149** (SEQ ID NO: 149), **FIG. 151** (SEQ ID NO: 151), **FIG. 153** (SEQ ID NO: 153), **FIG. 155** (SEQ ID NO: 155), **FIG. 157** (SEQ ID NO: 157), **FIG. 159** (SEQ ID NO: 159), **FIG. 161** (SEQ ID NO: 161), **FIG. 163** (SEQ ID NO: 163), **FIG. 165** (SEQ ID NO: 165), **FIG. 167** (SEQ ID NO: 167), **FIG. 169** (SEQ ID NO: 169), **FIG. 171** (SEQ ID NO: 171), **FIG. 173** (SEQ ID NO: 173), **FIG. 175** (SEQ ID NO: 175), **FIG. 177** (SEQ ID NO: 177), **FIG. 179** (SEQ ID NO: 179), **FIG. 181** (SEQ ID NO:

181), **FIG. 183** (SEQ ID NO: 183), **FIG. 185** (SEQ ID NO: 185), **FIG. 187** (SEQ ID NO: 187), **FIG. 189** (SEQ ID NO: 189), **FIG. 191** (SEQ ID NO: 191), **FIG. 193** (SEQ ID NO: 193), **FIG. 195** (SEQ ID NO: 195), **FIG. 197** (SEQ ID NO: 197), **FIG. 199** (SEQ ID NO: 199), **FIG. 201** (SEQ ID NO: 201), **FIG. 203** (SEQ ID NO: 203), **FIG. 205** (SEQ ID NO: 205), **FIG. 207** (SEQ ID NO: 207), **FIG. 209** (SEQ ID NO: 209), **FIG. 211** (SEQ ID NO: 211), **FIG. 213** (SEQ ID NO: 213), **FIG. 215** (SEQ ID NO: 215), **FIG. 217** (SEQ ID NO: 217), **FIG. 219** (SEQ ID NO: 219), **FIG. 221** (SEQ ID NO: 221), **FIG. 223** (SEQ ID NO: 223), **FIG. 225** (SEQ ID NO: 225), **FIG. 227** (SEQ ID NO: 227), **FIG. 229** (SEQ ID NO: 229), **FIG. 231** (SEQ ID NO: 231), **FIG. 233** (SEQ ID NO: 233), **FIG. 235** (SEQ ID NO: 235), **FIG. 237** (SEQ ID NO: 237), **FIG. 239** (SEQ ID NO: 239), **FIG. 241** (SEQ ID NO: 241), **FIG. 243** (SEQ ID NO: 243), **FIG. 245** (SEQ ID NO: 245), **FIG. 247** (SEQ ID NO: 247), **FIG. 249** (SEQ ID NO: 249), **FIG. 251** (SEQ ID NO: 251), **FIG. 253** (SEQ ID NO: 253), **FIG. 255** (SEQ ID NO: 255), **FIG. 257** (SEQ ID NO: 257), **FIG. 259** (SEQ ID NO: 259), **FIG. 261** (SEQ ID NO: 261), **FIG. 263** (SEQ ID NO: 263), **FIG. 265** (SEQ ID NO: 265), **FIG. 267** (SEQ ID NO: 267), **FIG. 269** (SEQ ID NO: 269), **FIG. 271** (SEQ ID NO: 271), **FIG. 273** (SEQ ID NO: 273), **FIG. 275** (SEQ ID NO: 275), **FIG. 277** (SEQ ID NO: 277), **FIG. 279** (SEQ ID NO: 279), **FIG. 281** (SEQ ID NO: 281), **FIG. 283** (SEQ ID NO: 283), **FIG. 285** (SEQ ID NO: 285), **FIG. 287** (SEQ ID NO: 287), **FIGS. 289A-289B** (SEQ ID NO: 289), **FIG. 291** (SEQ ID NO: 291), **FIG. 293** (SEQ ID NO: 293), **FIG. 295** (SEQ ID NO: 295), **FIG. 297** (SEQ ID NO: 297), **FIG. 299** (SEQ ID NO: 299), **FIG. 301** (SEQ ID NO: 301), **FIG. 303** (SEQ ID NO: 303), **FIG. 305** (SEQ ID NO: 305), **FIG. 307** (SEQ ID NO: 307), **FIG. 309** (SEQ ID NO: 309), **FIGS. 311A-311B** (SEQ ID NO: 311), **FIG. 313** (SEQ ID NO: 313), **FIG. 315** (SEQ ID NO: 315), **FIG. 317** (SEQ ID NO: 317), **FIG. 319** (SEQ ID NO: 319), **FIG. 321** (SEQ ID NO: 321), **FIG. 323** (SEQ ID NO: 323), **FIG. 325** (SEQ ID NO: 325), **FIG. 327** (SEQ ID NO: 327), **FIG. 329** (SEQ ID NO: 329), **FIG. 331** (SEQ ID NO: 331), **FIG. 333** (SEQ ID NO: 333), **FIG. 335** (SEQ ID NO: 335), **FIG. 337** (SEQ ID NO: 337), **FIG. 339** (SEQ ID NO: 339), **FIG. 341** (SEQ ID NO: 341), **FIG. 343** (SEQ ID NO: 343), **FIG. 345** (SEQ ID NO: 345), **FIG. 347** (SEQ ID NO: 347), **FIG. 349** (SEQ ID NO: 349), **FIGS. 351A-351B** (SEQ ID NO: 351), **FIG. 353** (SEQ ID NO: 353), **FIG. 355** (SEQ ID NO: 355), **FIG. 357** (SEQ ID NO: 357), **FIG. 359** (SEQ ID NO: 359), **FIG. 361** (SEQ ID NO: 361), **FIG. 363** (SEQ ID NO: 363), **FIG. 365** (SEQ ID NO: 365), **FIG. 367** (SEQ ID NO: 367), **FIG. 369** (SEQ ID NO: 369), **FIG. 371** (SEQ ID NO: 371), **FIG. 373** (SEQ ID NO: 373), **FIG. 375** (SEQ ID NO: 375), **FIG. 377** (SEQ ID NO: 377), **FIG. 379** (SEQ ID NO: 379), **FIG. 381** (SEQ ID NO: 381), **FIG. 383** (SEQ ID NO: 383), **FIG. 385** (SEQ ID NO: 385), **FIG. 387** (SEQ ID NO: 387), **FIG. 389** (SEQ ID NO: 389), **FIG. 391** (SEQ ID NO: 391), **FIG. 393** (SEQ ID NO: 393), **FIG. 395** (SEQ ID NO: 395), **FIG. 397** (SEQ ID NO: 397), **FIG. 399** (SEQ ID NO: 399), **FIG. 401** (SEQ ID NO: 401), **FIG. 403** (SEQ ID NO: 403), **FIG. 405** (SEQ ID NO: 405), **FIG. 407** (SEQ ID NO: 407), **FIG. 409** (SEQ ID NO: 409), **FIG. 411** (SEQ ID NO: 411), **FIG. 413** (SEQ ID NO: 413), **FIG. 415** (SEQ ID NO: 415), **FIG. 417** (SEQ ID NO: 417), **FIG. 419** (SEQ ID NO: 419), **FIG. 421** (SEQ ID NO: 421), **FIG. 423** (SEQ ID NO: 423), **FIG. 425** (SEQ ID NO: 425), **FIG. 427** (SEQ ID NO: 427), **FIG. 429** (SEQ ID NO: 429), **FIG. 431** (SEQ ID NO: 431), **FIG. 433** (SEQ ID NO: 433), **FIG. 435** (SEQ ID NO:

435), **FIG. 437** (SEQ ID NO: 437), **FIG. 439** (SEQ ID NO: 439), **FIG. 441** (SEQ ID NO: 441), **FIG. 443** (SEQ ID NO: 443), **FIG. 445** (SEQ ID NO: 445), **FIG. 447** (SEQ ID NO: 447), **FIG. 449** (SEQ ID NO: 449), **FIG. 451** (SEQ ID NO: 451), **FIG. 453** (SEQ ID NO: 453), **FIG. 455** (SEQ ID NO: 455), **FIG. 457** (SEQ ID NO: 457), **FIG. 459** (SEQ ID NO: 459), **FIG. 461** (SEQ ID NO: 461), **FIG. 463** (SEQ ID NO: 463), **FIG. 465** (SEQ ID NO: 465), **FIG. 467** (SEQ ID NO: 467), **FIG. 469** (SEQ ID NO: 469), **FIG. 471** (SEQ ID NO: 471), **FIG. 473** (SEQ ID NO: 473), **FIG. 475** (SEQ ID NO: 475), **FIG. 477** (SEQ ID NO: 477), **FIG. 479** (SEQ ID NO: 479), **FIG. 481** (SEQ ID NO: 481), **FIG. 483** (SEQ ID NO: 483), **FIG. 485** (SEQ ID NO: 485), **FIG. 487** (SEQ ID NO: 487), **FIG. 489** (SEQ ID NO: 489), **FIG. 491** (SEQ ID NO: 491), **FIG. 493** (SEQ ID NO: 493), **FIG. 495** (SEQ ID NO: 495), **FIG. 497** (SEQ ID NO: 497), **FIG. 499** (SEQ ID NO: 499), **FIG. 501** (SEQ ID NO: 501), **FIG. 503** (SEQ ID NO: 503), **FIG. 505** (SEQ ID NO: 505), **FIG. 507** (SEQ ID NO: 507), **FIG. 509** (SEQ ID NO: 509), **FIG. 511** (SEQ ID NO: 511), **FIG. 513** (SEQ ID NO: 513), **FIG. 515** (SEQ ID NO: 515), **FIG. 517** (SEQ ID NO: 517), **FIG. 519** (SEQ ID NO: 519), **FIG. 521** (SEQ ID NO: 521), **FIG. 523** (SEQ ID NO: 523), **FIGS. 525A-525B** (SEQ ID NO: 525), **FIG. 527** (SEQ ID NO: 527), **FIG. 529** (SEQ ID NO: 529), **FIG. 531** (SEQ ID NO: 531), **FIG. 533** (SEQ ID NO: 533), **FIG. 535** (SEQ ID NO: 535), **FIG. 537** (SEQ ID NO: 537), **FIG. 539** (SEQ ID NO: 539), **FIG. 541** (SEQ ID NO: 541), **FIG. 543** (SEQ ID NO: 543), **FIG. 545** (SEQ ID NO: 545), **FIG. 547** (SEQ ID NO: 547), **FIG. 549** (SEQ ID NO: 549), **FIG. 551** (SEQ ID NO: 551), **FIG. 553** (SEQ ID NO: 553), **FIG. 555** (SEQ ID NO: 555), **FIG. 557** (SEQ ID NO: 557), **FIG. 559** (SEQ ID NO: 559), **FIG. 561** (SEQ ID NO: 561), **FIG. 563** (SEQ ID NO: 563), **FIG. 565** (SEQ ID NO: 565), **FIG. 567** (SEQ ID NO: 567), **FIG. 569** (SEQ ID NO: 569), **FIG. 571** (SEQ ID NO: 571), **FIG. 573** (SEQ ID NO: 573), **FIG. 575** (SEQ ID NO: 575), **FIG. 577** (SEQ ID NO: 577), **FIG. 579** (SEQ ID NO: 579), **FIG. 581** (SEQ ID NO: 581), **FIG. 583** (SEQ ID NO: 583), **FIG. 585** (SEQ ID NO: 585), **FIG. 587** (SEQ ID NO: 587), **FIG. 589** (SEQ ID NO: 589), **FIG. 591** (SEQ ID NO: 591), **FIG. 593** (SEQ ID NO: 593), **FIG. 595** (SEQ ID NO: 595), **FIG. 597** (SEQ ID NO: 597), **FIG. 599** (SEQ ID NO: 599), **FIG. 601** (SEQ ID NO: 601), **FIG. 603** (SEQ ID NO: 603), **FIG. 605** (SEQ ID NO: 605), **FIG. 607** (SEQ ID NO: 607), and **FIG. 609** (SEQ ID NO: 609).

4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5. A vector comprising the nucleic acid of claim 1.

