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(54) COMPOSITIONS AND METHODS FOR DETECTING UNSTABLE ARTERIOSCLEROTIC PLAQUES

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(57) ABSTRACT

The present disclosure provides methods of detecting an unstable arteriosclerotic plaque in an individual, involving detecting in a biological sample from the individual an enzymatic cleavage product of a protein component of an arteriosclerotic plaque. The present disclosure provides methods of assessing the risk that an individual will develop an occlusive vascular event. The present disclosure further provides kits for carrying out a subject method.

Figure 1A

Homo sapiens
Alpha-1 (I) collagen (1464 aa)
GenBank AAB94054

```
   1 mfsfvdlrll lllaatallt hgqeegqveg qdedippitc vqnglryhdr dvwkpepcri
  61 cvcdngkvlc ddvicdetkn cpgaevpege ccpvcpdgse sptdqettgv egpkgdtgpr
 121 gprgpagppg rdgipgqpgl pgppgppgpp gppglggnfa pqlsygydek stggisvpgp
 181 mgpsgprglp gppgapgpqg fqgppgepge pgasgpmgpr gppgppgkng ddgeagkpgr
 241 pgergppgpq garglpgtag lpgmkghrgf sgldgakgda gpagpkgepg spgengapgq
 301 mgprglpger grpgapgpag argndgatga agppgptgpa gppgfpgavg akgeagpqgp
 361 rgsegpqgvr gepgppgpag aagpagnpga dgqpgakgan gapgiagapg fpgargpsgp
 421 qgpggppgpk gnsgepgapg skgdtgakge pgpvgvqgpp gpageegkrg argepgptgl
 481 pgppgerggp gsrgfpgadg vagpkgpage rgspgpagpk gspgeagrpg eaglpgakgl
 541 tgspgspgpd gktgppgpag qdgrpgppgp pgargqagvm gfpgpkgaag epgkagergv
 601 pgppgavgpa gkdgeagaqg ppgpagpage rgeqgpagsp gfqglpgpag ppgeagkpge
 661 qgvpgdlgap gpsgargerg fpgergvqgp pgpagprgan gapgndgakg dagapgapgs
 721 qgapglqgmp gergaaglpg pkgdrgdagp kgadgspgkd gvrgltgpig ppgpagapgd
 781 kgesgpsgpa gptgargapg drgepgppgp agfagppgad gqpgakgepg dagakgdagp
 841 pgpagpagpp gpignvgapg akgargsagp pgatgfpgaa grvgppgpsg nagppgppgp
 901 agkeggkgpr getgpagrpg evgppgppgp agekgspgad gpagapgtpg pqgiagqrgv
 961 vglpgqrger gfpglpgpsg epgkqgpsga sgergppgpm gppglagppg esgregapga
1021 egspgrdgsp gakgdrgetg pagppgapga pgapgpvgpa gksgdrgetg pagpagpvgp
1081 vgargpagpq gprgdkgetg eqgdrgikgh rgfsglqgpp gppgspgeqg psgasgpagp
1141 rgppgsagap gkdglnglpg pigppgprgr tgdagpvgpp gppgppgppg ppsagfdfsf
```

Figure 1B

```
1201 lpqppqekah dggryyradd anvvrdrdle vdttlkslsq qienirspeg srknpartcr
1261 dlkmchsdwk sgeywidpnq gcnldaikvf cnmetgetcv yptqpsvaqk nwyisknpkd
1321 krhvwfgesm tdgfqfeygg qgsdpadvai qltflrlmst easqnityhc knsvaymdqq
1381 tgnlkkalll kgsneieira egnsrftysv tvdgctshtg awgktvieyk ttktsrlpii
1441 dvapldvgap dqefgfdvgp vcfl (SEQ ID NO:1)
```

Figure 2A

Homo sapiens
Alpha-1 (II) collagen
GenBank AAC41772 (1487 aa)

```
   1 mirlgapqsl vlltllvaav lrcqgqdvqe agscvqdgqr yndkdvwkpe pcricvcdtg
  61 tvlcddiice dvkdclspei pfgeccpicp tdlatasgqp gpkgqkgepg dikdivgpkg
 121 ppgpqgpage qgprgdrgdk gekgapgprg rdgepgtpgn pgppgppgpp gppglggnfa
 181 aqmaggfdek aggaqlgvmq gpmgpmgprg ppgpagapgp qgfqgnpgep gepgvsgpmg
 241 prgppgppgk pgddgeagkp gkagergppg pqgargfpgt pglpgvkghr gypgldgakg
 301 eagapgvkge sgspgengsp gpmgprglpg ergrtgpaga agargndgqp gpagppgpvg
 361 paggpgfpga pgakgeagpt gargpegaqg prgepgtpgs pgpagasgnp gtdgipgakg
 421 sagapgiaga pgfpgprgpp gpqgatgplg pkgqtgepgi agfkgeqgpk gepgpagpqg
 481 apgpageegk rgargepggv gpigppgerg apgnrgfpgq dglagpkgap gergpsglag
 541 pkgangdpgr pgepglpgar gltgrpgdag pqgkvgpsga pgedgrpgpp gpqgargqpg
 601 vmgfpgpkga ngepgkagek glpgapglrg lpgkdgetga agppgpagpa gergeqgapg
 661 psgfqglpgp pgppgeggkp gdqgvpgeag apglvgprge rgfpgergsp gaqglqgprg
 721 lpgtpgtdgp kgasgpagpp gaqgppglqg mpgergaagi agpkgdrgdv gekgpegapg
 781 kdggrgltgp igppgpagan gekgevgppg pagsagarga pgergetgpp gpagfagppg
 841 adgqpgakge qgeagqkgda gapgpqgpsg apgpqgptgv tgpkgargaq gppgatgfpg
 901 aagrvgppgs ngnpgppgpp gpsgkdgpkg argdsgppgr agepglqgpa gppgekgepg
 961 ddgpsgaegp pgpqglagqr givglpgqrg ergfpglpgp sgepgkqgap gasgdrgppg
1021 pvgppgltgp agepgregsp gadgppgrdg aagvkgdrge tgavgapgap gppgspgpag
1081 ptgkqgdrge agaqgpmgps gpagargiqg pqgprgdkge agepgerglk ghrgftglqg
1141 lpgppgpsgd qgasgpagps gprgppgpvg psgkdgangi pgpigppgpr grsgetgpag
```

Figure 2B

```
1201 ppgnpgppgp pgppgpgidm safaglgpre kgpdplqymr adqaagglrq hdaevdatlk
1261 slnnqiesir spegsrknpa rtcrdlklch pewksgdywi dpnqgctlda mkvfcnmetg
1321 etcvypnpan vpkknwwssk skekkhiwfg etinggfhfs ygddnlapnt anvqmtflrl
1381 lstegsqnit yhcknsiayl deaagnlkka lliqgsndve iraegnsrft ytalkdgctk
1441 htgkwgktvi eyrsqktsrl piidiapmdi ggpeqefgvd igpvcfl (SEQ ID NO:2)
```

Figure 3A

Homo sapiens
Alpha-1(III) collagen (1466 aa)
GenBank AAL13167

```
   1 mmsfvqkgsw lllallhpti ilaqqeaveg gcshlgqsya drdvwkpepc qicvcdsgsv
  61 lcddiicddq eldcpnpeip fgeccavcpq pptaptrppn gqgpqgpkgd pgppgipgrn
 121 gdpgipgqpg spgspgppgi cescptgpqn yspqydsydv ksgvavggla gypgpagppg
 181 ppgppgtsgh pgspgspgyq gppgepgqag psgppgppga igpsgpagkd gesgrpgrpg
 241 erglpgppgi kgpagipgfp gmkghrgfdg rngekgetga pglkgenglp gengapgpmg
 301 prgapgergr pglpgaagar gndgargsdg qpgppgppgt agfpgspgak gevgpagspg
 361 sngapgqrge pgpqghagaq gppgppging spggkgemgp agipgapglm gargppgpag
 421 angapglrgg agepgkngak gepgprgerg eagipgvpga kgedgkdgsp gepganglpg
 481 aagergapgf rgpagpngip gekgpagerg apgpagprga agepgrdgvp ggpgmrgmpg
 541 spggpgsdgk pgppgsqges grpgppgpsg prgqpgvmgf pgpkgndgap gkngerggpg
 601 gpgpqgppgk ngetgpqgpp gptgpggdkg dtgppgpqgl qglpgtggpp gengkpgepg
 661 pkgdagapga pggkgdagap gergppglag apglrggagp pgpeggkgaa gppgppgaag
 721 tpglqgmpge rgglgspgpk gdkgepggpg adgvpgkdgp rgptgpigpp gpagqpgdkg
 781 eggapglpgi agprgspger getgppgpag fpgapgqnge pggkgergap gekgeggppg
 841 vagppggsgp agppgpqgvk gergspggpg aagfpgargl pgppgsngnp gppgpsgspg
 901 kdgppgpagn tgapgspgvs gpkgdagqpg ekgspgaqgp pgapgplgia gitgarglag
 961 ppgmpgprgs pgpqgvkges gkpganglsg ergppgpqgl pglagtagep grdgnpgsdg
1021 lpgrdgspgg kgdrgengsp gapgapghpg ppgpvgpagk sgdrgesgpa gpagapgpag
1081 srgapgpqgp rgdkgetger gaagikghrg fpgnpgapgs pgpagqqgai gspgpagprg
1141 pvgpsgppgk dgtsghpgpi gppgprgnrg ergsegspgh pgqpgppgpp gapgpccggv
```

Figure 3B

1201 gaaaiagigg ekaggfapyy gdepmdfkin tdeimtslks vngqieslis pdgsrknpar
1261 ncrdlkfchp elksgeywvd pnqgckldai kvfcnmetge tcisanplnv prkhwwtdss
1321 aekkhvwfge smdggfqfsy gnpelpedvl dvqlaflrll ssrasqnity hcknsiaymd
1381 qasgnvkkal klmgsnegef kaegnskfty tvledgctkh tgewsktvfe yrtrkavrlp
1441 ivdiapydig gpdqefgvdv gpvcfl (SEQ ID NO:3)