6. A host cell comprising the vector of claim 5.

7. The host cell of claim 6, wherein said cell is a CHO cell.

8. The host cell of claim 6, wherein said cell is an *E. coli*.

9. The host cell of claim 6, wherein said cell is a yeast cell.

10. A process for producing a PRO polypeptide comprising culturing the host cell of claim 6 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

11. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in **FIG. 2** (SEQ ID NO: 2), **FIG. 4** (SEQ ID NO: 4), **FIG. 6** (SEQ ID NO: 6), **FIG. 8** (SEQ ID NO: 8), **FIG. 10** (SEQ ID NO: 10), **FIG. 12** (SEQ ID NO: 12), **FIG. 14** (SEQ ID NO: 14), **FIG. 16** (SEQ ID NO: 16), **FIG. 18** (SEQ ID NO:

18), **FIG. 20** (SEQ ID NO: 20), **FIG. 22** (SEQ ID NO: 22), **FIG. 24** (SEQ ID NO: 24), **FIG. 26** (SEQ ID NO: 26), **FIG. 28** (SEQ ID NO: 28), **FIG. 30** (SEQ ID NO: 30), **FIG. 32** (SEQ ID NO: 32), **FIG. 34** (SEQ ID NO: 34), **FIG. 36** (SEQ ID NO: 36), **FIG. 38** (SEQ ID NO: 38), **FIG. 40** (SEQ ID NO: 40), **FIG. 42** (SEQ ID NO: 42), **FIG. 44** (SEQ ID NO: 44), **FIG. 46** (SEQ ID NO: 46), **FIG. 48** (SEQ ID NO: 48), **FIG. 50** (SEQ ID NO: 50), **FIG. 52** (SEQ ID NO: 52), **FIG. 54** (SEQ ID NO: 54), **FIG. 56** (SEQ ID NO: 56), **FIG. 58** (SEQ ID NO: 58), **FIG. 60** (SEQ ID NO: 60), **FIG. 62** (SEQ ID NO: 62), **FIG. 64** (SEQ ID NO: 64), **FIG. 66** (SEQ ID NO: 66), **FIG. 68** (SEQ ID NO: 68), **FIG. 70** (SEQ ID NO: 70), **FIG. 72** (SEQ ID NO: 72), **FIG. 74** (SEQ ID NO: 74), **FIG. 76** (SEQ ID NO: 76), **FIG. 78** (SEQ ID NO: 78), **FIG. 80** (SEQ ID NO: 80), **FIG. 82** (SEQ ID NO: 82), **FIG. 84** (SEQ ID NO: 84), **FIG. 86** (SEQ ID NO: 86), **FIG. 88** (SEQ ID NO: 88), **FIG. 90** (SEQ ID NO: 90), **FIG. 92** (SEQ ID NO: 92), **FIG. 94** (SEQ ID NO: 94), **FIG. 96** (SEQ ID NO: 96), **FIG. 98** (SEQ ID NO: 98), **FIG. 100** (SEQ ID NO: 100), **FIG. 102** (SEQ ID NO: 102), **FIG. 104** (SEQ ID NO: 104), **FIG. 106** (SEQ ID NO: 106), **FIG. 108** (SEQ ID NO: 108), **FIG. 110** (SEQ ID NO: 110), **FIG. 112** (SEQ ID NO: 112), **FIG. 114** (SEQ ID NO: 114), **FIG. 116** (SEQ ID NO: 116), **FIG. 118** (SEQ ID NO: 118), **FIG. 120** (SEQ ID NO: 120), **FIG. 122** (SEQ ID NO: 122), **FIG. 124** (SEQ ID NO: 124), **FIG. 126** (SEQ ID NO: 126), **FIG. 128** (SEQ ID NO: 128), **FIG. 130** (SEQ ID NO: 130), **FIG. 132** (SEQ ID NO: 132), **FIG. 134** (SEQ ID NO: 134), **FIG. 136** (SEQ ID NO: 136), **FIG. 138** (SEQ ID NO: 138), **FIG. 140** (SEQ ID NO: 140), **FIG. 142** (SEQ ID NO: 142), **FIG. 144** (SEQ ID NO: 144), **FIG. 146** (SEQ ID NO: 146), **FIG. 148** (SEQ ID NO: 148), **FIG. 150** (SEQ ID NO: 150), **FIG. 152** (SEQ ID NO: 152), **FIG. 154** (SEQ ID NO: 154), **FIG. 156** (SEQ ID NO: 156), **FIG. 158** (SEQ ID NO: 158), **FIG. 160** (SEQ ID NO: 160), **FIG. 162** (SEQ ID NO: 162), **FIG. 164** (SEQ ID NO: 164), **FIG. 166** (SEQ ID NO: 166), **FIG. 168** (SEQ ID NO: 168), **FIG. 170** (SEQ ID NO: 170), **FIG. 172** (SEQ ID NO: 172), **FIG. 174** (SEQ ID NO: 174), **FIG. 176** (SEQ ID NO: 176), **FIG. 178** (SEQ ID NO: 178), **FIG. 180** (SEQ ID NO: 180), **FIG. 182** (SEQ ID NO: 182), **FIG. 184** (SEQ ID NO: 184), **FIG. 186** (SEQ ID NO: 186), **FIG. 188** (SEQ ID NO: 188), **FIG. 190** (SEQ ID NO: 190), **FIG. 192** (SEQ ID NO: 192), **FIG. 194** (SEQ ID NO: 194), **FIG. 196** (SEQ ID NO: 196), **FIG. 198** (SEQ ID NO: 198), **FIG. 200** (SEQ ID NO: 200), **FIG. 202** (SEQ ID NO: 202), **FIG. 204** (SEQ ID NO: 204), **FIG. 206** (SEQ ID NO: 206), **FIG. 208** (SEQ ID NO: 208), **FIG. 210** (SEQ ID NO: 210), **FIG. 212** (SEQ ID NO: 212), **FIG. 214** (SEQ ID NO: 214), **FIG. 216** (SEQ ID NO: 216), **FIG. 218** (SEQ ID NO: 218), **FIG. 220** (SEQ ID NO: 220), **FIG. 222** (SEQ ID NO: 222), **FIG. 224** (SEQ ID NO: 224), **FIG. 226** (SEQ ID NO: 226), **FIG. 228** (SEQ ID NO: 228), **FIG. 230** (SEQ ID NO: 230), **FIG. 232** (SEQ ID NO: 232), **FIG. 234** (SEQ ID NO: 234), **FIG. 236** (SEQ ID NO: 236), **FIG. 238** (SEQ ID NO: 238), **FIG. 240** (SEQ ID NO: 240), **FIG. 242** (SEQ ID NO: 242), **FIG. 244** (SEQ ID NO: 244), **FIG. 246** (SEQ ID NO: 246), **FIG. 248** (SEQ ID NO: 248), **FIG. 250** (SEQ ID NO: 250), **FIG. 252** (SEQ ID NO: 252), **FIG. 254** (SEQ ID NO: 254), **FIG. 256** (SEQ ID NO: 256), **FIG. 258** (SEQ ID NO: 258), **FIG. 260** (SEQ ID NO: 260), **FIG. 262** (SEQ ID NO: 262), **FIG. 264** (SEQ ID NO: 264), **FIG. 266** (SEQ ID NO: 266), **FIG. 268** (SEQ ID NO: 268), **FIG. 270** (SEQ ID NO: 270), **FIG. 272** (SEQ ID NO: 272), **FIG. 274** (SEQ ID NO: 274), **FIG. 276** (SEQ ID NO: 276), **FIG. 278** (SEQ ID NO: 278), **FIG. 280** (SEQ ID NO:

280), **FIG. 282** (SEQ ID NO: 282), **FIG. 284** (SEQ ID NO: 284), **FIG. 286** (SEQ ID NO: 286), **FIG. 288** (SEQ ID NO: 288), **FIG. 290** (SEQ ID NO: 290), **FIG. 292** (SEQ ID NO: 292), **FIG. 294** (SEQ ID NO: 294), **FIG. 296** (SEQ ID NO: 296), **FIG. 298** (SEQ ID NO: 298), **FIG. 300** (SEQ ID NO: 300), **FIG. 302** (SEQ ID NO: 302), **FIG. 304** (SEQ ID NO: 304), **FIG. 306** (SEQ ID NO: 306), **FIG. 308** (SEQ ID NO: 308), **FIG. 310** (SEQ ID NO: 310), **FIG. 312** (SEQ ID NO: 312), **FIG. 314** (SEQ ID NO: 314), **FIG. 316** (SEQ ID NO: 316), **FIG. 318** (SEQ ID NO: 318), **FIG. 320** (SEQ ID NO: 320), **FIG. 322** (SEQ ID NO: 322), **FIG. 324** (SEQ ID NO: 324), **FIG. 326** (SEQ ID NO: 326), **FIG. 328** (SEQ ID NO: 328), **FIG. 330** (SEQ ID NO: 330), **FIG. 332** (SEQ ID NO: 332), **FIG. 334** (SEQ ID NO: 334), **FIG. 336** (SEQ ID NO: 336), **FIG. 338** (SEQ ID NO: 338), **FIG. 340** (SEQ ID NO: 340), **FIG. 342** (SEQ ID NO: 342), **FIG. 344** (SEQ ID NO: 344), **FIG. 346** (SEQ ID NO: 346), **FIG. 348** (SEQ ID NO: 348), **FIG. 350** (SEQ ID NO: 350), **FIG. 352** (SEQ ID NO: 352), **FIG. 354** (SEQ ID NO: 354), **FIG. 356** (SEQ ID NO: 356), **FIG. 358** (SEQ ID NO: 358), **FIG. 360** (SEQ ID NO: 360), **FIG. 362** (SEQ ID NO: 362), **FIG. 364** (SEQ ID NO: 364), **FIG. 366** (SEQ ID NO: 366), **FIG. 368** (SEQ ID NO: 368), **FIG. 370** (SEQ ID NO: 370), **FIG. 372** (SEQ ID NO: 372), **FIG. 374** (SEQ ID NO: 374), **FIG. 376** (SEQ ID NO: 376), **FIG. 378** (SEQ ID NO: 378), **FIG. 380** (SEQ ID NO: 380), **FIG. 382** (SEQ ID NO: 382), **FIG. 384** (SEQ ID NO: 384), **FIG. 386** (SEQ ID NO: 386), **FIG. 388** (SEQ ID NO: 388), **FIG. 390** (SEQ ID NO: 390), **FIG. 392** (SEQ ID NO: 392), **FIG. 394** (SEQ ID NO: 394), **FIG. 396** (SEQ ID NO: 396), **FIG. 398** (SEQ ID NO: 398), **FIG. 400** (SEQ ID NO: 400), **FIG. 402** (SEQ ID NO: 402), **FIG. 404** (SEQ ID NO: 404), **FIG. 406** (SEQ ID NO: 406), **FIG. 408** (SEQ ID NO: 408), **FIG. 410** (SEQ ID NO: 410), **FIG. 412** (SEQ ID NO: 412), **FIG. 414** (SEQ ID NO: 414), **FIG. 416** (SEQ ID NO: 416), **FIG. 418** (SEQ ID NO: 418), **FIG. 420** (SEQ ID NO: 420), **FIG. 422** (SEQ ID NO: 422), **FIG. 424** (SEQ ID NO: 424), **FIG. 426** (SEQ ID NO: 426), **FIG. 428** (SEQ ID NO: 428), **FIG. 430** (SEQ ID NO: 430), **FIG. 432** (SEQ ID NO: 432), **FIG. 434** (SEQ ID NO: 434), **FIG. 436** (SEQ ID NO: 436), **FIG. 438** (SEQ ID NO: 438), **FIG. 440** (SEQ ID NO: 440), **FIG. 442** (SEQ ID NO: 442), **FIG. 444** (SEQ ID NO: 444), **FIG. 446** (SEQ ID NO: 446), **FIG. 448** (SEQ ID NO: 448), **FIG. 450** (SEQ ID NO: 450), **FIG. 452** (SEQ ID NO: 452), **FIG. 454** (SEQ ID NO: 454), **FIG. 456** (SEQ ID NO: 456), **FIG. 458** (SEQ ID NO: 458), **FIG. 460** (SEQ ID NO: 460), **FIG. 462** (SEQ ID NO: 462), **FIG. 464** (SEQ ID NO: 464), **FIG. 466** (SEQ ID NO: 466), **FIG. 468** (SEQ ID NO: 468), **FIG. 470** (SEQ ID NO: 470), **FIG. 472** (SEQ ID NO: 472), **FIG. 474** (SEQ ID NO: 474), **FIG. 476** (SEQ ID NO: 476), **FIG. 478** (SEQ ID NO: 478), **FIG. 480** (SEQ ID NO: 480), **FIG. 482** (SEQ ID NO: 482), **FIG. 484** (SEQ ID NO: 484), **FIG. 486** (SEQ ID NO: 486), **FIG. 488** (SEQ ID NO: 488), **FIG. 490** (SEQ ID NO: 490), **FIG. 492** (SEQ ID NO: 492), **FIG. 494** (SEQ ID NO: 494), **FIG. 496** (SEQ ID NO: 496), **FIG. 498** (SEQ ID NO: 498), **FIG. 500** (SEQ ID NO: 500), **FIG. 502** (SEQ ID NO: 502), **FIG. 504** (SEQ ID NO: 504), **FIG. 506** (SEQ ID NO: 506), **FIG. 508** (SEQ ID NO: 508), **FIG. 510** (SEQ ID NO: 510), **FIG. 512** (SEQ ID NO: 512), **FIG. 514** (SEQ ID NO: 514), **FIG. 516** (SEQ ID NO: 516), **FIG. 518** (SEQ ID NO: 518), **FIG. 520** (SEQ ID NO: 520), **FIG. 522** (SEQ ID NO: 522), **FIG. 524** (SEQ ID NO: 524), **FIG. 526** (SEQ ID NO: 526), **FIG. 528** (SEQ ID NO: 528), **FIG. 530** (SEQ ID NO: 530), **FIG. 532** (SEQ ID NO: 532), **FIG. 534** (SEQ ID NO: 534), **FIG. 536** (SEQ ID NO: 536), **FIG. 538** (SEQ ID 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602), **FIG. 604** (SEQ ID NO: 604), **FIG. 606** (SEQ ID NO: 606), **FIG. 608** (SEQ ID NO: 608), and **FIG. 610** (SEQ ID NO: 610).