Figure 4A

Homo sapiens
Alpha-1 (IV) collagen (1669 aa)
GenBank AAA53098

```
   1 mgprlsvwll llpaalllhe ehsraaakgg cagsgcgkcd chgvkgqkge rglpglqgvi
  61 gfpgmqgpeg pqgppgqkgd tgepglpgtk gtrgppgasg ypgnpglpgi pgqdgppgpp
 121 gipgcngtkg ergplgppgl pgfagnpgpp glpgmkgdpg eilghvpgml lkgergfpgi
 181 pgtpgppglp glqgpvgppg ftgppgppgp pgppgekgqm glsfqgpkgd kgdqgvsgpp
 241 gvpgqaqvqe kgdfatkgek gqkgepgfqg mpgvgekgep gkpgprgkpg kdgdkgekgs
 301 pgfpgepgyp gligrqgpqg ekgeagppgp pgivigtgpl gekgergypg tpgprgepgp
 361 kgfpglpgqp gppglpvpgq agapgfpger gekgdrgfpg tslpgpsgrd glpgppgspg
 421 ppgqpgytng ivecqpgppg dqgppgipgq pgfigeigek gqkgesclic didgyrgppg
 481 pqgppgeigf pgqpgakgdr glpgrdgvag vpgpqgtpgl igqpgakgep gefyfdlrlk
 541 gdkgdpgfpg qpgmpgrags pgrdghpglp gpkgspgsvg lkgergppgg vgfpgsrgdt
 601 gppgppgygp agpigdkgqa gfpggpgspg lpgpkgepgk ivplpgppga eglpgspgfp
 661 gpqgdrgfpg tpgrpglpge kgavgqpgig fpgppgpkgv dglpgdmgpp gtpgrpgfng
 721 lpgnpgvqgq kgepgvglpg lkglpglpgi pgtpgekgsi gvpgvpgehg aigppglqgi
 781 rgepgppglp gsvgspgvpg igppgargpp ggqgppglsg ppgikgekgf pgfpgldmpg
 841 pkgdkgaqgl pgitgqsglp glpgqqgapg ipgfpgskge mgvmgtpgqp gspgpvgapg
 901 lpgekgdhgf pgssgprgdp glkgdkgdvg lpgkpgsmdk vdmgsmkgqk gdqgekgqig
 961 pigekgsrgd pgtpgvpgkd gqagqpgqpg pkgdpgisgt pgapglpgpk gsvggmglpg
1021 tpgekgvpgi pgpqgspglp gdkgakgekg qagppgigip glrgekgdqg iagfpgspge
1081 kgekgsigip gmpgspglkg spgsvgypgs pglpgekgdk glpgldgipg vkgeaglpgt
1141 pgptgpagqk gepgsdgipg sagekgepgl pgrgfpgfpg akgdkgskge vgfpglagsp
```

Figure 4B

```
1201 gipgskgeqg fmgppgpqgq pglpgspgha tegpkgdrgp qgqpglpglp gpmgppglpg
1261 idgvkgdkgn pgwpgapgvp gpkgdpgfqg mpgiggspgi tgskgdmgpp gvpgfqgpkg
1321 lpglqgikgd qgdqgvpgak glpgppgppg pydiikgepg lpgpegppgl kglqglpgpk
1381 gqqgvtglvg ipgppgipgf dgapgqkgem gpagptgprg fpgppgpdgl pgsmgppgtp
1441 svdhgflvtr hsqtiddpqc psgtkilyhg ysllyvqgne rahgqdlgta gsclrkfstm
1501 pflfcninnv cnfasrndys ywlstpepmp msmapitgen irpfisrcav ceapamvmav
1561 hsqtiqippc psgwsslwig ysfvmhtsag aegsgqalas pgscleefrs apfiechgrg
1621 tcnyyanays fwlatierse mfkkptpstl kagelrthvs rcqvcmrrt (SEQ ID NO:4)
```

Figure 5

Homo sapiens
Alpha-1 (VI) collagen (1028 aa)
GenBank NP_001839

1 mraarallpl llqacwtaaq depetprava fqdcpvdlff vldtsesval rlkpygalvd
61 kvksftkrfi dnlrdryyrc drnlvwnaga lhysdeveii qgltrmpggr dalkssvdav
121 kyfgkgtytd caikkgleql lvggshlken kylivvtdgh plegykepcg gledavneak
181 hlgvkvfsva itpdhleprl siiatdhtyr rnftaadwgq srdaeeaisq tidtivdmik
241 nnveqvccsf ecqpargppg lrgdpgfege rgkpglpgek geagdpgrpg dlgpvgyqgm
301 kgekgsrgek gsrgpkgykg ekgkrgidgv dgvkgemgyp glpgckgspg fdgiqgppgp
361 kgdpgafglk gekgepgadg eagrpgssgp sgdegqpgep gppgekgeag degnpgpdga
421 pgerggpger gprgtpgtrg prgdpgeagp qgdqgregpv gvpgdpgeag pigpkgyrgd
481 egppgsegar gapgpagppg dpglmgerge dgpagngteg fpgfpgypgn rgapgingtk
541 gypglkgdeg eagdpgddnn diaprgvkga kgyrgpegpq gppghqgppg pdeceildii
601 mkmcscceck cgpidllfvl dssesiglqn feiakdfvvk vidrlsrdel vkfepgqsya
661 gvvqyshsqm qehvslrsps irnvqelkea ikslqwmagg tftgealqyt rdqllppspn
721 nrialvitdg rsdtqrdttp lnvlcspgiq vvsvgikdvf dfipgsdqln viscqglaps
781 qgrpglslvk enyaelleda flknvtaqic idkkcpdytc pitfsspadi tilldgsasv
841 gshnfdttkr fakrlaerfl tagr**tdpahd** **vr**vavvqysg tgqqrperas lqflqnytal
901 asavdamdfi ndatdvndal gyvtrfyrea ssgaakkrll **lfsdgnsqga tpaaiek**avq
961 eaqragieif vvvvg**rqvne** **phirv**lvtgk taeydvayge shlfrvpsyq allr**gvfhqt**
1021 **vsr**kvalg (SEQ ID NO:5)

Figure 6A

Homo sapiens
Alpha-3 (VI) collagen (3177 aa)
GenBank NP_04360

```
   1 mrkhrhlplv avfclflsgf ptthaqqqqa dvkngaaadi iflvdsswti geehfqlvre
  61 flydvvksla vgendfhfal vqfngnphte fllntyrtkq evlshisnms yiggtnqtgk
 121 gleyimqshl tkaagsragd gvpqvivvlt dghskdglal psaelksadv nvfaigveda
 181 degalkeias eplnmhmfnl enftslhdiv gnlvscvhss vsperagdte tlkditaqds
 241 adiiflidgs nntgsvnfav ildflvnlle klpigtqqir vgvvqfsdep rtmfsldtys
 301 tkaqvlgavk algfaggela niglaldfvv enhftraggs rveegvpqvl vlisagpssd
 361 eirygvvalk qasvfsfglg aqaasraelq hiatddnlvf tvpefrsfgd lqekllpyiv
 421 gvaqrhivlk pptivtqvie vnkrdivflv dgssalglan fnairdfiak viqrleigqd
 481 liqvavaqya dtvrpefyfn thptkrevit avrkmkpldg salytgsald fvrnnlftss
 541 agyraaegip kllvlitggk sldeisqpaq elkrssimaf aignkgadqa eleeiafdss
 601 lvfipaefra aplqgmlpgl laplrtlsgt pevhsnkrdi iflldgsanv gktnfpyvrd
 661 fvmnlvnsld igndnirvgl vqfsdtpvte fslntyqtks dilghlrqlq lqggsglntg
 721 salsyvyanh fteaggsrir ehvpqlllll tagqsedsyl qaanaltrag iltfcvgasq
 781 ankaeleqia fnpslvylmd dfsslpalpq qliqplttyv sggveevpla qpeskrdilf
 841 lfdgsanlvg qfpvvrdfly kiidelnvkp egtriavaqy sddvkvesrf dehqskpeil
 901 nlvkrmkikt gkalnlgyal dyaqryifvk sagsriedgv lqflvllvag rssdrvdgpa
 961 snlkqsgvvp fifqaknadp aeleqivlsp afilaaeslp kigdlhpqiv nllksvhnga
1021 papvsgekdv vflldgsegv rsgfpllkef vqrvvesldv gqdrvrvavv qysdrtrpef
1081 ylnsymnkqd vvnavrqltl lggptpntga alefvlrnil vssagsrite gvpqllivlt
1141 adrsgddvrn psvvvkrgga vpigigigna ditemqtisf ipdfavaipt frqlgtvqqv
```

Figure 6B

```
1201 iservtqltr eelsrlqpvl qplpspgvgg krdvvflidg sqsagpefqy vrtlierlvd
1261 yldvgfdttr vaviqfsddp kvefllnahs skdevqnavq rlrpkggrqi nvgnaleyvs
1321 rnifkrplgs rieegvpqfl vlissgksdd evddpavelk qfgvapftia rnadqeelvk
1381 islspeyvfs vstfrelpsl eqklltpitt ltseqiqkll astrypppav esdaadivfl
1441 idssegvrpd gfahirdfvs rivrrlnigp skvrvgvvqf sndvfpefyl ktyrsqapvl
1501 dairrlrlrg gsplntgkal efvarnlfvk sagsriedgv pqhlvlvlgg ksqddvsrfa
1561 qvirssgivs lgvgdrnidr telqtitndp rlvftvrefr elpnieerim nsfgpsaatp
1621 appgvdtppp srpekkkadi vflldgsinf rrdsfqevlr fvseivdtvy edgdsiqvgl
1681 vqynsdptde fflkdfstkr qiidainkvv ykggrhantk vglehlrvnh fvpeagsrld
1741 qrvpqiafvi tggksvedaq dvslaltqrg vkvfavgvrn idseevgkia snsatafrvg
1801 nvqelselse qvletlhdam hetlcpgvtd aakacnldvi lgfdgsrdqn vfvaqkgfes
1861 kvdailnris qmhrvscsgg rsptvrvsvv antpsgpvea fdfdeyqpem lekfrnmrsq
1921 hpyvltedtl kvylnkfrqs spdsvkvvih ftdgadgdla dlhrasenlr qegvralilv
1981 glervvnler lmhlefgrgf mydrplrlnl ldldyelaeq ldniaekacc gvpckcsgqr
2041 gdrgpigsig pkgipgedgy rgypgdeggp gergppgvng tqgfqgcpgq rgvkgsrgfp
2101 gekgevgeig ldgldgedgd kglpgssgek gnpgrrgdkg prgekgergd vgirgdpgnp
2161 gqdsqergpk getgdlgpmg vpgrdgvpgg pgetgknggf grrgppgakg nkggpgqpgf
2221 egeqgtrgaq gpagpagppg ligeqgisgp rgsggaagap gergrtgplg rkgepgepgp
2281 kggignrgpr getgddgrdg vgsegrrgkk gergfpgypg pkgnpgepgl ngttgpkgir
2341 grrgnsgppg ivgqkgdpgy pgpagpkgnr gdsidqcali qsikdkcpcc ygplecpvfp
2401 telafaldts egvnqdtfgr mrdvvlsivn dltiaesncp rgarvavvty nnevtteirf
2461 adskrksvll dkiknlqval tskqqsleta msfvarntfk rvrngflmrk vavffsntpt
```