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

13. A chimeric molecule comprising a polypeptide according to claim 11 fused to a heterologous amino acid sequence.

14. The chimeric molecule of claim 13, wherein said heterologous amino acid sequence is an epitope tag sequence.

15. The chimeric molecule of claim 13, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

16. An antibody which specifically binds to a polypeptide according to claim 11.

17. The antibody of claim 16, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

18. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in **FIG. 2** (SEQ ID NO: 2), **FIG. 4** (SEQ ID NO: 4), **FIG. 6** (SEQ ID NO: 6), **FIG. 8** (SEQ ID NO: 8), **FIG. 10** (SEQ ID NO: 10), **FIG. 12** (SEQ ID NO: 12), **FIG. 14** (SEQ ID NO: 14), **FIG. 16** (SEQ ID NO: 16), **FIG. 18** (SEQ ID NO: 18), **FIG. 20** (SEQ ID NO: 20), **FIG. 22** (SEQ ID NO: 22), **FIG. 24** (SEQ ID NO: 24), **FIG. 26** (SEQ ID NO: 26), **FIG. 28** (SEQ ID NO: 28), **FIG. 30** (SEQ ID NO: 30), **FIG. 32** (SEQ ID NO: 32), **FIG. 34** (SEQ ID NO: 34), **FIG. 36** (SEQ ID NO: 36), **FIG. 38** (SEQ ID NO: 38), **FIG. 40** (SEQ ID NO: 40), **FIG. 42** (SEQ ID NO: 42), **FIG. 44** (SEQ ID NO: 44), **FIG. 46** (SEQ ID NO: 46), **FIG. 48** (SEQ ID NO: 48), **FIG. 50** (SEQ ID NO: 50), **FIG. 52** (SEQ ID NO: 52), **FIG. 54** (SEQ ID NO: 54), **FIG. 56** (SEQ ID NO: 56), **FIG. 58** (SEQ ID NO: 58), **FIG. 60** (SEQ ID NO: 60), **FIG. 62** (SEQ ID NO: 62), **FIG. 64** (SEQ ID NO: 64), **FIG. 66** (SEQ ID NO: 66), **FIG. 68** (SEQ ID NO: 68), **FIG. 70** (SEQ ID NO: 70), **FIG. 72** (SEQ ID NO: 72), **FIG. 74** (SEQ ID NO: 74), **FIG. 76** (SEQ ID NO: 76), **FIG. 78** (SEQ ID NO: 78), **FIG. 80** (SEQ ID NO: 80), **FIG. 82** (SEQ ID NO: 82), **FIG. 84** (SEQ ID NO: 84), **FIG. 86** (SEQ ID NO: 86), **FIG. 88** (SEQ ID NO: 88), **FIG. 90** (SEQ ID NO: 90), **FIG. 92** (SEQ ID NO: 92), **FIG. 94** (SEQ ID NO: 94), **FIG. 96** (SEQ ID NO: 96), **FIG.**

NO: 558), **FIG. 560** (SEQ ID NO: 560), **FIG. 562** (SEQ ID NO: 562), **FIG. 564** (SEQ ID NO: 564), **FIG. 566** (SEQ ID NO: 566), **FIG. 568** (SEQ ID NO: 568), **FIG. 570** (SEQ ID NO: 570), **FIG. 572** (SEQ ID NO: 572), **FIG. 574** (SEQ ID NO: 574), **FIG. 576** (SEQ ID NO: 576), **FIG. 578** (SEQ ID NO: 578), **FIG. 580** (SEQ ID NO: 580), **FIG. 582** (SEQ ID NO: 582), **FIG. 584** (SEQ ID NO: 584), **FIG. 586** (SEQ ID NO: 586), **FIG. 588** (SEQ ID NO: 588), **FIG. 590** (SEQ ID NO: 590), **FIG. 592** (SEQ ID NO: 592), **FIG. 594** (SEQ ID NO: 594), **FIG. 596** (SEQ ID NO: 596), **FIG. 598** (SEQ ID NO: 598), **FIG. 600** (SEQ ID NO: 600), **FIG. 602** (SEQ ID NO: 602), **FIG. 604** (SEQ ID NO: 604), **FIG. 606** (SEQ ID NO: 606), **FIG. 608** (SEQ ID NO: 608), or **FIG. 610** (SEQ ID NO: 610), lacking its associated signal peptide;

- (b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in **FIG. 2** (SEQ ID NO: 2), **FIG. 4** (SEQ ID NO: 4), **FIG. 6** (SEQ ID NO: 6), **FIG. 8** (SEQ ID NO: 8), **FIG. 10** (SEQ ID NO: 10), **FIG. 12** (SEQ ID NO: 12), **FIG. 14** (SEQ ID NO: 14), **FIG. 16** (SEQ ID NO: 16), **FIG. 18** (SEQ ID NO: 18), **FIG. 20** (SEQ ID NO: 20), **FIG. 22** (SEQ ID NO: 22), **FIG. 24** (SEQ ID NO: 24), **FIG. 26** (SEQ ID NO: 26), **FIG. 28** (SEQ ID NO: 28), **FIG. 30** (SEQ ID NO: 30), **FIG. 32** (SEQ ID NO: 32), **FIG. 34** (SEQ ID NO: 34), **FIG. 36** (SEQ ID NO: 36), **FIG. 38** (SEQ ID NO: 38), **FIG. 40** (SEQ ID NO: 40), **FIG. 42** (SEQ ID NO: 42), **FIG. 44** (SEQ ID NO: 44), **FIG. 46** (SEQ ID NO: 46), **FIG. 48** (SEQ ID NO: 48), **FIG. 50** (SEQ ID NO: 50), **FIG. 52** (SEQ ID NO: 52), **FIG. 54** (SEQ ID NO: 54), **FIG. 56** (SEQ ID NO: 56), **FIG. 58** (SEQ ID NO: 58), **FIG. 60** (SEQ ID NO: 60), **FIG. 62** (SEQ ID NO: 62), **FIG. 64** (SEQ ID NO: 64), **FIG. 66** (SEQ ID NO: 66), **FIG. 68** (SEQ ID NO: 68), **FIG. 70** (SEQ ID NO: 70), **FIG. 72** (SEQ ID NO: 72), **FIG. 74** (SEQ ID NO: 74), **FIG. 76** (SEQ ID NO: 76), **FIG. 78** (SEQ ID NO: 78), **FIG. 80** (SEQ ID NO: 80), **FIG. 82** (SEQ ID NO: 82), **FIG. 84** (SEQ ID NO: 84), **FIG. 86** (SEQ ID NO: 86), **FIG. 88** (SEQ ID NO: 88), **FIG. 90** (SEQ ID NO: 90), **FIG. 92** (SEQ ID NO: 92), **FIG. 94** (SEQ ID NO: 94), **FIG. 96** (SEQ ID NO: 96), **FIG. 98** (SEQ ID NO: 98), **FIG. 100** (SEQ ID NO: 100), **FIG. 102** (SEQ ID NO: 102), **FIG. 104** (SEQ ID NO: 104), **FIG. 106** (SEQ ID NO: 106), **FIG. 108** (SEQ ID NO: 108), **FIG. 110** (SEQ ID NO: 110), **FIG. 112** (SEQ ID NO: 112), **FIG. 114** (SEQ ID NO: 114), **FIG. 116** (SEQ ID NO: 116), **FIG. 118** (SEQ ID NO: 118), **FIG. 120** (SEQ ID NO: 120), **FIG. 122** (SEQ ID NO: 122), **FIG. 124** (SEQ ID NO: 124), **FIG. 126** (SEQ ID NO: 126), **FIG. 128** (SEQ ID NO: 128), **FIG. 130** (SEQ ID NO: 130), **FIG. 132** (SEQ ID NO: 132), **FIG. 134** (SEQ ID NO: 134), **FIG. 136** (SEQ ID NO: 136), **FIG. 138** (SEQ ID NO: 138), **FIG. 140** (SEQ ID NO: 140), **FIG. 142** (SEQ ID NO: 142), **FIG. 144** (SEQ ID NO: 144), **FIG. 146** (SEQ ID NO: 146), **FIG. 148** (SEQ ID NO: 148), **FIG. 150** (SEQ ID NO: 150), **FIG. 152** (SEQ ID NO: 152), **FIG. 154** (SEQ ID NO: 154), **FIG. 156** (SEQ ID NO: 156), **FIG. 158** (SEQ ID NO: 158), **FIG. 160** (SEQ ID NO: 160), **FIG. 162** (SEQ ID NO: 162), **FIG. 164** (SEQ ID NO: 164), **FIG. 166** (SEQ ID NO: 166), **FIG. 168** (SEQ ID NO: 168), **FIG. 170** (SEQ ID NO: 170), **FIG. 172** (SEQ ID NO: 172), **FIG. 174** (SEQ ID NO: 174), **FIG. 176** (SEQ ID NO: 176), **FIG. 178** (SEQ ID NO: 178),

FIG. 180 (SEQ ID NO: 180), **FIG. 182** (SEQ ID NO: 182), **FIG. 184** (SEQ ID NO: 184), **FIG. 186** (SEQ ID NO: 186), **FIG. 188** (SEQ ID NO: 188), **FIG. 190** (SEQ ID NO: 190), **FIG. 192** (SEQ ID NO: 192), **FIG. 194** (SEQ ID NO: 194), **FIG. 196** (SEQ ID NO: 196), **FIG. 198** (SEQ ID NO: 198), **FIG. 200** (SEQ ID NO: 200), **FIG. 202** (SEQ ID NO: 202), **FIG. 204** (SEQ ID NO: 204), **FIG. 206** (SEQ ID NO: 206), **FIG. 208** (SEQ ID NO: 208), **FIG. 210** (SEQ ID NO: 210), **FIG. 212** (SEQ ID NO: 212), **FIG. 214** (SEQ ID NO: 214), **FIG. 216** (SEQ ID NO: 216), **FIG. 218** (SEQ ID NO: 218), **FIG. 220** (SEQ ID NO: 220), **FIG. 222** (SEQ ID NO: 222), **FIG. 224** (SEQ ID NO: 224), **FIG. 226** (SEQ ID NO: 226), **FIG. 228** (SEQ ID NO: 228), **FIG. 230** (SEQ ID NO: 230), **FIG. 232** (SEQ ID NO: 232), **FIG. 234** (SEQ ID NO: 234), **FIG. 236** (SEQ ID NO: 236), **FIG. 238** (SEQ ID NO: 238), **FIG. 240** (SEQ ID NO: 240), **FIG. 242** (SEQ ID NO: 242), **FIG. 244** (SEQ ID NO: 244), **FIG. 246** (SEQ ID NO: 246), **FIG. 248** (SEQ ID NO: 248), **FIG. 250** (SEQ ID NO: 250), **FIG. 252** (SEQ ID NO: 252), **FIG. 254** (SEQ ID NO: 254), **FIG. 256** (SEQ ID NO: 256), **FIG. 258** (SEQ ID NO: 258), **FIG. 260** (SEQ ID NO: 260), **FIG. 262** (SEQ ID NO: 262), **FIG. 264** (SEQ ID NO: 264), **FIG. 266** (SEQ ID NO: 266), **FIG. 268** (SEQ ID NO: 268), **FIG. 270** (SEQ ID NO: 270), **FIG. 272** (SEQ ID NO: 272), **FIG. 274** (SEQ ID NO: 274), **FIG. 276** (SEQ ID NO: 276), **FIG. 278** (SEQ ID NO: 278), **FIG. 280** (SEQ ID NO: 280), **FIG. 282** (SEQ ID NO: 282), **FIG. 284** (SEQ ID NO: 284), **FIG. 286** (SEQ ID NO: 286), **FIG. 288** (SEQ ID NO: 288), **FIG. 290** (SEQ ID NO: 290), **FIG. 292** (SEQ ID NO: 292), **FIG. 294** (SEQ ID NO: 294), **FIG. 296** (SEQ ID NO: 296), **FIG. 298** (SEQ ID NO: 298), **FIG. 300** (SEQ ID NO: 300), **FIG. 302** (SEQ ID NO: 302), **FIG. 304** (SEQ ID NO: 304), **FIG. 306** (SEQ ID NO: 306), **FIG. 308** (SEQ ID NO: 308), **FIG. 310** (SEQ ID NO: 310), **FIG. 312** (SEQ ID NO: 312), **FIG. 314** (SEQ ID NO: 314), **FIG. 316** (SEQ ID NO: 316), **FIG. 318** (SEQ ID NO: 318), **FIG. 320** (SEQ ID NO: 320), **FIG. 322** (SEQ ID NO: 322), **FIG. 324** (SEQ ID NO: 324), **FIG. 326** (SEQ ID NO: 326), **FIG. 328** (SEQ ID NO: 328), **FIG. 330** (SEQ ID NO: 330), **FIG. 332** (SEQ ID NO: 332), **FIG. 334** (SEQ ID NO: 334), **FIG. 336** (SEQ ID NO: 336), **FIG. 338** (SEQ ID NO: 338), **FIG. 340** (SEQ ID NO: 340), **FIG. 342** (SEQ ID NO: 342), **FIG. 344** (SEQ ID NO: 344), **FIG. 346** (SEQ ID NO: 346), **FIG. 348** (SEQ ID NO: 348), **FIG. 350** (SEQ ID NO: 350), **FIG. 352** (SEQ ID NO: 352), **FIG. 354** (SEQ ID NO: 354), **FIG. 356** (SEQ ID NO: 356), **FIG. 358** (SEQ ID NO: 358), **FIG. 360** (SEQ ID NO: 360), **FIG. 362** (SEQ ID NO: 362), **FIG. 364** (SEQ ID NO: 364), **FIG. 366** (SEQ ID NO: 366), **FIG. 368** (SEQ ID NO: 368), **FIG. 370** (SEQ ID NO: 370), **FIG. 372** (SEQ ID NO: 372), **FIG. 374** (SEQ ID NO: 374), **FIG. 376** (SEQ ID NO: 376), **FIG. 378** (SEQ ID NO: 378), **FIG. 380** (SEQ ID NO: 380), **FIG. 382** (SEQ ID NO: 382), **FIG. 384** (SEQ ID NO: 384), **FIG. 386** (SEQ ID NO: 386), **FIG. 388** (SEQ ID NO: 388), **FIG. 390** (SEQ ID NO: 390), **FIG. 392** (SEQ ID NO: 392), **FIG. 394** (SEQ ID NO: 394), **FIG. 396** (SEQ ID NO: 396), **FIG. 398** (SEQ ID NO: 398), **FIG. 400** (SEQ ID NO: 400), **FIG. 402** (SEQ ID NO: 402), **FIG. 404** (SEQ ID NO: 404), **FIG. 406** (SEQ ID NO: 406), **FIG. 408** (SEQ ID NO: 408),

408), **FIG. 410** (SEQ ID NO: 410), **FIG. 412** (SEQ ID NO: 412), **FIG. 414** (SEQ ID NO: 414), **FIG. 416** (SEQ ID NO: 416), **FIG. 418** (SEQ ID NO: 418), **FIG. 420** (SEQ ID NO: 420), **FIG. 422** (SEQ ID NO: 422), **FIG. 424** (SEQ ID NO: 424), **FIG. 426** (SEQ ID NO: 426), **FIG. 428** (SEQ ID NO: 428), **FIG. 430** (SEQ ID NO: 430), **FIG. 432** (SEQ ID NO: 432), **FIG. 434** (SEQ ID NO: 434), **FIG. 436** (SEQ ID NO: 436), **FIG. 438** (SEQ ID NO: 438), **FIG. 440** (SEQ ID NO: 440), **FIG. 442** (SEQ ID NO: 442), **FIG. 444** (SEQ ID NO: 444), **FIG. 446** (SEQ ID NO: 446), **FIG. 448** (SEQ ID NO: 448), **FIG. 450** (SEQ ID NO: 450), **FIG. 452** (SEQ ID NO: 452), **FIG. 454** (SEQ ID NO: 454), **FIG. 456** (SEQ ID NO: 456), **FIG. 458** (SEQ ID NO: 458), **FIG. 460** (SEQ ID NO: 460), **FIG. 462** (SEQ ID NO: 462), **FIG. 464** (SEQ ID NO: 464), **FIG. 466** (SEQ ID NO: 466), **FIG. 468** (SEQ ID NO: 468), **FIG. 470** (SEQ ID NO: 470), **FIG. 472** (SEQ ID NO: 472), **FIG. 474** (SEQ ID NO: 474), **FIG. 476** (SEQ ID NO: 476), **FIG. 478** (SEQ ID NO: 478), **FIG. 480** (SEQ ID NO: 480), **FIG. 482** (SEQ ID NO: 482), **FIG. 484** (SEQ ID NO: 484), **FIG. 486** (SEQ ID NO: 486), **FIG. 488** (SEQ ID NO: 488), **FIG. 490** (SEQ ID NO: 490), **FIG. 492** (SEQ ID NO: 492), **FIG. 494** (SEQ ID NO: 494), **FIG. 496** (SEQ ID NO: 496), **FIG. 498** (SEQ ID NO: 498), **FIG. 500** (SEQ ID NO: 500), **FIG. 502** (SEQ ID NO: 502), **FIG. 504** (SEQ ID NO: 504), **FIG. 506** (SEQ ID NO: 506), **FIG. 508** (SEQ ID NO: 508), **FIG. 510** (SEQ ID NO: 510), **FIG. 512** (SEQ ID NO: 512), **FIG. 514** (SEQ ID NO: 514), **FIG. 516** (SEQ ID NO: 516), **FIG. 518** (SEQ ID NO: 518), **FIG. 520** (SEQ ID NO: 520), **FIG. 522** (SEQ ID NO: 522), **FIG. 524** (SEQ ID NO: 524), **FIG. 526** (SEQ ID NO: 526), **FIG. 528** (SEQ ID NO: 528), **FIG. 530** (SEQ ID NO: 530), **FIG. 532** (SEQ ID NO: 532), **FIG. 534** (SEQ ID NO: 534), **FIG. 536** (SEQ ID NO: 536), **FIG. 538** (SEQ ID NO: 538), **FIG. 540** (SEQ ID NO: 540), **FIG. 542** (SEQ ID NO: 542), **FIG. 544** (SEQ ID NO: 544), **FIG. 546** (SEQ ID NO: 546), **FIG. 548** (SEQ ID NO: 548), **FIG. 550** (SEQ ID NO: 550), **FIG. 552** (SEQ ID NO: 552), **FIG. 554** (SEQ ID NO: 554), **FIG. 556** (SEQ ID NO: 556), **FIG. 558** (SEQ ID NO: 558), **FIG. 560** (SEQ ID NO: 560), **FIG. 562** (SEQ ID NO: 562), **FIG. 564** (SEQ ID NO: 564), **FIG. 566** (SEQ ID NO: 566), **FIG. 568** (SEQ ID NO: 568), **FIG. 570** (SEQ ID NO: 570), **FIG. 572** (SEQ ID NO: 572), **FIG. 574** (SEQ ID NO: 574), **FIG. 576** (SEQ ID NO: 576), **FIG. 578** (SEQ ID NO: 578), **FIG. 580** (SEQ ID NO: 580), **FIG. 582** (SEQ ID NO: 582), **FIG. 584** (SEQ ID NO: 584), **FIG. 586** (SEQ ID NO: 586), **FIG. 588** (SEQ ID NO: 588), **FIG. 590** (SEQ ID NO: 590), **FIG. 592** (SEQ ID NO: 592), **FIG. 594** (SEQ ID NO: 594), **FIG. 596** (SEQ ID NO: 596), **FIG. 598** (SEQ ID NO: 598), **FIG. 600** (SEQ ID NO: 600), **FIG. 602** (SEQ ID NO: 602), **FIG. 604** (SEQ ID NO: 604), **FIG. 606** (SEQ ID NO: 606), **FIG. 608** (SEQ ID NO: 608), or **FIG. 610** (SEQ ID NO: 610), with its associated signal peptide; or

- (c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in **FIG. 2** (SEQ ID NO: 2), **FIG. 4** (SEQ ID NO: 4), **FIG. 6** (SEQ ID NO: 6), **FIG. 8** (SEQ ID NO: 8), **FIG. 10** (SEQ ID NO: 10), **FIG. 12** (SEQ ID NO: 12), **FIG. 14** (SEQ ID NO: 14), **FIG. 16** (SEQ ID NO: 16), **FIG. 18** (SEQ ID NO: 18), **FIG. 20** (SEQ ID NO: 20), **FIG. 22** (SEQ ID NO: 22),