Figure 6C

```
2521 raspqlreav lklsdagitp lfltrqedrq linalqinnt avghalvlpa grdltdflen
2581 vltchvcldi cnidpscgfg swrpsfrdrr aagsdvdidm afildsaett tlfqfnemkk
2641 yiaylvrqld mspdpkasqh farvavvqha psesvdnasm ppvkvefslt dygskeklvd
2701 flsrgmtqlq gtralgsaie ytienvfesa pnprdlkivv lmltgevpeq qleeaqrvil
2761 qakckgyffv vlgigrkvni kevytfasep ndvffklvdk stelneeplm rfgrllpsfv
2821 ssenafylsp dirkqcdwfq gdqptknlvk fghkqvnvpn nvtssptsnp vtttkpvttt
2881 kpvttttkpv ttttkpvtii nqpsvkpaaa kpapakpvaa kpvatkmatv rppvavkpat
2941 aakpvaakpa avrppaaaaa kpvatkpevp rpqaakpaat kpattkpmvk msrevqvfei
3001 tensaklhwe raeppgpyfy dltvtsahdq slvlkqnltv tdrviggtla gqtyhvavvc
3061 ylrsqvraty hgsfstkksq ppppqparsa ssstinlmvs teplaltetd icklpkdegt
3121 crdfilkwyy dpntkscarf wyggcggnen kfgsqkecek vcapvlakpg visvmgt (SEQ
ID NO:6)
```

Figure 7A

Homo sapiens
Alpha-1 (XII) collagen (3063 aa)
GenBank CAI19898

```
   1 mrsrlppala algaalllss ieaevdppsd lnfkiident vhmswakpvd pivgyritvd
  61 pttdgptkef tlsasttetl lselvpetey vvtitsydev eesvpvigql tiqtgsstkp
 121 vekkpgktei qkcsvsawtd lvflvdgsws vgrnnfkyil dfiaalvsaf digeektrvg
 181 vvqyssdtrt efnlnqyyqr dellaaikki pykggntmtg daidylvknt ftesagarvg
 241 fpkvaiiitd gksqdeveip arelrnvgve vfslgikaad akelkqiast pslnhvfnva
 301 nfdaivdiqn eiisqvcsgv deqlgelvsg eevveppsnl iamevsskyv klnwnpspsp
 361 vtgykviltp mtagsrqhal svgpqtttls vrdlsadtey qisvsamkgm tssepisime
 421 ktqpmkvqve csrgvdikad ivflvdgsys igianfvkvr aflevlvksf eispnrvqis
 481 lvqysrdpht eftlkkftkv ediieaintf pyrggstntg kamtyvreki fvpskgsrsn
 541 vpkvmilitd gkssdafrdp aiklrnsdve ifavgvkdav rseleaiasp paethvftve
 601 dfdafqrisf eltqsiclri eqelaaikkk ayvppkdlsf sevtsygfkt nwspagenvf
 661 syhitykeaa gddevtvvep asstsvvlss lkpetlylvn vtaeyedgfs iplageette
 721 evkgaprnlk vtdettdsfk itwtqapgrv lryriiyrpv aggesrevtt ppnqrrrtle
 781 nlipdtkyev svipeyfsgp gtpltgnaat eevrgnprdl rvsdpttstm klswsgapgk
 841 vkqylvtytp vaggetqevt vrgdttntvl qglkegtqya lsvtalyasg agdalfgegt
 901 tleergspqd lvtkditdts igaywtsapg mvrgyrvswk slyddvdtge knlpedaiht
 961 mienlqpetk yrisvfatys sgegepltgd attelsqdsk tlkvdeeten tmrvtwkpap
1021 gkvvnyrvvy rphgrgkqmv akvpptvtst vlkrlqpqtt yditvlpiyk mgegklrqgs
1081 gttasrfksp rnlktsdptm ssfrvtwepa pgevkgykvt fhptgddrrl gelvvgpydn
1141 tvvleelrag ttykvnvfgm fdggessplv gqemttlsdt tvmpilssgm ecltraeadi
```

Figure 7B

```
1201 vllvdgswsi granfrtvrs fisrivevfd igpkrvqial aqysgdprte wqlnahrdkk
1261 sllqavanlp ykggntltgm alnfirqqnf rtqagmrpra rkigvlitdg ksqddveaps
1321 kklkdegvel faigiknade velkmiatdp ddthaynvad feslsrivdd ltinlcnsvk
1381 gpgdleapsn lviserthrs frvswtppsd svdrykveyy pvsggkrqef yvsrmetstv
1441 lkdlkpetey vvnvysvved eyseplkgte ktlpvpvvsl niydvgpttm hvqwqpvgga
1501 tgyilsykpv kdteptrpke vrlgptvndm qltdlvpnte yavtvqavlh dltsepvtvr
1561 evtlplprpq dlklrdvths tmnvfwepvp gkvrkyivry ktpeedvkev evdrsetsts
1621 lkdlfsqtly tvsvsavhde gesppvtaqe ttrpvpaptn lkitevtseg frgtwdhgas
1681 dvslyritwa pfgssdkmet ilngdentlv fenlnpntiy evsitaiypd esesddligs
1741 ertlpilttq apksgprnlq vynatsnslt vkwdpasgrv qkyrityqps tgegneqttt
1801 iggrqnsvvl qklkpdtpyt itvsslypdg eggrmtgrgk tkplntvrnl rvydpststl
1861 nvrwdhaegn prqyklfyap aaggpeelvp ipgntnyail rnlqpdtsyt vtvvpvyteg
1921 dggrtsdtgr tlmrglarnv qvynptpnsl dvrwdpapgp vlqyrvvysp vdgtrpsesi
1981 vvpgntrmvh lerlipdtly svnlvalysd gegnpspaqg rtlprsgprn lrvfgettns
2041 lsvawdhadg pvqqyriiys ptvgdpidey ttvpgrrnnv ilqplqpdtp ykitviavye
2101 dgdgghltgn grtvgllppq nihisdewyt rfrvswdpsp spvlgykivy kpvgsnepme
2161 afvgemtsyt lhnlnpstty dvnvyaqyds glsvpltdqg ttlylnvtdl ktyqigwdtf
2221 cvkwsphraa tsyrlklspa dgtrgqeitv rgsetshcft glspdtdygv tvfvqtpnle
2281 gpgvsvkeht tvkpteapte pptppppti ppardvckga kadivfltda swsigddnfn
2341 kvvkfifntv ggfdeispag iqvsfvqysd evksefklnt yndkalalga lqniryrggn
2401 trtgkaltfi kekvltwesg mrknvpkvlv vvtdgrsqde vkkaalviqq sgfsvfvvgv
2461 advdynelan iaskpserhv fivddfesfe kiednlitfv cetatsscpl iyldgytspg
```

Figure 7C

```
2521 fkmleaynlt eknfasvqgv slesgsfpsy sayriqknaf vnqptadlhp nglppsytii
2581 llfrllpetp sdpfaiwqit drdykpqvgv iadpssktls ffnkdtrgev qtvtfdteev
2641 ktlfygsfhk vhivvtsksv kiyidcyeii ekdikeagni ttdgyeilgk llkgerksaa
2701 fqiqsfdivc spvwtsrdrc cdipsrrdeg kcpafpnsct ctqdsvgppg ppgpaggpga
2761 kgprgergis gaigppgprg digppgpqgp pgpqgpngls ipgeqgrqgm kgdagepglp
2821 grtgtpglpg ppgpmgppgd rgftgkdgam gprgppgppg spgspgvtgp sgkpgkpgdh
2881 grpgpsglkg ekgdrgdias qnmmravarq vceqlisgqm nrfnqmlnqi pndyqssrnq
2941 pgppgppgpp gsagargepg pggrpgfpgt pgmqgppger glpgekgerg tgssgprglp
3001 gppgpqgesr tgppgstgsr gppgppgrpg nsgirgppgp pgycdssqca sipyngqgyp
3061 gsg (SEQ ID NO:7)
```

Figure 8A

Homo sapiens
Alpha-1 (XIV) collagen (1796 aa)
GenBank AAI40894

```
   1 mkifqrkmry wllppflaiv yfctivqgqv apptrlrynv ishdsiqisw kaprgkfggy
  61 kllvtptsgg ktnqlnlqnt atkaiiqglm pdqnytvqii aynkdkeskp aqgqfrikdl
 121 ekrkdpkprv kvvdrgngsr psspeevkfv cqtpaiadiv ilvdgswsig rfnfrlvrhf
 181 lenlvtafdv gsektrigla qysgdpriew hlnafstkde vieavrnlpy kggntltgla
 241 lnyifensfk peagsrtgvs kigilitdgk sqddiippsr nlresgvelf aigvknadvn
 301 elqeiasepd sthvynvaef dlmhtvvesl trtlcsrvee qdreikasah aitgppteli
 361 tsevtarsfm vnwthapgnv ekyrvvyypt rggkpdevvv dgtvsstvlk nlmslteyqi
 421 avfaiyahta seglrgtett lalpmasdll lydvtensmr vkwdavpgas gylilyaplt
 481 eglagdekem kigethtdie lsgllpntey tvtvyamfge easdpvtgqe ttlalspprn
 541 lrisnvgsns arltwdptsr qingyrivyn nadgteinev evdpittfpl kgltplteyt
 601 iaifsiydeg qsepltgvft teevpaqqyl eidevttdsf rvtwhplsad eglhklmwip
 661 vyggkteevv lkeeqdshvi eglepgteye vsllavlddg sesevvtavg ttldsfwtep
 721 attivpttsv tsvfqtgirn lvvgdettss lrvkwdisds dvqqfrvtym taqgdpeeev
 781 igtvmvpgsq nnlllkpllp dteykvtvtp iytdgegvsv sapgktlpss gpqnlrvsee
 841 wynrlritwd ppsspvkgyr ivykpvsvpg ptletfvgad intilitnll sgmdynvkif
 901 asqasgfsda ltgmvktlfl gvtnlqakhv emtslcahwq vhrhatayrv vieslqdrqk
 961 qestvgggtt rhcfyglqpd seykisvytk lqeiegpsvs imektqslpt rpptfpptip
1021 pakevckaak adlvfmvdgs wsigdenfnk iisflystvg alnkigtdgt qvamvqftdd
1081 prtefklnay ktketlldai khisykggnt ktgkaikyvr dtlftaesgt rrgipkvivv
1141 itdgrsqddv nkisremqld gysifaigva dadyselvsi gskpsarhvf fvddfdafkk
```