FIG. 24 (SEQ ID NO: 24), **FIG. 26** (SEQ ID NO: 26), **FIG. 28** (SEQ ID NO: 28), **FIG. 30** (SEQ ID NO: 30), **FIG. 32** (SEQ ID NO: 32), **FIG. 34** (SEQ ID NO: 34), **FIG. 36** (SEQ ID NO: 36), **FIG. 38** (SEQ ID NO: 38), **FIG. 40** (SEQ ID NO: 40), **FIG. 42** (SEQ ID NO: 42), **FIG. 44** (SEQ ID NO: 44), **FIG. 46** (SEQ ID NO: 46), **FIG. 48** (SEQ ID NO: 48), **FIG. 50** (SEQ ID NO: 50), **FIG. 52** (SEQ ID NO: 52), **FIG. 54** (SEQ ID NO: 54), **FIG. 56** (SEQ ID NO: 56), **FIG. 58** (SEQ ID NO: 58), **FIG. 60** (SEQ ID NO: 60), **FIG. 62** (SEQ ID NO: 62), **FIG. 64** (SEQ ID NO: 64), **FIG. 66** (SEQ ID NO: 66), **FIG. 68** (SEQ ID NO: 68), **FIG. 70** (SEQ ID NO: 70), **FIG. 72** (SEQ ID NO: 72), **FIG. 74** (SEQ ID NO: 74), **FIG. 76** (SEQ ID NO: 76), **FIG. 78** (SEQ ID NO: 78), **FIG. 80** (SEQ ID NO: 80), **FIG. 82** (SEQ ID NO: 82), **FIG. 84** (SEQ ID NO: 84), **FIG. 86** (SEQ ID NO: 86), **FIG. 88** (SEQ ID NO: 88), **FIG. 90** (SEQ ID NO: 90), **FIG. 92** (SEQ ID NO: 92), **FIG. 94** (SEQ ID NO: 94), **FIG. 96** (SEQ ID NO: 96), **FIG. 98** (SEQ ID NO: 98), **FIG. 100** (SEQ ID NO: 100), **FIG. 102** (SEQ ID NO: 102), **FIG. 104** (SEQ ID NO: 104), **FIG. 106** (SEQ ID NO: 106), **FIG. 108** (SEQ ID NO: 108), **FIG. 110** (SEQ ID NO: 110), **FIG. 112** (SEQ ID NO: 112), **FIG. 114** (SEQ ID NO: 114), **FIG. 116** (SEQ ID NO: 116), **FIG. 118** (SEQ ID NO: 118), **FIG. 120** (SEQ ID NO: 120), **FIG. 122** (SEQ ID NO: 122), **FIG. 124** (SEQ ID NO: 124), **FIG. 126** (SEQ ID NO: 126), **FIG. 128** (SEQ ID NO: 128), **FIG. 130** (SEQ ID NO: 130), **FIG. 132** (SEQ ID NO: 132), **FIG. 134** (SEQ ID NO: 134), **FIG. 136** (SEQ ID NO: 136), **FIG. 138** (SEQ ID NO: 138), **FIG. 140** (SEQ ID NO: 140), **FIG. 142** (SEQ ID NO: 142), **FIG. 144** (SEQ ID NO: 144), **FIG. 146** (SEQ ID NO: 146), **FIG. 148** (SEQ ID NO: 148), **FIG. 150** (SEQ ID NO: 150), **FIG. 152** (SEQ ID NO: 152), **FIG. 154** (SEQ ID NO: 154), **FIG. 156** (SEQ ID NO: 156), **FIG. 158** (SEQ ID NO: 158), **FIG. 160** (SEQ ID NO: 160), **FIG. 162** (SEQ ID NO: 162), **FIG. 164** (SEQ ID NO: 164), **FIG. 166** (SEQ ID NO: 166), **FIG. 168** (SEQ ID NO: 168), **FIG. 170** (SEQ ID NO: 170), **FIG. 172** (SEQ ID NO: 172), **FIG. 174** (SEQ ID NO: 174), **FIG. 176** (SEQ ID NO: 176), **FIG. 178** (SEQ ID NO: 178), **FIG. 180** (SEQ ID NO: 180), **FIG. 182** (SEQ ID NO: 182), **FIG. 184** (SEQ ID NO: 184), **FIG. 186** (SEQ ID NO: 186), **FIG. 188** (SEQ ID NO: 188), **FIG. 190** (SEQ ID NO: 190), **FIG. 192** (SEQ ID NO: 192), **FIG. 194** (SEQ ID NO: 194), **FIG. 196** (SEQ ID NO: 196), **FIG. 198** (SEQ ID NO: 198), **FIG. 200** (SEQ ID NO: 200), **FIG. 202** (SEQ ID NO: 202), **FIG. 204** (SEQ ID NO: 204), **FIG. 206** (SEQ ID NO: 206), **FIG. 208** (SEQ ID NO: 208), **FIG. 210** (SEQ ID NO: 210), **FIG. 212** (SEQ ID NO: 212), **FIG. 214** (SEQ ID NO: 214), **FIG. 216** (SEQ ID NO: 216), **FIG. 218** (SEQ ID NO: 218), **FIG. 220** (SEQ ID NO: 220), **FIG. 222** (SEQ ID NO: 222), **FIG. 224** (SEQ ID NO: 224), **FIG. 226** (SEQ ID NO: 226), **FIG. 228** (SEQ ID NO: 228), **FIG. 230** (SEQ ID NO: 230), **FIG. 232** (SEQ ID NO: 232), **FIG. 234** (SEQ ID NO: 234), **FIG. 236** (SEQ ID NO: 236), **FIG. 238** (SEQ ID NO: 238), **FIG. 240** (SEQ ID NO: 240), **FIG. 242** (SEQ ID NO: 242), **FIG. 244** (SEQ ID NO: 244), **FIG. 246** (SEQ ID NO: 246), **FIG. 248** (SEQ ID NO: 248), **FIG. 250** (SEQ ID NO: 250), **FIG. 252** (SEQ ID NO: 252), **FIG. 254** (SEQ ID NO: 254), **FIG. 256** (SEQ ID NO: 256), **FIG. 258** (SEQ ID NO: 258), **FIG. 260** (SEQ ID NO: 260),

FIG. 262 (SEQ ID NO: 262), **FIG. 264** (SEQ ID NO: 264), **FIG. 266** (SEQ ID NO: 266), **FIG. 268** (SEQ ID NO: 268), **FIG. 270** (SEQ ID NO: 270), **FIG. 272** (SEQ ID NO: 272), **FIG. 274** (SEQ ID NO: 274), **FIG. 276** (SEQ ID NO: 276), **FIG. 278** (SEQ ID NO: 278), **FIG. 280** (SEQ ID NO: 280), **FIG. 282** (SEQ ID NO: 282), **FIG. 284** (SEQ ID NO: 284), **FIG. 286** (SEQ ID NO: 286), **FIG. 288** (SEQ ID NO: 288), **FIG. 290** (SEQ ID NO: 290), **FIG. 292** (SEQ ID NO: 292), **FIG. 294** (SEQ ID NO: 294), **FIG. 296** (SEQ ID NO: 296), **FIG. 298** (SEQ ID NO: 298), **FIG. 300** (SEQ ID NO: 300), **FIG. 302** (SEQ ID NO: 302), **FIG. 304** (SEQ ID NO: 304), **FIG. 306** (SEQ ID NO: 306), **FIG. 308** (SEQ ID NO: 308), **FIG. 310** (SEQ ID NO: 310), **FIG. 312** (SEQ ID NO: 312), **FIG. 314** (SEQ ID NO: 314), **FIG. 316** (SEQ ID NO: 316), **FIG. 318** (SEQ ID NO: 318), **FIG. 320** (SEQ ID NO: 320), **FIG. 322** (SEQ ID NO: 322), **FIG. 324** (SEQ ID NO: 324), **FIG. 326** (SEQ ID NO: 326), **FIG. 328** (SEQ ID NO: 328), **FIG. 330** (SEQ ID NO: 330), **FIG. 332** (SEQ ID NO: 332), **FIG. 334** (SEQ ID NO: 334), **FIG. 336** (SEQ ID NO: 336), **FIG. 338** (SEQ ID NO: 338), **FIG. 340** (SEQ ID NO: 340), **FIG. 342** (SEQ ID NO: 342), **FIG. 344** (SEQ ID NO: 344), **FIG. 346** (SEQ ID NO: 346), **FIG. 348** (SEQ ID NO: 348), **FIG. 350** (SEQ ID NO: 350), **FIG. 352** (SEQ ID NO: 352), **FIG. 354** (SEQ ID NO: 354), **FIG. 356** (SEQ ID NO: 356), **FIG. 358** (SEQ ID NO: 358), **FIG. 360** (SEQ ID NO: 360), **FIG. 362** (SEQ ID NO: 362), **FIG. 364** (SEQ ID NO: 364), **FIG. 366** (SEQ ID NO: 366), **FIG. 368** (SEQ ID NO: 368), **FIG. 370** (SEQ ID NO: 370), **FIG. 372** (SEQ ID NO: 372), **FIG. 374** (SEQ ID NO: 374), **FIG. 376** (SEQ ID NO: 376), **FIG. 378** (SEQ ID NO: 378), **FIG. 380** (SEQ ID NO: 380), **FIG. 382** (SEQ ID NO: 382), **FIG. 384** (SEQ ID NO: 384), **FIG. 386** (SEQ ID NO: 386), **FIG. 388** (SEQ ID NO: 388), **FIG. 390** (SEQ ID NO: 390), **FIG. 392** (SEQ ID NO: 392), **FIG. 394** (SEQ ID NO: 394), **FIG. 396** (SEQ ID NO: 396), **FIG. 398** (SEQ ID NO: 398), **FIG. 400** (SEQ ID NO: 400), **FIG. 402** (SEQ ID NO: 402), **FIG. 404** (SEQ ID NO: 404), **FIG. 406** (SEQ ID NO: 406), **FIG. 408** (SEQ ID NO: 408), **FIG. 410** (SEQ ID NO: 410), **FIG. 412** (SEQ ID NO: 412), **FIG. 414** (SEQ ID NO: 414), **FIG. 416** (SEQ ID NO: 416), **FIG. 418** (SEQ ID NO: 418), **FIG. 420** (SEQ ID NO: 420), **FIG. 422** (SEQ ID NO: 422), **FIG. 424** (SEQ ID NO: 424), **FIG. 426** (SEQ ID NO: 426), **FIG. 428** (SEQ ID NO: 428), **FIG. 430** (SEQ ID NO: 430), **FIG. 432** (SEQ ID NO: 432), **FIG. 434** (SEQ ID NO: 434), **FIG. 436** (SEQ ID NO: 436), **FIG. 438** (SEQ ID NO: 438), **FIG. 440** (SEQ ID NO: 440), **FIG. 442** (SEQ ID NO: 442), **FIG. 444** (SEQ ID NO: 444), **FIG. 446** (SEQ ID NO: 446), **FIG. 448** (SEQ ID NO: 448), **FIG. 450** (SEQ ID NO: 450), **FIG. 452** (SEQ ID NO: 452), **FIG. 454** (SEQ ID NO: 454), **FIG. 456** (SEQ ID NO: 456), **FIG. 458** (SEQ ID NO: 458), **FIG. 460** (SEQ ID NO: 460), **FIG. 462** (SEQ ID NO: 462), **FIG. 464** (SEQ ID NO: 464), **FIG. 466** (SEQ ID NO: 466), **FIG. 468** (SEQ ID NO: 468), **FIG. 470** (SEQ ID NO: 470), **FIG. 472** (SEQ ID NO: 472), **FIG. 474** (SEQ ID NO: 474), **FIG. 476** (SEQ ID NO: 476), **FIG. 478** (SEQ ID NO: 478), **FIG. 480** (SEQ ID NO: 480), **FIG. 482** (SEQ ID NO: 482), **FIG. 484** (SEQ ID NO: 484), **FIG. 486** (SEQ ID NO: 486), **FIG. 488** (SEQ ID NO: 488), **FIG. 490** (SEQ ID NO: 490), **FIG.**

492 (SEQ ID NO: 492), **FIG. 494** (SEQ ID NO: 494), **FIG. 496** (SEQ ID NO: 496), **FIG. 498** (SEQ ID NO: 498), **FIG. 500** (SEQ ID NO: 500), **FIG. 502** (SEQ ID NO: 502), **FIG. 504** (SEQ ID NO: 504), **FIG. 506** (SEQ ID NO: 506), **FIG. 508** (SEQ ID NO: 508), **FIG. 510** (SEQ ID NO: 510), **FIG. 512** (SEQ ID NO: 512), **FIG. 514** (SEQ ID NO: 514), **FIG. 516** (SEQ ID NO: 516), **FIG. 518** (SEQ ID NO: 518), **FIG. 520** (SEQ ID NO: 520), **FIG. 522** (SEQ ID NO: 522), **FIG. 524** (SEQ ID NO: 524), **FIG. 526** (SEQ ID NO: 526), **FIG. 528** (SEQ ID NO: 528), **FIG. 530** (SEQ ID NO: 530), **FIG. 532** (SEQ ID NO: 532), **FIG. 534** (SEQ ID NO: 534), **FIG. 536** (SEQ ID NO: 536), **FIG. 538** (SEQ ID NO: 538), **FIG. 540** (SEQ ID NO: 540), **FIG. 542** (SEQ ID NO: 542), **FIG. 544** (SEQ ID NO: 544), **FIG. 546** (SEQ ID NO: 546), **FIG. 548** (SEQ ID NO: 548), **FIG. 550** (SEQ ID NO: 550), **FIG. 552** (SEQ ID NO: 552), **FIG. 554** (SEQ ID NO: 554), **FIG. 556** (SEQ ID NO: 556), **FIG. 558** (SEQ ID NO: 558), **FIG. 560** (SEQ ID NO: 560), **FIG. 562** (SEQ ID NO: 562), **FIG. 564** (SEQ ID NO: 564), **FIG. 566** (SEQ ID NO: 566), **FIG. 568** (SEQ ID NO: 568), **FIG. 570** (SEQ ID NO: 570), **FIG. 572** (SEQ ID NO: 572), **FIG. 574** (SEQ ID NO: 574), **FIG. 576** (SEQ ID NO: 576), **FIG. 578** (SEQ ID NO: 578), **FIG. 580** (SEQ ID NO: 580), **FIG. 582** (SEQ ID NO: 582), **FIG. 584** (SEQ ID NO: 584), **FIG. 586** (SEQ ID NO: 586), **FIG. 588** (SEQ ID NO: 588), **FIG. 590** (SEQ ID NO: 590), **FIG. 592** (SEQ ID NO: 592), **FIG. 594** (SEQ ID NO: 594), **FIG. 596** (SEQ ID NO: 596), **FIG. 598** (SEQ ID NO: 598), **FIG. 600** (SEQ ID NO: 600), **FIG. 602** (SEQ ID NO: 602), **FIG. 604** (SEQ ID NO: 604), **FIG. 606** (SEQ ID NO: 606), **FIG. 608** (SEQ ID NO: 608), or **FIG. 610** (SEQ ID NO: 610), lacking its associated signal peptide.

19. An isolated polypeptide having at least 80% amino acid sequence identity to:

- (a) an amino acid sequence of the polypeptide shown in **FIG. 2** (SEQ ID NO: 2), **FIG. 4** (SEQ ID NO: 4), **FIG. 6** (SEQ ID NO: 6), **FIG. 8** (SEQ ID NO: 8), **FIG. 10** (SEQ ID NO: 10), **FIG. 12** (SEQ ID NO: 12), **FIG. 14** (SEQ ID NO: 14), **FIG. 16** (SEQ ID NO: 16), **FIG. 18** (SEQ ID NO: 18), **FIG. 20** (SEQ ID NO: 20), **FIG. 22** (SEQ ID NO: 22), **FIG. 24** (SEQ ID NO: 24), **FIG. 26** (SEQ ID NO: 26), **FIG. 28** (SEQ ID NO: 28), **FIG. 30** (SEQ ID NO: 30), **FIG. 32** (SEQ ID NO: 32), **FIG. 34** (SEQ ID NO: 34), **FIG. 36** (SEQ ID NO: 36), **FIG. 38** (SEQ ID NO: 38), **FIG. 40** (SEQ ID NO: 40), **FIG. 42** (SEQ ID NO: 42), **FIG. 44** (SEQ ID NO: 44), **FIG. 46** (SEQ ID NO: 46), **FIG. 48** (SEQ ID NO: 48), **FIG. 50** (SEQ ID NO: 50), **FIG. 52** (SEQ ID NO: 52), **FIG. 54** (SEQ ID NO: 54), **FIG. 56** (SEQ ID NO: 56), **FIG. 58** (SEQ ID NO: 58), **FIG. 60** (SEQ ID NO: 60), **FIG. 62** (SEQ ID NO: 62), **FIG. 64** (SEQ ID NO: 64), **FIG. 66** (SEQ ID NO: 66), **FIG. 68** (SEQ ID NO: 68), **FIG. 70** (SEQ ID NO: 70), **FIG. 72** (SEQ ID NO: 72), **FIG. 74** (SEQ ID NO: 74), **FIG. 76** (SEQ ID NO: 76), **FIG. 78** (SEQ ID NO: 78), **FIG. 80** (SEQ ID NO: 80), **FIG. 82** (SEQ ID NO: 82), **FIG. 84** (SEQ ID NO: 84), **FIG. 86** (SEQ ID NO: 86), **FIG. 88** (SEQ ID NO: 88), **FIG. 90** (SEQ ID NO: 90), **FIG. 92** (SEQ ID NO: 92), **FIG. 94** (SEQ ID NO: 94), **FIG. 96** (SEQ ID NO: 96), **FIG. 98** (SEQ ID NO: 98), **FIG. 100** (SEQ ID NO: 100), **FIG. 102** (SEQ ID NO: 102), **FIG. 104** (SEQ ID NO: 104), **FIG. 106** (SEQ ID NO: 106), **FIG. 108** (SEQ ID NO: 108),

(SEQ ID NO: 570), **FIG. 572** (SEQ ID NO: 572), **FIG. 574** (SEQ ID NO: 574), **FIG. 576** (SEQ ID NO: 576), **FIG. 578** (SEQ ID NO: 578), **FIG. 580** (SEQ ID NO: 580), **FIG. 582** (SEQ ID NO: 582), **FIG. 584** (SEQ ID NO: 584), **FIG. 586** (SEQ ID NO: 586), **FIG. 588** (SEQ ID NO: 588), **FIG. 590** (SEQ ID NO: 590), **FIG. 592** (SEQ ID NO: 592), **FIG. 594** (SEQ ID NO: 594), **FIG. 596** (SEQ ID NO: 596), **FIG. 598** (SEQ ID NO: 598), **FIG. 600** (SEQ ID NO: 600), **FIG. 602** (SEQ ID NO: 602), **FIG. 604** (SEQ ID NO: 604), **FIG. 606** (SEQ ID NO: 606), **FIG. 608** (SEQ ID NO: 608), or **FIG. 610** (SEQ ID NO: 610), lacking its associated signal peptide;

- (b) an amino acid sequence of an extracellular domain of the polypeptide shown in **FIG. 2** (SEQ ID NO: 2), **FIG. 4** (SEQ ID NO: 4), **FIG. 6** (SEQ ID NO: 6), **FIG. 8** (SEQ ID NO: 8), **FIG. 10** (SEQ ID NO: 10), **FIG. 12** (SEQ ID NO: 12), **FIG. 14** (SEQ ID NO: 14), **FIG. 16** (SEQ ID NO: 16), **FIG. 18** (SEQ ID NO: 18), **FIG. 20** (SEQ ID NO: 20), **FIG. 22** (SEQ ID NO: 22), **FIG. 24** (SEQ ID NO: 24), **FIG. 26** (SEQ ID NO: 26), **FIG. 28** (SEQ ID NO: 28), **FIG. 30** (SEQ ID NO: 30), **FIG. 32** (SEQ ID NO: 32), **FIG. 34** (SEQ ID NO: 34), **FIG. 36** (SEQ ID NO: 36), **FIG. 38** (SEQ ID NO: 38), **FIG. 40** (SEQ ID NO: 40), **FIG. 42** (SEQ ID NO: 42), **FIG. 44** (SEQ ID NO: 44), **FIG. 46** (SEQ ID NO: 46), **FIG. 48** (SEQ ID NO: 48), **FIG. 50** (SEQ ID NO: 50), **FIG. 52** (SEQ ID NO: 52), **FIG. 54** (SEQ ID NO: 54), **FIG. 56** (SEQ ID NO: 56), **FIG. 58** (SEQ ID NO: 58), **FIG. 60** (SEQ ID NO: 60), **FIG. 62** (SEQ ID NO: 62), **FIG. 64** (SEQ ID NO: 64), **FIG. 66** (SEQ ID NO: 66), **FIG. 68** (SEQ ID NO: 68), **FIG. 70** (SEQ ID NO: 70), **FIG. 72** (SEQ ID NO: 72), **FIG. 74** (SEQ ID NO: 74), **FIG. 76** (SEQ ID NO: 76), **FIG. 78** (SEQ ID NO: 78), **FIG. 80** (SEQ ID NO: 80), **FIG. 82** (SEQ ID NO: 82), **FIG. 84** (SEQ ID NO: 84), **FIG. 86** (SEQ ID NO: 86), **FIG. 88** (SEQ ID NO: 88), **FIG. 90** (SEQ ID NO: 90), **FIG. 92** (SEQ ID NO: 92), **FIG. 94** (SEQ ID NO: 94), **FIG. 96** (SEQ ID NO: 96), **FIG. 98** (SEQ ID NO: 98), **FIG. 100** (SEQ ID NO: 100), **FIG. 102** (SEQ ID NO: 102), **FIG. 104** (SEQ ID NO: 104), **FIG. 106** (SEQ ID NO: 106), **FIG. 108** (SEQ ID NO: 108), **FIG. 110** (SEQ ID NO: 110), **FIG. 112** (SEQ ID NO: 112), **FIG. 114** (SEQ ID NO: 114), **FIG. 116** (SEQ ID NO: 116), **FIG. 118** (SEQ ID NO: 118), **FIG. 120** (SEQ ID NO: 120), **FIG. 122** (SEQ ID NO: 122), **FIG. 124** (SEQ ID NO: 124), **FIG. 126** (SEQ ID NO: 126), **FIG. 128** (SEQ ID NO: 128), **FIG. 130** (SEQ ID NO: 130), **FIG. 132** (SEQ ID NO: 132), **FIG. 134** (SEQ ID NO: 134), **FIG. 136** (SEQ ID NO: 136), **FIG. 138** (SEQ ID NO: 138), **FIG. 140** (SEQ ID NO: 140), **FIG. 142** (SEQ ID NO: 142), **FIG. 144** (SEQ ID NO: 144), **FIG. 146** (SEQ ID NO: 146), **FIG. 148** (SEQ ID NO: 148), **FIG. 150** (SEQ ID NO: 150), **FIG. 152** (SEQ ID NO: 152), **FIG. 154** (SEQ ID NO: 154), **FIG. 156** (SEQ ID NO: 156), **FIG. 158** (SEQ ID NO: 158), **FIG. 160** (SEQ ID NO: 160), **FIG. 162** (SEQ ID NO: 162), **FIG. 164** (SEQ ID NO: 164), **FIG. 166** (SEQ ID NO: 166), **FIG. 168** (SEQ ID NO: 168), **FIG. 170** (SEQ ID NO: 170), **FIG. 172** (SEQ ID NO: 172), **FIG. 174** (SEQ ID NO: 174), **FIG. 176** (SEQ ID NO: 176), **FIG. 178** (SEQ ID NO: 178), **FIG. 180** (SEQ ID NO: 180), **FIG. 182** (SEQ ID NO: 182), **FIG. 184** (SEQ ID NO: 184), **FIG. 186** (SEQ ID NO: 186), **FIG. 188** (SEQ ID NO: 188), **FIG. 190** (SEQ ID NO: 190),

FIG. 192 (SEQ ID NO: 192), **FIG. 194** (SEQ ID NO: 194), **FIG. 196** (SEQ ID NO: 196), **FIG. 198** (SEQ ID NO: 198), **FIG. 200** (SEQ ID NO: 200), **FIG. 202** (SEQ ID NO: 202), **FIG. 204** (SEQ ID NO: 204), **FIG. 206** (SEQ ID NO: 206), **FIG. 208** (SEQ ID NO: 208), **FIG. 210** (SEQ ID NO: 210), **FIG. 212** (SEQ ID NO: 212), **FIG. 214** (SEQ ID NO: 214), **FIG. 216** (SEQ ID NO: 216), **FIG. 218** (SEQ ID NO: 218), **FIG. 220** (SEQ ID NO: 220), **FIG. 222** (SEQ ID NO: 222), **FIG. 224** (SEQ ID NO: 224), **FIG. 226** (SEQ ID NO: 226), **FIG. 228** (SEQ ID NO: 228), **FIG. 230** (SEQ ID NO: 230), **FIG. 232** (SEQ ID NO: 232), **FIG. 234** (SEQ ID NO: 234), **FIG. 236** (SEQ ID NO: 236), **FIG. 238** (SEQ ID NO: 238), **FIG. 240** (SEQ ID NO: 240), **FIG. 242** (SEQ ID NO: 242), **FIG. 244** (SEQ ID NO: 244), **FIG. 246** (SEQ ID NO: 246), **FIG. 248** (SEQ ID NO: 248), **FIG. 250** (SEQ ID NO: 250), **FIG. 252** (SEQ ID NO: 252), **FIG. 254** (SEQ ID NO: 254), **FIG. 256** (SEQ ID NO: 256), **FIG. 258** (SEQ ID NO: 258), **FIG. 260** (SEQ ID NO: 260), **FIG. 262** (SEQ ID NO: 262), **FIG. 264** (SEQ ID NO: 264), **FIG. 266** (SEQ ID NO: 266), **FIG. 268** (SEQ ID NO: 268), **FIG. 270** (SEQ ID NO: 270), **FIG. 272** (SEQ ID NO: 272), **FIG. 274** (SEQ ID NO: 274), **FIG. 276** (SEQ ID NO: 276), **FIG. 278** (SEQ ID NO: 278), **FIG. 280** (SEQ ID NO: 280), **FIG. 282** (SEQ ID NO: 282), **FIG. 284** (SEQ ID NO: 284), **FIG. 286** (SEQ ID NO: 286), **FIG. 288** (SEQ ID NO: 288), **FIG. 290** (SEQ ID NO: 290), **FIG. 292** (SEQ ID NO: 292), **FIG. 294** (SEQ ID NO: 294), **FIG. 296** (SEQ ID NO: 296), **FIG. 298** (SEQ ID NO: 298), **FIG. 300** (SEQ ID NO: 300), **FIG. 302** (SEQ ID NO: 302), **FIG. 304** (SEQ ID NO: 304), **FIG. 306** (SEQ ID NO: 306), **FIG. 308** (SEQ ID NO: 308), **FIG. 310** (SEQ ID NO: 310), **FIG. 312** (SEQ ID NO: 312), **FIG. 314** (SEQ ID NO: 314), **FIG. 316** (SEQ ID NO: 316), **FIG. 318** (SEQ ID NO: 318), **FIG. 320** (SEQ ID NO: 320), **FIG. 322** (SEQ ID NO: 322), **FIG. 324** (SEQ ID NO: 324), **FIG. 326** (SEQ ID NO: 326), **FIG. 328** (SEQ ID NO: 328), **FIG. 330** (SEQ ID NO: 330), **FIG. 332** (SEQ ID NO: 332), **FIG. 334** (SEQ ID NO: 334), **FIG. 336** (SEQ ID NO: 336), **FIG. 338** (SEQ ID NO: 338), **FIG. 340** (SEQ ID NO: 340), **FIG. 342** (SEQ ID NO: 342), **FIG. 344** (SEQ ID NO: 344), **FIG. 346** (SEQ ID NO: 346), **FIG. 348** (SEQ ID NO: 348), **FIG. 350** (SEQ ID NO: 350), **FIG. 352** (SEQ ID NO: 352), **FIG. 354** (SEQ ID NO: 354), **FIG. 356** (SEQ ID NO: 356), **FIG. 358** (SEQ ID NO: 358), **FIG. 360** (SEQ ID NO: 360), **FIG. 362** (SEQ ID NO: 362), **FIG. 364** (SEQ ID NO: 364), **FIG. 366** (SEQ ID NO: 366), **FIG. 368** (SEQ ID NO: 368), **FIG. 370** (SEQ ID NO: 370), **FIG. 372** (SEQ ID NO: 372), **FIG. 374** (SEQ ID NO: 374), **FIG. 376** (SEQ ID NO: 376), **FIG. 378** (SEQ ID NO: 378), **FIG. 380** (SEQ ID NO: 380), **FIG. 382** (SEQ ID NO: 382), **FIG. 384** (SEQ ID NO: 384), **FIG. 386** (SEQ ID NO: 386), **FIG. 388** (SEQ ID NO: 388), **FIG. 390** (SEQ ID NO: 390), **FIG. 392** (SEQ ID NO: 392), **FIG. 394** (SEQ ID NO: 394), **FIG. 396** (SEQ ID NO: 396), **FIG. 398** (SEQ ID NO: 398), **FIG. 400** (SEQ ID NO: 400), **FIG. 402** (SEQ ID NO: 402), **FIG. 404** (SEQ ID NO: 404), **FIG. 406** (SEQ ID NO: 406), **FIG. 408** (SEQ ID NO: 408), **FIG. 410** (SEQ ID NO: 410), **FIG. 412** (SEQ ID NO: 412), **FIG. 414** (SEQ ID NO: 414), **FIG. 416** (SEQ ID NO: 416), **FIG. 418** (SEQ ID NO: 418), **FIG. 420** (SEQ ID NO: 420),