Figure 8B

```
1201 iedelitfvc etasatcpvv hkdgidlagf kmmemfglve kdfssvegvs mepgtfnvfp
1261 cyqlhkdalv sqptrylhpe glpsdytisf lfrilpdtpq epfalweiln knsdplvgvi
1321 ldnggktlty fnydqsgdfq tvtfegpeir kifygsfhkl hivvsetlvk vvidckqvge
1381 kamnasanit sdgvevlgkm vrsrgpggns apfqlqmfdi vcstswantd kccelpglrd
1441 descpdlphs cscsetneva lgpagppggp glrgpkgqqg epgpkgpdgp rgeiglpgpq
1501 gppgpqgpsg lsiqgmpgmp gekgekgdtg lpgpqgipgg vgspgrdgsp gqrglpgkdg
1561 ssgppgppgp igipgtpgvp gitgsmgpqg algppgvpga kgergergdl qsqamvrsva
1621 rqvceqliqs hmarytailn qipshsssir tvqgppgepg rpgspgapge qgppgtpgfp
1681 gnagvpgtpg ergltgikge kgnpgvgtqg prgppgpagp sgesrpgspg ppgspgprgp
1741 pghlgvpgpq gpsgqpgycd psscsaygvr aphpdqpeft pvqdeleame lwgpgv(SEQ
ID NO:8)
```

Figure 9A

Homo sapiens
Alpha-1 (XV) collagen (1388 aa)
GenBank CAI17044

```
   1 maprrnngqc wcllmllsvs tplpavtqtr gatetasqgh ldltqligvp lpssvsfvtg
  61 yggfpaysfg pganvgrpar tlipstffrd faisvvvkps strggvlfai tdafqkviyl
 121 glrlsgvedg hqriilyyte pgshvsqeaa afsvpvmthr wnrfamivqg eevtllvnce
 181 ehsripfqrs sqalafessa gifmgnagat glerftgslq qltvhpdprt peelcdpees
 241 sasgetsglq eadgvaeile avtytqaspk eakvepintp ptpsspfedm elsgepvpeg
 301 tlettnmsii qhsspkqgsg eilndtlegv hsvdgdpitd sgsgagafld iaeeknlaat
 361 aaglaevpis tageaeassv ptggptlsms tenpeegvtp gpdneerlaa taageaeala
 421 smpgeveasg vapgeldlsm saqslgeeat vgpssedslt taaaatevsl stfedeeasg
 481 vptdglaplt atmaperavt sgpgdeedla aatteeplit aggeesgspp pdgpplplpt
 541 vaperwitpa qrehvgmkgq agpkgekgda geelpgppep sgpvgptaga eaegsglgwg
 601 sdvgsgsgdl vgseqllrgp pgppgppglp gipgkpgtdv fmgppgspge dgpagepgpp
 661 gpegqpgvdg atglpgmkge kgargpngsv gekgdpgnrg lpgppgkkgq agppgvmgpp
 721 gppgppgppg pgctmglgfe dtegsgstql lnepklsrpt aaiglkgekg drgpkgergm
 781 dgasivgppg prgppghikv lsnslinith gfmnfsdipe lvgppgpdgl pglpgfpgpr
 841 gpkgdtglpg fpglkgeqge kgepgailte diplerlmgk kgepgmhgap gpmgpkgppg
 901 hkgefglpgr pgrpglnglk gtkgdpgvim qgppglpgpp gppgppgavi nikgaifpip
 961 vrphckmpvd tahpgspeli tfhgvkgekg swglpgskge kgdqgaqgpp gppldlaylr
1021 hflnnlkgen gdkgfkgekg ekgdingsfl msgppglpgn pgpagqkget vvgpqgppga
1081 pglpgppgfg rpgdpgppgp pgppgppail gaavalpgpp gppgqpglpg srnlvtafsn
1141 mddmlqkahl viegtfiylr dsteffirvr dgwkklqlge lipipadspp ppalssnphq
```

Figure 9B

1201 llpppnpiss anyekpalhl aalnmpfsgd iradfqcfkq araagllsty raflsshlqd
1261 lstivrkaer yslpivnlkg qvlfnnwdsi fsghggqfnm hipiysfdgr dimtdpswpq
1321 kviwhgssph gvrlvdnyce awrtadtavt glasplstgk ildqkaysca nrlivlcien
1381 sfmtdark (SEQ ID NO:9)

Figure 10A

Homo sapiens
Alpha-1 (XVIII) collagen (1751 aa)
GenBank NP_569711

```
   1 mapypcgchi llllfcclaa aranllnlnw lwfnnedtsh aattipepqg plpvqptadt
  61 tthvtprngs tepatapgsp eppselledg qdtptsaesp dapeeniagv gaeilnvakg
 121 irsfvqlwnd tvpteslara etlvletpvg plalagpsst pqengttlwp srgipsspga
 181 htteagtlpa ptpsppslgr pwapltgpsv pppssgrasl ssllggappw gslqdpdsqg
 241 lspaaaapsq qlqrpdvrlr tpllhplvmg slgkhaapsa fssglpgals qvavttltrd
 301 sgawvshvan svgpglanns allgadpeap agrclplpps lpvcghlgis rfwlpnhlhh
 361 esgeqvraga rawggllqth chpflawffc lllvppcgsv pppapppccq fcealqdacw
 421 srlggrlpv acaslptqed gycvligpaa eriseevgll qllgdpppqq vtqtddpdvg
 481 layvfgpdan sgqvaryhfp slffrdfsll fhirpategp gvlfaitdsa qamvllgvkl
 541 sgvqdghqdi sllytepgag qthtaasfrl pafvgqwthl alsvaggfva lyvdceefqr
 601 mplarssrgl elepgaglfv aqaggadpdk fqgviaelkv rrdpqvspmh cldeegddsd
 661 gasgdsgsgl gdarellree tgaalkprlp apppvttppl aggsstedsr seeveeqttv
 721 aslgaqtlpg sdsvstwdgs vrtpggrvke gglkgqkgep gvpgppgrag ppgspclpgp
 781 pglpcpvspl gpagpalqtv pgpqgppgpp grdgtpgrdg epgdpgedgk pgdtgpqgfp
 841 gtpgdvgpkg dkgdpgvger gppgpqgppg ppgpsfrhdk ltfidmegsg fggdlealrg
 901 prgfpgppgp pgvpglpgep grfgvnssdv pgpaglpgvp gregppgfpg lpgppgppgr
 961 egppgrtgqk gslgeagapg hkgskgapgp agargesgla gapgpagppg ppgppgppgp
1021 glpagfddme gsggpfwsta rsadgpqgpp glpglkgdpg vpglpgakge vgadgvpgfp
1081 glpgregiag pqgpkgdrgs rgekgdpgkd gvgqpglpgp pgppgpvvyv seqdgsvlsv
1141 pgpegrpgfa gfpgpagpkg nlgskgergs pgpkgekgep gsifspdgga lgpaqkgakg
```

Figure 10B

```
1201 epgfrgppgp ygrpgykgei gfpgrpgrpg mnglkgekge pgdaslgfgm rgmpgppgpp
1261 gppgppgtpv ydsnvfaess rpgppglpgn qgppgpkgak gevgppgppg qfpfdflqle
1321 aemkgekgdr gdagqkgerg epggggffgs slpgppgppg prgypgipgp kgesirgqpg
1381 ppgpqgppgi gyegrqgppg ppgppgppsf pgphrqtisv pgppgppgpp gppgtmgass
1441 gvrlwatrqa mlgqvhevpe gwlifvaeqe elyvrvqngf rkvqleartp lprgtdneva
1501 alqppvvqlh dsnpyprreh phptarpwra ddilaspprl pepqpypgap hhssyvhlrp
1561 arptsppahs hrdfqpvlhl valnsplsgg mrgirgadfq cfqqaravgl agtfraflss
1621 rlqdlysivr radraavpiv nlkdellfps wealfsgseg plkpgarifs fdgkdvlrhp
1681 twpqksvwhg sdpngrrlte sycetwrtea psatgqassl lggrllgqsa aschhayivl
1741 ciensfmtas k (SEQ ID NO:10)
```

Figure 11

Homo sapiens
Alpha-1 (XIX) collagen (1142 aa)
GenBank CAI42716

```
   1 mrltgpwklw lwmsifllpa stsvtvrdkt eescpilrie ghqltydnin klevsgfdlg
  61 dsfslrrafc esdktcfklg sallirdtik ifpkglpeey svaamfrvrr nakkerwflw
 121 qvlnqqnipq isivvdggkk vvefmfqate gdvlnyifrn relrplfdrq whklgisiqs
 181 qvislymdcn liarrqtdek dtvdfhgrtv iatrasdgkp vdielhqlki ycsanliaqe
 241 tcceisdtkc peqdgfgnia sswvtahask mssylpakqe lkdqcqcipn kgeaglpgap
 301 gspgqkghkg epgenglhga pgfpgqkgeq gfegskgetg ekgeqgekgd palaglngen
 361 glkgdlgphg ppgpkgekgd tgppgppalp gslgiqgpqg ppgkegqrgr rgktgppgkp
 421 gppgppgppg iqgihqtlgg yynkdnkgnd eheagglkgd kgetglpgfp gsvgpkgqkg
 481 epgepftkge kgdrgepgvi gsqgvkgepg dpgppgligs pglkgqqgsa gsmgprgppg
 541 dvglpgehgi pgkqgikgek gdpggiigpp glpgpkgeag ppgkslpgep gldgnpgapg
 601 prgpkgergl pgvhgspgdi gpqgigipgr tgaqgpagep giqgprglpg lpgtpgtpgn
 661 dgvpgrdgkp glpgppgdpi alpllgdiga llknfcgncq asvpglksnk geeggagepg
 721 kydsmarkgd igprgppgip gregpkgskg ergypgipge kgdeglqgip gipgapgptg
 781 ppglmgrtgh pgptgakgek gsdgppgkpg ppgppgipfn erngmsslyk ikggvnvpsy
 841 pgppgppgpk gdpgpvgepg amglpglegf pgvkgdrgpa gppgiagmsg kpgapgppgv
 901 pgepgergpv gdigfpgpeg psgkpgingk dgipgaqgim gkpgdrgpkg ergdqgipgd
 961 rgsqgergkp gltgmkgaig pmgppgnkgs mgspghqgpp gspgipgipa davsfeeikk
1021 yinqevlrif eermavflsq lklpaamlaa qaygrpgppg kdglpgppgd pgpqgyrgqk
1081 gergepgigl pgspglpgts alglpgspga pgpqgppgps grcnpedcly pvshahqrtg
1141 gn (SEQ ID NO:11)
```

Figure 12A

Homo sapiens
Alpha-2 (I) collagen (1366 aa)
GenBank NP_000080

```
   1 mlsfvdtrtl lllavtlcla tcqslqeetv rkgpagdrgp rgergppgpp grdgedgptg
  61 ppgppgppgp pglggnfaaq ydgkgvglgp gpmglmgprg ppgaagapgp qgfqgpagep
 121 gepgqtgpag argpagppgk agedghpgkp grpgergvvg pqgargfpgt pglpgfkgir
 181 ghngldglkg qpgapgvkge pgapgengtp gqtgarglpg ergrvgapgp agargsdgsv
 241 gpvgpagpig sagppgfpga pgpkgeigav gnagpagpag prgevglpgl sgpvgppgnp
 301 gangltgakg aaglpgvaga pglpgprgip gpvgaagatg arglvgepgp agskgesgnk
 361 gepgsagpqg ppgpsgeegk rgpngeagsa gppgppglrg spgsrglpga dgragvmgpp
 421 gsrgasgpag vrgpngdagr pgepglmgpr glpgspgnig pagkegpvgl pgidgrpgpi
 481 gpagargepg nigfpgpkgp tgdpgkngdk ghaglagarg apgpdgnnga qgppgpqgvq
 541 ggkgeqgppg ppgfqglpgp sgpagevgkp gerglhgefg lpgpagprge rgppgesgaa
 601 gptgpigsrg psgppgpdgn kgepgvvgav gtagpsgpsg lpgergaagi pggkgekgep
 661 glrgeignpg rdgargapga vgapgpagat gdrgeagaag pagpagprgs pgergevgpa
 721 gpngfagpag aagqpgakge rgakgpkgen gvvgptgpvg aagpagpngp pgpagsrgdg
 781 gppgmtgfpg aagrtgppgp sgisgppgpp gpagkeglrg prgdqgpvgr tgevgavgpp
 841 gfagekgpsg eagtagppgt pgpqgllgap gilglpgsrg erglpgvaga vgepgplgia
 901 gppgargppg avgspgvnga pgeagrdgnp gndgppgrdg qpghkgergy pgnigpvgaa
 961 gapgphgpvg pagkhgnrge tgpsgpvgpa gavgprgpsg pqgirgdkge pgekgprglp
1021 glkghnglqg lpgiaghhgd qgapgsvgpa gprgpagpsg pagkdgrtgh pgtvgpagir
1081 gpqghqgpag ppgppgppgp pgvsgggydf gydgdfyrad qprsapslrp kdyevdatlk
1141 slnnqietll tpegsrknpa rtcrdlrlsh pewssgyywi dpnqgctmda ikvycdfstg
```

Figure 12B

```
1201 etciraqpen ipaknwyrss kdkkhvwlge tinagsqfey nvegvtskem atqlafmrll
1261 anyasqnity hcknsiaymd eetgnlkkav ilqgsndvel vaegnsrfty tvlvdgcskk
1321 tnewgktiie yktnkpsrlp fldiapldig gadqeffvdi gpvcfk (SEQ ID NO:12)
```

Figure 13A

Homo sapiens
Fibronectin (2386 aa)
GenBank P02751

```
   1 mlrgpgpgll llavqclgta vpstgasksk rqaqqmvqpq spvavsqskp gcydngkhyq
  61 inqqwertyl gnalvctcyg gsrgfncesk peaeetcfdk ytgntyrvgd tyerpkdsmi
 121 wdctcigagr grisctianr cheggqsyki gdtwrrphet ggymlecvcl gngkgewtck
 181 piaekcfdha agtsyvvget wekpyqgwmm vdctclgegs gritctsrnr cndqdtrtsy
 241 rigdtwskkd nrgnllqcic tgngrgewkc erhtsvqtts sgsgpftdvr aavyqpqphp
 301 qpppyghcvt dsgvvysvgm qwlktqgnkq mlctclgngv scqetavtqt yggnsngepc
 361 vlpftyngrt fyscttegrq dghlwcstts nyeqdqkysf ctdhtvlvqt rggnsngalc
 421 hfpflynnhn ytdctsegrr dnmkwcgttq nydadqkfgf cpmaaheeic ttnegvmyri
 481 gdqwdkqhdm ghmmrctcvg ngrgewtcia ysqlrdqciv dditynvndt fhkrheeghm
 541 lnctcfgqgr grwkcdpvdq cqdsetgtfy qigdswekyv hgvryqcycy grgigewhcq
 601 plqtypsssg pvevfitetp sqpnshpiqw napqpshisk yilrwrpkns vgrwkeatip
 661 ghlnsytikg lkpgvvyegq lisiqqyghq evtrfdfttt ststpvtsnt vtgettpfsp
 721 lvatsesvte itassfvvsw vsasdtvsgf rveyelseeg depqyldlps tatsvnipdl
 781 lpgrkyivnv yqisedgeqs lilstsqtta pdappdttvd qvddtsivvr wsrpqapitg
 841 yrivyspsve gsstelnlpe tansvtlsdl qpgvqyniti yaveenqest pvviqqettg
 901 tprsdtvpsp rdlqfvevtd vkvtimwtpp esavtgyrvd vipvnlpgeh gqrlpisrnt
 961 faevtglspg vtyyfkvfav shgreskplt aqqttkldap tnlqfvnetd stvlvrwtpp
1021 raqitgyrlt vgltrrgqpr qynvgpsvsk yplrnlqpas eytvslvaik gnqespkatg
1081 vfttlqpgss ippyntevte ttivitwtpa prigfklgvr psqggeapre vtsdsgsivv
1141 sgltpgveyv ytiqvlrdgq erdapivnkv vtplspptnl hleanpdtgv ltvswerstt
```

Figure 13B

1201 pditgyritt tptngqqgns leevvhadqs sctfdnlspg leynvsvytv kddkesvpis
1261 dtiipavppp tdlrftnigp dtmrvtwapp psidltnflv ryspvkneed vaelsispsd
1321 navvltnllp gteyvvsvss vyeqhestpl rgrqktglds ptgidfsdit ansftvhwia
1381 pratitgyri rhhpehfsgr predrvphsr nsitltnltp gteyvvsiva lngreespll
1441 igqqstvsdv prdlevvaat ptslliswda pavtvryyri tygetggnsp vqeftvpgsk
1501 statisglkp gvdytitvya vtgrgdspas skpisinyrt eidkpsqmqv tdvqdnsisv
1561 kwlpssspvt gyrvtttpkn gpgptktkta gpdqtemtie glqptveyvv svyaqnpsge
1621 sqplvqtavt nidrpkglaf tdvdvdsiki awespqgqvs ryrvtysspe dgihelfpap
1681 dgeedtaelq glrpgseytv svvalhddme sqpligtqst aipaptdlkf tqvtptslsa
1741 qwtppnvqlt gyrvrvtpke ktgpmkeinl apdsssvvvs glmvatkyev svyalkdtlt
1801 srpaqgvvtt lenvspprra rvtdatetti tiswrtktet itgfqvdavp angqtpiqrt
1861 ikpdvrsyti tglqpgtdyk iylytlndna rsspvvidas taidapsnlr flattpnsll
1921 vswqpprari tgyiikyekp gspprevvpr prpgvteati tglepgteyt iyvialknnq
1981 ksepligrkk tdelpqlvtl phpnlhgpei ldvpstvqkt pfvthpgydt gngiqlpgts
2041 gqqpsvgqqm ifeehgfrrt tpttatpir hrprpyppnv geeiqighip redvdyhlyp

Figure 13C

2101 hgpglnpnas tgqealsqtt iswapfqdts eyiischpvg tdeeplqfrv pgtstsatlt
2161 gltrgatynv ivealkdqqr hkvreevvtv gnsvneglnq ptddscfdpy tvshyavgde
2221 wermsesgfk llcqclgfgs ghfrcdssrw chdngvnyki gekwdrqgen gqmmsctclg
2281 ngkgefkcdp heatcyddgk tyhvgeqwqk eylgaicsct cfggqrgwrc dncrrpggep
2341 spegttgqsy nqysqryhqr tntnvncpie cfmpldvqad redsre (SEQ ID NO:13)

Figure 14A

Homo sapiens
Fibrillin-1 (2871 aa)
GenBank NP_000129

```
   1 mrrgrlleia lgftvllasy tshgadanle agnvketras rakrrggggh dalkgpnvcg
  61 srynayccpg wktlpggnqc ivpicrhscg dgfcsrpnmc tcpsgqiaps cgsrsiqhcn
 121 ircmnggscs ddhclcqkgy igthcgqpvc esgclnggrc vapnrcacty gftgpqcerd
 181 yrtgpcftvi snqmcqgqls givctktlcc atvgrawghp cemcpaqphp crrgfipnir
 241 tgacqdvdec qaipglcqgg ncintvgsfe ckcpaghkln evsqkcedid ecstipgice
 301 ggectntvss yfckcppgfy tspdgtrcid vrpgycytal tngrcsnqlp qsitkmqccc
 361 dagrcwspgv tvapemcpir atedfnklcs vpmvipgrpe yppppplgpip pvlpvppgfp
 421 pgpqipvprp pveylypsre pprvlpvnvt dycqlvrylc qngrciptpg syrcecnkgf
 481 qldlrgecid vdeceknpca ggecinnqgs ytcqcragyq stltrtecrd ideclqngri
 541 cnngrcintd gsfhcvcnag fhvtrdgknc edmdecsirn mclngmcine dgsfkcickp
 601 gfqlasdgry ckdinecetp gicmngrcvn tdgsyrcecf pglavgldgr vcvdthmrst
 661 cyggykrgqc ikplfgavtk secccastey afgepcqpcp aqnsaeyqal cssgpgmtsa
 721 gsdinecald pdicpngice nlrgtykcic nsgyevdstg kncvdinecv lnsllcdngq
 781 crntpgsfvc tcpkgfiykp dlktcedide cesspcingv cknspgsfic ecssestldp
 841 tkticietik gtcwqtvidg rceiningat lksqccsslg aawgspctlc qvdpicgkgy
 901 srikgtqced idecevfpgv ckngicvntr gsfkcqcpsg mtldatgric ldirletcfl
 961 ryedeectlp iagrhrmdac ccsvgaawgt eeceecpmrn tpeyeelcpr gpgfatkeit
1021 ngkpffkdin eckmipslct hgkcrntigs fkcrcdsgfa ldseernctd idecrispdl
1081 cgrgqcvntp gdfeckcdeg yesgfmmmkn cmdidecqrd pllcrggvch ntegsyrcec
1141 ppghqlspni sacidinece lsahlcpngr cvnligkyqc acnpgyhstp drlfcvdide
```