420), **FIG. 422** (SEQ ID NO: 422), **FIG. 424** (SEQ ID NO: 424), **FIG. 426** (SEQ ID NO: 426), **FIG. 428** (SEQ ID NO: 428), **FIG. 430** (SEQ ID NO: 430), **FIG. 432** (SEQ ID NO: 432), **FIG. 434** (SEQ ID NO: 434), **FIG. 436** (SEQ ID NO: 436), **FIG. 438** (SEQ ID NO: 438), **FIG. 440** (SEQ ID NO: 440), **FIG. 442** (SEQ ID NO: 442), **FIG. 444** (SEQ ID NO: 444), **FIG. 446** (SEQ ID NO: 446), **FIG. 448** (SEQ ID NO: 448), **FIG. 450** (SEQ ID NO: 450), **FIG. 452** (SEQ ID NO: 452), **FIG. 454** (SEQ ID NO: 454), **FIG. 456** (SEQ ID NO: 456), **FIG. 458** (SEQ ID NO: 458), **FIG. 460** (SEQ ID NO: 460), **FIG. 462** (SEQ ID NO: 462), **FIG. 464** (SEQ ID NO: 464), **FIG. 466** (SEQ ID NO: 466), **FIG. 468** (SEQ ID NO: 468), **FIG. 470** (SEQ ID NO: 470), **FIG. 472** (SEQ ID NO: 472), **FIG. 474** (SEQ ID NO: 474), **FIG. 476** (SEQ ID NO: 476), **FIG. 478** (SEQ ID NO: 478), **FIG. 480** (SEQ ID NO: 480), **FIG. 482** (SEQ ID NO: 482), **FIG. 484** (SEQ ID NO: 484), **FIG. 486** (SEQ ID NO: 486), **FIG. 488** (SEQ ID NO: 488), **FIG. 490** (SEQ ID NO: 490), **FIG. 492** (SEQ ID NO: 492), **FIG. 494** (SEQ ID NO: 494), **FIG. 496** (SEQ ID NO: 496), **FIG. 498** (SEQ ID NO: 498), **FIG. 500** (SEQ ID NO: 500), **FIG. 502** (SEQ ID NO: 502), **FIG. 504** (SEQ ID NO: 504), **FIG. 506** (SEQ ID NO: 506), **FIG. 508** (SEQ ID NO: 508), **FIG. 510** (SEQ ID NO: 510), **FIG. 512** (SEQ ID NO: 512), **FIG. 514** (SEQ ID NO: 514), **FIG. 516** (SEQ ID NO: 516), **FIG. 518** (SEQ ID NO: 518), **FIG. 520** (SEQ ID NO: 520), **FIG. 522** (SEQ ID NO: 522), **FIG. 524** (SEQ ID NO: 524), **FIG. 526** (SEQ ID NO: 526), **FIG. 528** (SEQ ID NO: 528), **FIG. 530** (SEQ ID NO: 530), **FIG. 532** (SEQ ID NO: 532), **FIG. 534** (SEQ ID NO: 534), **FIG. 536** (SEQ ID NO: 536), **FIG. 538** (SEQ ID NO: 538), **FIG. 540** (SEQ ID NO: 540), **FIG. 542** (SEQ ID NO: 542), **FIG. 544** (SEQ ID NO: 544), **FIG. 546** (SEQ ID NO: 546), **FIG. 548** (SEQ ID NO: 548), **FIG. 550** (SEQ ID NO: 550), **FIG. 552** (SEQ ID NO: 552), **FIG. 554** (SEQ ID NO: 554), **FIG. 556** (SEQ ID NO: 556), **FIG. 558** (SEQ ID NO: 558), **FIG. 560** (SEQ ID NO: 560), **FIG. 562** (SEQ ID NO: 562), **FIG. 564** (SEQ ID NO: 564), **FIG. 566** (SEQ ID NO: 566), **FIG. 568** (SEQ ID NO: 568), **FIG. 570** (SEQ ID NO: 570), **FIG. 572** (SEQ ID NO: 572), **FIG. 574** (SEQ ID NO: 574), **FIG. 576** (SEQ ID NO: 576), **FIG. 578** (SEQ ID NO: 578), **FIG. 580** (SEQ ID NO: 580), **FIG. 582** (SEQ ID NO: 582), **FIG. 584** (SEQ ID NO: 584), **FIG. 586** (SEQ ID NO: 586), **FIG. 588** (SEQ ID NO: 588), **FIG. 590** (SEQ ID NO: 590), **FIG. 592** (SEQ ID NO: 592), **FIG. 594** (SEQ ID NO: 594), **FIG. 596** (SEQ ID NO: 596), **FIG. 598** (SEQ ID NO: 598), **FIG. 600** (SEQ ID NO: 600), **FIG. 602** (SEQ ID NO: 602), **FIG. 604** (SEQ ID NO: 604), **FIG. 606** (SEQ ID NO: 606), **FIG. 608** (SEQ ID NO: 608), or **FIG. 610** (SEQ ID NO: 610), with its associated signal peptide; or

- (c) an amino acid sequence of an extracellular domain of the polypeptide shown in **FIG. 2** (SEQ ID NO: 2), **FIG. 4** (SEQ ID NO: 4), **FIG. 6** (SEQ ID NO: 6), **FIG. 8** (SEQ ID NO: 8), **FIG. 10** (SEQ ID NO: 10), **FIG. 12** (SEQ ID NO: 12), **FIG. 14** (SEQ ID NO: 14), **FIG. 16** (SEQ ID NO: 16), **FIG. 18** (SEQ ID NO: 18), **FIG. 20** (SEQ ID NO: 20), **FIG. 22** (SEQ ID NO: 22), **FIG. 24** (SEQ ID NO: 24), **FIG. 26** (SEQ ID NO: 26), **FIG. 28** (SEQ ID NO: 28), **FIG. 30** (SEQ ID NO: 30), **FIG. 32** (SEQ ID NO: 32), **FIG. 34** (SEQ ID NO: 34), **FIG. 36**

(SEQ ID NO: 36), **FIG. 38** (SEQ ID NO: 38), **FIG. 40** (SEQ ID NO: 40), **FIG. 42** (SEQ ID NO: 42), **FIG. 44** (SEQ ID NO: 44), **FIG. 46** (SEQ ID NO: 46), **FIG. 48** (SEQ ID NO: 48), **FIG. 50** (SEQ ID NO: 50), **FIG. 52** (SEQ ID NO: 52), **FIG. 54** (SEQ ID NO: 54), **FIG. 56** (SEQ ID NO: 56), **FIG. 58** (SEQ ID NO: 58), **FIG. 60** (SEQ ID NO: 60), **FIG. 62** (SEQ ID NO: 62), **FIG. 64** (SEQ ID NO: 64), **FIG. 66** (SEQ ID NO: 66), **FIG. 68** (SEQ ID NO: 68), **FIG. 70** (SEQ ID NO: 70), **FIG. 72** (SEQ ID NO: 72), **FIG. 74** (SEQ ID NO: 74), **FIG. 76** (SEQ ID NO: 76), **FIG. 78** (SEQ ID NO: 78), **FIG. 80** (SEQ ID NO: 80), **FIG. 82** (SEQ ID NO: 82), **FIG. 84** (SEQ ID NO: 84), **FIG. 86** (SEQ ID NO: 86), **FIG. 88** (SEQ ID NO: 88), **FIG. 90** (SEQ ID NO: 90), **FIG. 92** (SEQ ID NO: 92), **FIG. 94** (SEQ ID NO: 94), **FIG. 96** (SEQ ID NO: 96), **FIG. 98** (SEQ ID NO: 98), **FIG. 100** (SEQ ID NO: 100), **FIG. 102** (SEQ ID NO: 102), **FIG. 104** (SEQ ID NO: 104), **FIG. 106** (SEQ ID NO: 106), **FIG. 108** (SEQ ID NO: 108), **FIG. 110** (SEQ ID NO: 110), **FIG. 112** (SEQ ID NO: 112), **FIG. 114** (SEQ ID NO: 114), **FIG. 116** (SEQ ID NO: 116), **FIG. 118** (SEQ ID NO: 118), **FIG. 120** (SEQ ID NO: 120), **FIG. 122** (SEQ ID NO: 122), **FIG. 124** (SEQ ID NO: 124), **FIG. 126** (SEQ ID NO: 126), **FIG. 128** (SEQ ID NO: 128), **FIG. 130** (SEQ ID NO: 130), **FIG. 132** (SEQ ID NO: 132), **FIG. 134** (SEQ ID NO: 134), **FIG. 136** (SEQ ID NO: 136), **FIG. 138** (SEQ ID NO: 138), **FIG. 140** (SEQ ID NO: 140), **FIG. 142** (SEQ ID NO: 142), **FIG. 144** (SEQ ID NO: 144), **FIG. 146** (SEQ ID NO: 146), **FIG. 148** (SEQ ID NO: 148), **FIG. 150** (SEQ ID NO: 150), **FIG. 152** (SEQ ID NO: 152), **FIG. 154** (SEQ ID NO: 154), **FIG. 156** (SEQ ID NO: 156), **FIG. 158** (SEQ ID NO: 158), **FIG. 160** (SEQ ID NO: 160), **FIG. 162** (SEQ ID NO: 162), **FIG. 164** (SEQ ID NO: 164), **FIG. 166** (SEQ ID NO: 166), **FIG. 168** (SEQ ID NO: 168), **FIG. 170** (SEQ ID NO: 170), **FIG. 172** (SEQ ID NO: 172), **FIG. 174** (SEQ ID NO: 174), **FIG. 176** (SEQ ID NO: 176), **FIG. 178** (SEQ ID NO: 178), **FIG. 180** (SEQ ID NO: 180), **FIG. 182** (SEQ ID NO: 182), **FIG. 184** (SEQ ID NO: 184), **FIG. 186** (SEQ ID NO: 186), **FIG. 188** (SEQ ID NO: 188), **FIG. 190** (SEQ ID NO: 190), **FIG. 192** (SEQ ID NO: 192), **FIG. 194** (SEQ ID NO: 194), **FIG. 196** (SEQ ID NO: 196), **FIG. 198** (SEQ ID NO: 198), **FIG. 200** (SEQ ID NO: 200), **FIG. 202** (SEQ ID NO: 202), **FIG. 204** (SEQ ID NO: 204), **FIG. 206** (SEQ ID NO: 206), **FIG. 208** (SEQ ID NO: 208), **FIG. 210** (SEQ ID NO: 210), **FIG. 212** (SEQ ID NO: 212), **FIG. 214** (SEQ ID NO: 214), **FIG. 216** (SEQ ID NO: 216), **FIG. 218** (SEQ ID NO: 218), **FIG. 220** (SEQ ID NO: 220), **FIG. 222** (SEQ ID NO: 222), **FIG. 224** (SEQ ID NO: 224), **FIG. 226** (SEQ ID NO: 226), **FIG. 228** (SEQ ID NO: 228), **FIG. 230** (SEQ ID NO: 230), **FIG. 232** (SEQ ID NO: 232), **FIG. 234** (SEQ ID NO: 234), **FIG. 236** (SEQ ID NO: 236), **FIG. 238** (SEQ ID NO: 238), **FIG. 240** (SEQ ID NO: 240), **FIG. 242** (SEQ ID NO: 242), **FIG. 244** (SEQ ID NO: 244), **FIG. 246** (SEQ ID NO: 246), **FIG. 248** (SEQ ID NO: 248), **FIG. 250** (SEQ ID NO: 250), **FIG. 252** (SEQ ID NO: 252), **FIG. 254** (SEQ ID NO: 254), **FIG. 256** (SEQ ID NO: 256), **FIG. 258** (SEQ ID NO: 258), **FIG. 260** (SEQ ID NO: 260), **FIG. 262** (SEQ ID NO: 262), **FIG. 264** (SEQ ID NO: 264), **FIG. 266** (SEQ ID NO: 266), **FIG. 268** (SEQ ID NO: 268), **FIG. 270** (SEQ ID NO: 270), **FIG. 272** (SEQ ID NO: 272),