Figure 14B

1201 csimnggcet fctnsegsye cscqpgfalm pdqrsctdid ecednpnicd ggqctnipge
1261 yrclcydgfm asedmktcvd vnecdlnpni clsgtcentk gsfichcdmg ysgkkgktgc
1321 tdineceiga hncgkhavct ntagsfkcsc spgwigdgik ctdldecsng thmcsqhadc
1381 kntmgsyrcl ckegytgdgf tctdldecse nlnlcgngqc lnapggyrce cdmgfvpsad
1441 gkacedidec slpnicvfgt chnlpglfrc eceigyeldr sggnctdvne cldpttcisg
1501 ncvntpgsyi cdcppdfeln ptrvgcvdtr sgncyldirp rgdngdtacs neigvgvska
1561 scccslgkaw gtpcemcpav ntseykilcp ggegfrpnpi tviledidec qelpglcqgg
1621 kcintfgsfq crcptgyyln edtrvcddvn ecetpgicgp gtcyntvgny tcicppdymq
1681 vnggnncmdm rrslcyrnyy adnqtcdgel lfnmtkkmcc csynigrawn kpceqcpips
1741 tdefatlcgs qrpgfvidiy tglpvdidec reipgvceng vcinmvgsfr cecpvgffyn
1801 dkllvcedid ecqngpvcqr naecintags yrcdckpgyr ftstgqcndr necqeipnic
1861 shgqcidtvg sfyclchtgf ktnddqtmcl dinecerdac gngtcrntig sfncrcnhgf
1921 ilshnndcid vdecasgngn lcrngqcint vgsfqcqcne gyevapdgrt cvdineclle
1981 prkcapgtcq nldgsyrcic ppgyslqnek cedidecvee peicalgtcs ntegsfkclc
2041 pegfslsssg rrcqdlrmsy cyakfeggkc sspksrnhsk qecccalkge gwgdpcelcp
2101 tepdeafrqi cpygsgiivg pddsavdmde ckepdvckhg qcintdgsyr cecpfgyila
2161 gnecvdtdec svgnpcgngt cknviggfec tceegfepgp mmtcedinec aqnpllcafr
2221 cvntygsyec kcpvgyvlre drrmckdede ceegkhdcte kqmecknlig tymcicgpgy
2281 qrrpdgegcv denecqtkpg icengrclnt rgsytcecnd gftaspnqde cldnregycf
2341 tevlqnmcqi gssnrnpvtk secccdggrg wgphceicpf qgtvafkklc phgrgfmtng

Figure 14C

2401 adideckvih dvcrngecvn drgsyhcick tgytpditgt scvdlnecnq apkpcnfick
2461 ntegsyqcsc pkgyilqedg rsckdldeca tkqhncqflc vntiggftck cppgftqhht
2521 scidnnects dinlcgskgi cqntpgsftc ecqrgfsldq tgsscedvde cegnhrcqhg
2581 cqniiggyrc scpqgylqhy qwnqcvdene clsahicgga schntlgsyk cmcpagfqye
2641 qfsggcqdin ecgsaqapcs ygcsnteggy lcgcppgyfr igqghcvsgm gmgrgnpepp
2701 vsgemddnsl speacyecki ngypkrgrkr rstnetdasn iedqsetean vslaswdvek
2761 taifafnish vsnkvrilel lpalttltnh nryliesgne dgffkinqke gisylhftkk
2821 kpvagtyslq isstplykkk elnqledkyd kdylsgelgd nlkmkiqvll h (SEQ ID
NO:14)

Figure 15
Homo sapiens
Dermatopontin (201 aa)
GenBank CAA 80487

1 mdlsllwvlm plvtmawgqy gdygypyqqy hdysddgwvn lnrqgfsyqc pqgqvivavr
61 sifskkegsd rqwnyacmpt pqslgeptec wweeinragm ewyqtcsnng lvagfqsryf
121 esvldrewqf yccryskrcp yscwltteyp ghygeemdmi synydyyirg atttfsaver
181 drqwkfimcr mteydcefan v (SEQ ID NO:15)

Figure 16
Homo sapiens
Metalloproteinase inhibitor-1 (207 aa)
GenBank NP_003245
1 mapfeplasg illllwliap sractcvpph pqtafcnsdl virakfvgtp evnqttlyqr
61 yeikmtkmyk gfqalgdaad irfvytpame svcgyfhrsh nrseefliag klqdgllhit
121 tcsfvapwns lslaqrrgft ktytvgceec tvfpclsipc klqsgthclw tdqllqgsek
181 gfqsrhlacl prepglctwq slrsqia (SEQ ID NO:16)

Figure 17
Homo sapiens
Galectin-1 (135 aa)
GenBank NP_003396
1 macglvasnl nlkpgeclrv rgevapdaks fvlnlgkdsn nlclhfnprf nahgdantiv
61 cnskdggawg teqreavfpf qpgsvaevci tfdqanltvk lpdgyefkfp nrlnleainy
121 maadgdfkik cvafd (SEQ ID NO:17)

Figure 18

Homo sapiens

Lumican (338 aa)

GenBank AAA85268

1 mslsaftlfl aliggtsgqy ydydfppsiy gqsspncape cncpesypsa mycdelklks

61 vpmvppgiky lylrnnqidh idekafenvt dlqwlildhn vlenskikgr vfsklkqlkk

121 lhinhnnlte svgplpksle dlqlthnkit klgsfeglvn ltfihlqhnr lkedavsaaf

181 kglksleyld lsfnqiarlp sglpvslltl yldnnkisni pdeyfkrfna lqylrlshne

241 ladsgipgns fnvsslveld lsynklknip tvnenlenyy levnqlekfd iksfckilgp

301 lsyskikhlr ldgnrisets lppdmyeclr vanevtln (SEQ ID NO:18)

Figure 19

Homo sapiens

Prolargin (382 aa)

GenBank AAC18782

1 mrsplcwllp llilasvaqg qptrrprpgt gpgrrprprp rptpsfpqpd epaeptdlpp

61 plppgppsif pdcprecycp pdfpsalycd srnlrkvpvi pprihylylq nnfitelpve

121 sfqnatglrw inldnnrirk idqrvleklp glvflymekn qle**evpsalp** **r**nleql**rlsq**

181 **nhisrippgv** **fsk**lenllll dlqhnr**lsdg** **vfkpdt**fhgl knlmql**nlah** **nilr**kmpprv

241 ptaihqly**ld** **snkietipng** **yfksfpnlaf** **ir**lnynkltd rglpknsfni snllvlhlsh

301 nrissvpain nrlehly**lnn** **nsiek**ingtq icpn**dlvafh** **dfssdlenvp** **hlr**ylrldgn

361 ylkppipldl mmcfrllqsv vi (SEQ ID NO:19)

Figure 20A
Homo sapiens
Tenascin (2201 aa)
GenBank NP_002151

1 mgamtqllag vflaflalat eggvlkkvir hkrqsgvnat lpeenqpvvf nhvyniklpv
61 gsqcsvdles asgekdlapp sepsesfqeh tvdgenqivf thriniprra cgcaaapdvk
121 ellsrleele nlvsslreqc tagagcclqp atgrldtrpf csgrgnfste gcgcvcepgw
181 kgpncsepec pgnchlrgrc idgqcicddg ftgedcsqla cpsdcndqgk cvngvcicfe
241 gyagadcsre icpvpcseeh gtcvdglcvc hdgfagddcn kplclnncyn rgrcvenecv
301 cdegftgedc selicpndcf drgrcingtc yceegftged cgkptcphac htqgrceegq
361 cvcdegfagv dcsekrcpad chnrgrcvdg rcecddgftg adcgelkcpn gcsghgrcvn
421 gqcvcdegyt gedcsqlrcp ndchsrgrcv egkcvceqgf kgydcsdmsc pndchqhgrc
481 vngmcvcddg ytgedcrdrq cprdcsnrgl cvdgqcvced gftgpdcael scpndchgqg
541 rcvngqcvch egfmgkdcke qrcpsdchgq grcvdgqcic hegftgldcg qhscpsdcnn
601 lgqcvsgrci cnegysgedc sevsppkdlv vtevteetvn lawdnemrvt eylvvytpth
661 egglemqfrv pgdqtstiiq **elepgveyfi r**vfailenkk sipvsarvat ylpapeglkf
721 ksiketsvev ewdpldiafe tweiifrnmn kedegeitks lrrpetsyrq tglapgqeye
781 islhivknnt rgpglkrvtt trldapsqie vkdvtdttal itwfkplaei dgieltygik
841 dvpgdrttid ltedenqysi gnlkpdteye vslisrrgdm ssnpaketft tgldaprnlr
901 rvsqtdnsit lewrngkaai dsyrikyapi sggdhaevdv pksqqattkt tltglrpgte
961 ygigvsavke dkesnpatin aateldtpkd lqvsetaets ltllwktpla kfdryrlnys
1021 lptgqwvgvq lprnttsyvl rglepgqeyn vlltaekgrh kskparvkas teqapelenl
1081 tvtevgwdgl rlnwtaadqa yehfiiqvqe ankveaarnl tvpgslravd ipglkaatpy
1141 **tvsiygviqg yr**tpvlsaea stgetpnlge vvvaevgwda lklnwtapeg ayeyffiqvq

Figure 20B

1201 eadtveaaqn ltvpgglrst dlpglkaath ytitirgvtq dfsttplsve vlteevpdmg
1261 nltvtevswd alrlnwttpd gtydqftiqv qeadqveeah nltvpgslrs meipglragt
1321 py**tvtlhgev** **r**ghstrplav evvtedlpql gdlavsevgw dglrlnwtaa dnayehfviq
1381 vqevnkveaa qnltlpgslr avdipgleaa tpyrvsiygv irgyrtpvls aeastakepe
1441 ignlnvsdit pesfnlswma tdgifetfti eiidsnrlle tveynisgae rtahisglpp
1501 stdfivylsg lapsirtkti satattealp llenltisdi npygftvswm asenafdsfl
1561 vtvvdsgkll dpqeftlsgt qrklelrgli tgigyevmvs gftqghqtkp lraeivteae
1621 pevdnllvsd atpdgfrlsw tadegvfdnf vlkirdtkkq sepleitlla pertrditgl
1681 reateyeiel ygiskgrrsq tvsaiattam gspkevifsd itensatvsw raptaqves**f**
1741 **rityvpitgg** **tpsmvtvdgt** **k**tqtrlvkli pgveylvsii amkgfeesep vsgsfttald
1801 gpsglvtani tdsealarwq paiatvdsyv isytgekvpe itrtvsgntv eyaltdlepa
1861 teytlrifae kgpqksstit akfttdldsp rdltatevqs etalltwrpp rasvtgyllv
1921 yesvdgtvke vivgpdttsy sladlspsth ytakiqalng plrsnmiqti fttigllypf
1981 pkdcsqamln gdttsglyti ylngdkaeal evfcdmtsdg ggwivflrrk ngrenfyqnw
2041 kayaagfgdr reefwlgldn lnkitaqggy elrvdlrdhg etafavydkf svgdaktryk
2101 lkvegysgta gdsmayhngr sfstfdkdtd saitncalsy kgafwyrnch rvnlmgrygd
2161 nnhsqgvnwf hwkghehsiq faemklrpsn frnlegrrkr a (SEQ ID NO:20)

Figure 21
Homo sapiens
Vitronectin (478 aa)
GenBank ADL14521

1 maplrpllil allawvalad qesckgrcte gfnvdkkcqc delcsyyqsc **ctdytaeckp**
61 **qvtr**gdvftm pedeytvydd geeknnatvh eqvggpslts dlqaqskgnp eqtpvlkpee
121 eapapevgas kpegidsrpe tlhpgrpqpp aeeelcsgkp fdaftdlkng slfafrgqyc
181 yeldekavrp gypklirdvw giegpidaaf trincqgkty lfkgsqywrf edgvldpdyp
241 rnisdgfdgi pdnvdaalal pahsysgrer vyffkgkqyw eyqfqhqpsq eecegsslsa
301 vfehfammqr dswedifell fwgrtsagtr qpqfisrdwh gvpgqvdaam agr**iyisgma**
361 **prps**lakkqr frhrnrkgyr sqrghsrgrn qnsrrpsrat wlslfssees nlgannyddy
421 rmdwlvpa**tc** **epiqsvfffs** **gdk**yyrvnlr trrvdtvdpp ypr**siaqywl** **gcpapgh**l (SEQ
ID NO:21)

Figure 22A

Homo sapiens

Tenascin-X (4289 aa)

GenBank P22105

1 mmpaqyalts slvllvllst aragpfssrs nvtlpaprpp pqpgghtvga gvgspssqly

61 ehtveggekq vvfthrinlp pstgcgcppg teppvlasev qalrvrleil eelvkglkeq

121 ctggccpasa qagtgqtdvr tlcslhgvfd lsrctcscep gwggptcsdp tdaeippssp

181 psasgscpdd cndqgrcvrg rcvcfpgytg pscgwpscpg dcqgrgrcvq gvcvcragfs

241 gpdcsqrscp rgcsqrgrce ggrcvcdpgy tgddcgmrsc prgcsqrgrc engrcvcnpg

301 ytgedcgvrs cprgcsqrgr ckdgrcvcdp gytgedcgtr scpwdcgegg rcvdgrcvcw

361 pgytgedcst rtcprdcrgr grcedgecic dtgysgddcg vrscpgdcnq rgrcedgrcv

421 cwpgytgtdc gsracprdcr grgrcengvc vcnagysged cgvrscpgdc rgrgrcesgr

481 cmcwpgytgr dcgtracpgd crgrgrcvdg rcvcnpgftg edcgsrrcpg dcrghglced

541 gvcvcdagys gedcstrscp ggcrgrgqcl dgrcvcedgy sgedcgvrqc pndcsqhgvc

601 qdgvcicweg yvsedcsirt cpsnchgrgr ceegrclcdp gytgptcatr mcpadcrgrg

661 rcvqgvclch vgyggedcgq eeppasacpg gcgprelcra gqcvcvegfr gpdcaiqtcp

721 gdcrgrgech dgscvckdgy agedcgearv pssasaydqr glapgqeyqv tvralrgtsw

781 glpasktitt midgpqdlrv vavtpttlel gwlrpqaevd rfvvsyvsag nqrvrlevpp

841 eadgtlltdl mpgveyvvtv taergravsy pasvrantee reeespprps lsqpprrpwg

901 nltaelsrfr gtvqdlerhl rahgyplran qtytsvarhi heylqrqvlg ssadgallvs

961 ldglrgqfer vvlr**wrpqpp aegpggeltv pgttrtvs**lp dlrpgttyhv evhgvragqt

1021 sksyafittt gpsttqgaqa pllqqrpqel gelrvlgrde tgrlrvvwta qpdtfayfql

1081 rmrvpegpga heevlpgdvr qalvppppg tpyelslhgv ppggkpsdpi iyqgimdkde

1141 ekpgkssgpp rlgeltvtdr tsdslllrwt vpegefdsfv iqykdrdgqp qvvpvegpqr

Figure 22B

1201 savitsldpg rkykfvlygf vgkkrhgplv aeakilpqsd pspgtpphlg nlwvtdptpd
1261 slhlswtvpe gqfdtfmvqy rdrdgrpqvv pvegpersfv vssldpdhky rftlfgiank
1321 krygpltadg ttaperkeep prpefleqpl lgeltvtgvt pdslrlswtv aqgpfdsfmv
1381 qykdaqgqpq avpvagdene vtvpgldpdr kykmnlyglr grqrvgpesv vaktapqedv
1441 detpsptelg teapespeep llgeltvtgs spdslslfwt vpqgs**fdsft** **vqyk**drdgrp
1501 ravrvggkes evtvgglepg hkykmhlygl hegqrvgpvs avgvtapqqe etppatespl
1561 eprlgeltvt dvtpnsvgls wtvpegqfds fivqykdkdg qpqvvpvaad qrevtvynle
1621 perkykmnmy glhdgqrmgp lsvvivtapa teaskpplep rlgeltvtdi tpdsvglswt
1681 vpegefdsfv vqykdrdgqp qvvpvaadqr evtipdleps rkykfllfgi qdgkrrspvs
1741 veaktvargd aspgapprlg elwvtdptpd slrlswtvpe gqfdsfvvqf kdkdgpqvvp
1801 veghersvtv tpldagrkyr fllygllgkk rhgpltadgt tearsamddt gtkrppkprl
1861 geelqvttvt qnsvglswtv pegqfdsfvv qykdrdgqpq vvpvegslre vsvpgldpah
1921 ryklllyglh hgkrvgpisa vaitagreet etettaptpp apephlgelt veeatshtlh
1981 lswmvtegef dsfeiqytdr dgqlqmvrig gdrnditlsg lesdhrylvt lygfsdgkhv
2041 gpvhvealtv peeekpsepp tatpeppikp rlgeltvtda tpdslslswt vpegqfdhfl
2101 vqyrngdgqp kavrvpghee gvtisglepd hkykmnlygf hggqrmgpvs vvgvtepsme
2161 apepaeepll geltvtgssp dslslswtvp qgrfdsftvq ykdrdgrpqv vrvg**geesev**
2221 **tvgglepgr**k ykmhlyglhe grrvgpvsav gvtapeeesp daplaklrlg qmtvrditsd
2281 slslswtvpe gqfdhflvqf kngdgqpkav rvpghedgvt isglepdhky kmnlygfhgg
2341 qrvgpvsavg ltastepptp eppikprlee ltvtdatpds lslswtvpeg qfdhflvqyk

Figure 22C

2401 ngdgqpkatr vpghedrvti sglepdnkyk mnlygfhggq rvgpvsaigv teeetpspte
2461 psmeapeppe epllgeltvt gsspdslsls wtvpqgrfds ftvqykdrdg rpqvvrvgge
2521 esevtvggle pgrkykmhly glhegrrvgp vstvgvtapq edvdetpspt epgteapgpp
2581 eepllgeltv tgsspdslsl swtvpqgrfd sftvqykdrd grpqavrvgg qeskvtvrgl
2641 epgrkykmhl yglhegrrlg pvsavgvted eaettqavpt mtpeppikpr lgeltmtdat
2701 pdslslswtv pegqfdhflv qyrngdgqpk avrvpghedg vtisglepdh kykmnlygfh
2761 ggqrvgpisv igvteeetps ptelsteape ppeepllgel tvtgsspdsl slswtipqgh
2821 fdsftvqykd rdgrpqvmrv rgeesevtvg glepgrkykm hlyglhegrr vgpvstvgvt
2881 vptttp**eppn** **kpr**lgeltvt datpdslsls wmvpegqfdh flvqyrngdg qpkvvrvpgh
2941 edgvtisgle pdhkykmnly gfhggqrvgp isvigvteee tpaptepste apeppeepll
3001 geltvtgssp dslslswtip qgrfdsftvq ykdrdgrpqv vrvrgeesev tvgglepgck
3061 ykmhlyglhe gqrvgpvsav gvtapkdeae ttqavptmtp eppikprlge ltvtdatpds
3121 lslswmvpeg qfdhflvqyr ngdgqpkavr vpghedgvti sglepdhkyk mnlygfhggq
3181 rvgpvsaigv teeetpspte psteapeape epllgeltvt gsspdslsls wtvpqgrfds
3241 ftvqykdrdg qpqvvrvrge esevtvggle pgrkykmhly glhegqrvgp vstvgitapl
3301 ptplpveprl gelavaavts dsvglswtva qgpfdsflvq yrdaqgqpqa vpvsgdlrav
3361 avsgldpark ykfllfglqn gkrhgpvpve artapdtkps prlgeltvtd atpdsvglsw
3421 tvpegefdsf vvqykdkdgr lqvvpvaanq revtvqglep srkyrfllyg lsgrkrlgpi
3481 sadsttaple kelpphlgel tvaeetsssl rlswtvaqgp fdsfvvqyrd tdgqpravpv
3541 aadqrtvtve dlepgkkykf llygllggkr lgpvsalgmt apeedtpape lapeapeppe

Figure 22D

3601 eprlgvltvt dttpdsmrls wsvaqgpfds fvvqyedtng qpqallvdgd qskilisgle
3661 pstpyrflly glhegkrlgp lsaegttgla pagqtseesr prlsqlsvtd vttsslrlnw
3721 eappgafdsf llrfgvpsps tlephprpll qrelmvpgtr hsavlrdlrs gtlysltlyg
3781 lrgphkadsi qgtartlspv lesprdlqfs eiretsakvn wmpppsrads fkvsyqladg
3841 gepqsvqvdg qartqklqgl ipgaryevtv vsvr**gfeese pltgflttvp dgptq**lraln
3901 ltegfavlhw kppqnpvdty dvqvtapgap plqaetpgsa vdyplhdlvl htnytatvrg
3961 lrgpnltspa sitfttglea prdleakevt prtalltwte ppvrpagyll sfhtpggqnq
4021 eillpggits hqllglfpst synarlqamw gqsllppvst sfttgglrip fprdcgeemq
4081 ngagasrtst iflngnrerp lnvfcdmetd gggwlvfqrr mdgqtdfwrd wedyahgfgn
4141 isgefwlgne alhsltqagd ysmrvdlrag deavfaqyds fhvdsaaeyy rlhlegyhgt
4201 agdsmsyhsg svfsardrdp nslliscavs yrgawwyrnc hyanlnglyg stvdhqgvsw
4261 yhwkgfefsv pftemklrpr nfrspaggg (SEQ ID NO:22)

Figure 23A

Homo sapiens

Collagen alpha-2(IV) (1712 amino acids)