FIG. 274 (SEQ ID NO: 274), **FIG. 276** (SEQ ID NO: 276), **FIG. 278** (SEQ ID NO: 278), **FIG. 280** (SEQ ID NO: 280), **FIG. 282** (SEQ ID NO: 282), **FIG. 284** (SEQ ID NO: 284), **FIG. 286** (SEQ ID NO: 286), **FIG. 288** (SEQ ID NO: 288), **FIG. 290** (SEQ ID NO: 290), **FIG. 292** (SEQ ID NO: 292), **FIG. 294** (SEQ ID NO: 294), **FIG. 296** (SEQ ID NO: 296), **FIG. 298** (SEQ ID NO: 298), **FIG. 300** (SEQ ID NO: 300), **FIG. 302** (SEQ ID NO: 302), **FIG. 304** (SEQ ID NO: 304), **FIG. 306** (SEQ ID NO: 306), **FIG. 308** (SEQ ID NO: 308), **FIG. 310** (SEQ ID NO: 310), **FIG. 312** (SEQ ID NO: 312), **FIG. 314** (SEQ ID NO: 314), **FIG. 316** (SEQ ID NO: 316), **FIG. 318** (SEQ ID NO: 318), **FIG. 320** (SEQ ID NO: 320), **FIG. 322** (SEQ ID NO: 322), **FIG. 324** (SEQ ID NO: 324), **FIG. 326** (SEQ ID NO: 326), **FIG. 328** (SEQ ID NO: 328), **FIG. 330** (SEQ ID NO: 330), **FIG. 332** (SEQ ID NO: 332), **FIG. 334** (SEQ ID NO: 334), **FIG. 336** (SEQ ID NO: 336), **FIG. 338** (SEQ ID NO: 338), **FIG. 340** (SEQ ID NO: 340), **FIG. 342** (SEQ ID NO: 342), **FIG. 344** (SEQ ID NO: 344), **FIG. 346** (SEQ ID NO: 346), **FIG. 348** (SEQ ID NO: 348), **FIG. 350** (SEQ ID NO: 350), **FIG. 352** (SEQ ID NO: 352), **FIG. 354** (SEQ ID NO: 354), **FIG. 356** (SEQ ID NO: 356), **FIG. 358** (SEQ ID NO: 358), **FIG. 360** (SEQ ID NO: 360), **FIG. 362** (SEQ ID NO: 362), **FIG. 364** (SEQ ID NO: 364), **FIG. 366** (SEQ ID NO: 366), **FIG. 368** (SEQ ID NO: 368), **FIG. 370** (SEQ ID NO: 370), **FIG. 372** (SEQ ID NO: 372), **FIG. 374** (SEQ ID NO: 374), **FIG. 376** (SEQ ID NO: 376), **FIG. 378** (SEQ ID NO: 378), **FIG. 380** (SEQ ID NO: 380), **FIG. 382** (SEQ ID NO: 382), **FIG. 384** (SEQ ID NO: 384), **FIG. 386** (SEQ ID NO: 386), **FIG. 388** (SEQ ID NO: 388), **FIG. 390** (SEQ ID NO: 390), **FIG. 392** (SEQ ID NO: 392), **FIG. 394** (SEQ ID NO: 394), **FIG. 396** (SEQ ID NO: 396), **FIG. 398** (SEQ ID NO: 398), **FIG. 400** (SEQ ID NO: 400), **FIG. 402** (SEQ ID NO: 402), **FIG. 404** (SEQ ID NO: 404), **FIG. 406** (SEQ ID NO: 406), **FIG. 408** (SEQ ID NO: 408), **FIG. 410** (SEQ ID NO: 410), **FIG. 412** (SEQ ID NO: 412), **FIG. 414** (SEQ ID NO: 414), **FIG. 416** (SEQ ID NO: 416), **FIG. 418** (SEQ ID NO: 418), **FIG. 420** (SEQ ID NO: 420), **FIG. 422** (SEQ ID NO: 422), **FIG. 424** (SEQ ID NO: 424), **FIG. 426** (SEQ ID NO: 426), **FIG. 428** (SEQ ID NO: 428), **FIG. 430** (SEQ ID NO: 430), **FIG. 432** (SEQ ID NO: 432), **FIG. 434** (SEQ ID NO: 434), **FIG. 436** (SEQ ID NO: 436), **FIG. 438** (SEQ ID NO: 438), **FIG. 440** (SEQ ID NO: 440), **FIG. 442** (SEQ ID NO: 442), **FIG. 444** (SEQ ID NO: 444), **FIG. 446** (SEQ ID NO: 446), **FIG. 448** (SEQ ID NO: 448), **FIG. 450** (SEQ ID NO: 450), **FIG. 452** (SEQ ID NO: 452), **FIG. 454** (SEQ ID NO: 454), **FIG. 456** (SEQ ID NO: 456), **FIG. 458** (SEQ ID NO: 458), **FIG. 460** (SEQ ID NO: 460), **FIG. 462** (SEQ ID NO: 462), **FIG. 464** (SEQ ID NO: 464), **FIG. 466** (SEQ ID NO: 466), **FIG. 468** (SEQ ID NO: 468), **FIG. 470** (SEQ ID NO: 470), **FIG. 472** (SEQ ID NO: 472), **FIG. 474** (SEQ ID NO: 474), **FIG. 476** (SEQ ID NO: 476), **FIG. 478** (SEQ ID NO: 478), **FIG. 480** (SEQ ID NO: 480), **FIG. 482** (SEQ ID NO: 482), **FIG. 484** (SEQ ID NO: 484), **FIG. 486** (SEQ ID NO: 486), **FIG. 488** (SEQ ID NO: 488),

FIG. 490 (SEQ ID NO: 490), **FIG. 492** (SEQ ID NO: 492), **FIG. 494** (SEQ ID NO: 494), **FIG. 496** (SEQ ID NO: 496), **FIG. 498** (SEQ ID NO: 498), **FIG. 500** (SEQ ID NO: 500), **FIG. 502** (SEQ ID NO: 502), **FIG. 504** (SEQ ID NO: 504), **FIG. 506** (SEQ ID NO: 506), **FIG. 508** (SEQ ID NO: 508), **FIG. 510** (SEQ ID NO: 510), **FIG. 512** (SEQ ID NO: 512), **FIG. 514** (SEQ ID NO: 514), **FIG. 516** (SEQ ID NO: 516), **FIG. 518** (SEQ ID NO: 518), **FIG. 520** (SEQ ID NO: 520), **FIG. 522** (SEQ ID NO: 522), **FIG. 524** (SEQ ID NO: 524), **FIG. 526** (SEQ ID NO: 526), **FIG. 528** (SEQ ID NO: 528), **FIG. 530** (SEQ ID NO: 530), **FIG. 532** (SEQ ID NO: 532), **FIG. 534** (SEQ ID NO: 534), **FIG. 536** (SEQ ID NO: 536), **FIG. 538** (SEQ ID NO: 538), **FIG. 540** (SEQ ID NO: 540), **FIG. 542** (SEQ ID NO: 542), **FIG. 544** (SEQ ID NO: 544), **FIG. 546** (SEQ ID NO: 546), **FIG. 548** (SEQ ID NO: 548), **FIG. 550** (SEQ ID NO: 550), **FIG. 552** (SEQ ID NO: 552), **FIG. 554** (SEQ ID NO: 554), **FIG. 556** (SEQ ID NO: 556), **FIG. 558** (SEQ ID NO: 558), **FIG. 560** (SEQ ID NO: 560), **FIG. 562** (SEQ ID NO: 562), **FIG. 564** (SEQ ID NO: 564), **FIG. 566** (SEQ ID NO: 566), **FIG. 568** (SEQ ID NO: 568), **FIG. 570** (SEQ ID NO: 570), **FIG. 572** (SEQ ID NO: 572), **FIG. 574** (SEQ ID NO: 574), **FIG. 576** (SEQ ID NO: 576), **FIG. 578** (SEQ ID NO: 578), **FIG. 580** (SEQ ID NO: 580), **FIG. 582** (SEQ ID NO: 582), **FIG. 584** (SEQ ID NO: 584), **FIG. 586** (SEQ ID NO: 586), **FIG. 588** (SEQ ID NO: 588), **FIG. 590** (SEQ ID NO: 590), **FIG. 592** (SEQ ID NO: 592), **FIG. 594** (SEQ ID NO: 594), **FIG. 596** (SEQ ID NO: 596), **FIG. 598** (SEQ ID NO: 598), **FIG. 600** (SEQ ID NO: 600), **FIG. 602** (SEQ ID NO: 602), **FIG. 604** (SEQ ID NO: 604), **FIG. 606** (SEQ ID NO: 606), **FIG. 608** (SEQ ID NO: 608), or **FIG. 610** (SEQ ID NO: 610), lacking its associated signal peptide.

20. A method for stimulating the release of TNF- α from human blood, said method comprising contacting said blood with a PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or PRO4333 polypeptide, wherein the release of TNF- α from said blood is stimulated.

21. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO6029 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

22. A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

23. The method of claim 22, wherein said tumor is adrenal tumor, lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, cervical tumor or liver tumor.

24. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

* * * * *

专利名称(译)	分泌的和跨膜的多肽和编码它们的核酸		
公开(公告)号	US20030027262A1	公开(公告)日	2003-02-06
申请号	US10/173700	申请日	2002-06-17
[标]申请(专利权)人(译)	健泰科生物技术公司		
申请(专利权)人(译)	基因泰克, INC.		
当前申请(专利权)人(译)	基因泰克, INC.		
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摘要(译)

本发明涉及新的多肽和编码这些多肽的核酸分子。本文还提供了包含那些核酸序列的载体和宿主细胞，包含与异源多肽序列融合的本发明多肽的嵌合多肽分子，与本发明多肽结合的抗体和产生本发明多肽的方法发明。

MAALMRSKDSSCCLLLLAAVLNVESQIGSSRAKLNSTKSLGGETPGQAANRSAGHYQGLAFGGSKKGNLGA
YPCSSDKCEVGRYCHSPHQSSACNVCRKKKCRDGMCCPSTRCNGICIPVTESLITPHIPALDGTTRHRDR
NHGHYSNHDLGWQNLGRPHTKMSHIKGHBDEPLRSSDCTEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGL
EIFQRCDCAKGLSCKVWKDATYSSKARLHYCQKI

Signal peptide:
amino acids 1-25