GenBank NP_001837

```
   1 mgrdqravag palrrwlllg tvtvgflaqs vlagvkkfdv pcggrdcsgg cqcypekggr
  61 gqpgpvgpqg yngppglqgf pglqgrkgdk gergapgvtg pkgdvgargv sgfpgadgip
 121 ghpgqggprg rpgydgcngt qgdsgpqgpp gsegftgppg pqgpkgqkge pyalpkeerd
 181 ryrgepgepg lvgfqgppgr pghvgqmgpv gapgrpgppg ppgpkgqqgn rglgfygvkg
 241 ekgdvgqpgp ngipsdtlhp iiaptgvtfh pdqykgekgs egepgirgis lkgeegimgf
 301 pglrgypgls gekgspgqkg srgldgyqgp dgprgpkgea gdpgppglpa ysphpslakg
 361 argdpgfpga qgepgsqgep gdpglpgppg lsigdgdqrr glpgemgpkg figdpgipal
 421 yggppgpdgk rgppgppglp gppgpdgflf glkgakgrag fpglpgspga rgpkgwkgda
 481 gecrctegde aikglpglpg pkgfaginge pgrkgdrgdp gqhglpgfpg lkgvpgniga
 541 pgpkgakgds rtittkgerg qpgvpgvpgm kgddgspgrd gldgfpglpg ppgdgikgpp
 601 gdpgypgipg tkgtpgemgp pglglpglkg qrgfpgdagl pgppgflgpp gpagtpgqid
 661 cdtdvkravg gdrqeaiqpg ciggpkglpg lpgppgptga kglrgipgfa gadggpgprg
 721 lpgdagregf pgppgfigpr gskgavglpg pdgspgpigl pgpdgppger glpgevlgaq
 781 pgprgdagvp gqpglkglpg drgppgfrgs qgmpgmpglk gqpglpgpsg qpglygppgl
 841 hgfpgapgqe gplglpgipg reglpgdrgd pgdtgapgpv gmkglsgdrg dagftgeqgh
 901 pgspgfkgid gmpgtpglkg drgspgmdgf qgmpglkgrp gfpgskgeag ffgipglkgl
 961 agepgfkgsr gdpgppgppp vilpgmkdik gekgdegpmg lkgylgakgi qgmpgipgls
1021 gipglpgrpg hikgvkgdig vpgipglpgf pgvagppgit gfpgfigsrg dkgapgragl
1081 ygeigatgdf gdigdtinlp grpglkgerg ttgipglkgf fgekgtegdi gfpgitgvtg
1141 vqgppglkgq tgfpgltgpp gsqgelgrig lpggkgddgw pgapglpgfp glrgirglhg
```

Figure 23B

```
1201 lpgtkgfpgs pgsdihgdpg fpgppgergd pgeantlpgp vgvpgqkgdq gapgergppg
1261 spglqgfpgi tppsnisgap gdkgapgifg lkgyrgppgp pgsaalpgsk gdtgnpgapg
1321 tpgtkgwagd sgpqgrpgvf glpgekgprg eqgfmgntgp tgavgdrgpk gpkgdpgfpg
1381 apgtvgapgi agipqkiavq pgtvgpqgrr gppgapgemg pqgppgepgf rgapgkagpq
1441 grggvsavpg frgdegpigh qgpigqegap grpgspglpg mpgrsvsigy llvkhsqtdq
1501 epmcpvgmnk lwsgysllyf egqekahnqd lglagsclar fstmpflycn pgdvcyyasr
1561 ndksywlstt aplpmmpvae deikpyisrc svceapaiai avhsqdvsip hcpagwrslw
1621 igysflmhta agdegggqsl vspgscledf ratpfiecng grgtchyyan kysfwlttip
1681 eqsfqgspsa dtlkaglirt hisrcqvcmk nl (SEQ ID NO:23)
```

Figure 24A
Homo sapiens
Collagen alpha-5(IV) (1691 amino acids)
GenBank AAF66217

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   1 mklrgvslaa glfllalslw gqpaeaaacy gcspgskcdc sgikgekger gfpgleghpg
  61 lpgfpgpegp pgprgqkgdd gipgppgpkg irgppglpgf pgtpglpgmp ghdgapgpqg
 121 ipgcngtkge rgfpgspgfp glqgppgppg ipgmkgepgs iimsslpgpk gnpgypgppg
 181 iqglpgptgi pgpigppgpp glmgppgppg lpgpkgnmgl nfqgpkgekg eqglqgppgp
 241 pgqiseqkrp idvefqkgdq glpgdrgppg ppgirgppgp pggekgekge qgepgkrgkp
 301 gkdgengqpg ipglpgdpgy pgepgrdgek gqkgdtgppg ppglviprpg tgitigekgn
 361 iglpglpgek gergfpgiqg ppglpgppga avmgppgppg fpgergqkgd egppgisipg
 421 ppgldgqpga pglpgppgpa gphippsdei cepgppgppg spgdkglqge qgvkgdkgdt
 481 cfncigtgis gppgqpglpg lpgppgslgf pgqkgekgqa gatgpkglpg ipgapgapgf
 541 pgskgepgdi ltfpgmkgdk gelgspgapg lpglpgtpgq dglpglpgpk gepggitfkg
 601 ergppgnpgl pglpgnigpm gppgfgppgp vgekgiqgva gnpgqpgipg pkgdpgqtit
 661 qpgkpglpgn pgrdgdvglp gdpglpgqpg lpgipgskge pgipgiglpg ppgpkgfpgi
 721 pgppgapgtp grigleg ppg ppgfpgpkge pgfalpgppg ppglpgfkga lgpkgdrgfp
 781 gppgppgrtg ldglpgpkgd vgpngqpgpm gppglpgigv qgppgppgip gpigqpglhg
 841 ipgekgdpgp pgldvpgppg ergspgipga pgpigppgsp glpgkagasg fpgtkgemgm
 901 mgppgppgpl gipgrsgvpg lkgddglqgq pglpgptgek gskgepglpg ppgpmdpnll
 961 gskgekgepg lpgipgvsgp kgyqglpgdp gqpglsgqpg lpgppgpkgn pglpgqpgli
1021 gppglkgtig dmgfpgpqgv egppgpsgvp gqpgspglpg qkgdkgdpgi ssiglpglpg
1081 pkgepglpgy pgnpgikgsv gdpglpglpg tpgakgqpgl pgfpgtpgpp gpkgisgppg
1141 npglpgepgp vggghpgqp gppgekgkpg qdgipgpagq kgepgqpgfg npgppglpgl
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Figure 24B

1201 sgqkgdgglp gipgnpglpg pkgepgfhgf pgvqgppgpp gspgpalegp kgnpgpqgpp
1261 grpgptgfqg lpgpegppgl pgnggikgek gnpgqpglpg lpglkgdqgp pglqgnpgrp
1321 glngmkgdpg lpgvpgfpgm kgpsgvpgsa gpegepglig ppgppglpgp sgqsiiikgd
1381 agppgipgqp glkglpgpqg pqglpgptgp pgdpgrnglp gfdgaggrkg dpglpgqpgt
1441 rgldgppgpd glqgppgppg tssvahgfli trhsqttdap qcpqgtlqvy egfsllyvqg
1501 nkrahgqdlg tagsclrrfs tmpfmfcnin nvcnfasrnd ysywlstpep mpmsmqplkg
1561 qsiqpfisrc avceapavvi avhsqtiqip hcpqgwdslw igysfmmhts agaegsgqal
1621 aspgscleef rsapfiechg rgtcnyyans ysfwlatvdv sdmfskpqse tlkagdlrtr
1681 isrcqvcmkr t (SEQ ID NO:24)

Figure 25
Homo sapiens
Elastin (730 amino acids)
GenBank AAA52382

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  1 magltaaapr pgvllllllsi lhpsrpggvp gaipggvpgg vfypgaglga lgggalgpgg
 61 kplkpvpggl agaglgaglg afpavtfpga lvpggvadaa aaykaakaga glggvpgvgg
121 lgvsagavvp qpgagvkpgk vpgvglpgvy pggvlpgarf pgvgvlpgvp tgagvkpkap
181 gvggafagip gvgpfggpqp gvplgypika pklpggyglp yttgklpygy gpggvagaag
241 kagyptgtgv gpqaaaaaaa kaaakfgaga agvlpgvgga gvpgvpgaip giggiagvgt
301 paaaaaaaaa akaakygaaa glvpggpgfg pgvvgvpgag vpgvgvpgag ipvvpgagip
361 gaavpgvvsp eaaakaaaka akygarpgvg vggiptygvg aggfpgfgvg vggipgvagv
421 psvggvpgvg gvpgvgispe aqaaaaakaa kygvgtpaaa aakaaakaaq fallnlaglv
481 pgvgvapgvg vapgvgvapg vglapgvgva pgvgvapgvg vapgigpggv aaaaksaakv
541 aakaqlraaa glgagipglg vgvgvpglgv gagvpglgvg agvpgfgavp galaaakaak
601 ygaavpgvlg glgalggvgi pggvvgagpa aaaaaakaaa kaaqfglvga aglgglgvgg
661 lgvpgvgglg gippaaaaka akygaaglgg vlggagqfpl ggvaarpgfg lspifpggac
721 lgkacgrkrk (SEQ ID NO:25)
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COMPOSITIONS AND METHODS FOR DETECTING UNSTABLE ARTERIOSCLEROTIC PLAQUES

CROSS-REFERENCE

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 61/635,645, filed Apr. 19, 2012, which application is incorporated herein by reference in its entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[0002] This invention was made with government support under Grant No. P41 RR001614 awarded by the National Institutes of Health, National Center for Research Resources. The government has certain rights in the invention.

INTRODUCTION

[0003] Cardiovascular disease (CVD) is the general term for heart and blood vessel diseases, including atherosclerosis, coronary artery disease, cerebrovascular disease, aorto-iliac disease, and peripheral vascular disease. Individuals with CVD may develop a number of complications, such as myocardial infarction, stroke, angina pectoris, transient ischemic attacks, congestive heart failure, aortic aneurysm, and death.

[0004] Arterial plaque instability is a critical element in occlusive vascular disease events, including myocardial ischemia, myocardial infarction, stroke, and peripheral arterial disease. As plaques become unstable, they erode or rupture, exposing prothrombotic stimuli to the blood, which in turn initiates thrombi.

[0005] Levels of the acute phase reactant C-reactive protein (CRP) have been used to estimate an individual's risk of developing a cardiovascular disorder. However, CRP may be found in the blood of individuals with inflammation due to causes other than CVD; as such, the value of CRP as a diagnostic or prognostic tool is limited.

[0006] There is a need in the art for methods of determining an individual's risk of developing an occlusive vascular event.

LITERATURE

[0007] U.S. Patent Publication No. 2010/0323377; Libby et al. (2010) *Circ. J.* 74:213; Galis et al. (1994) *J. Clin. Invest.* 94:2493; Skølt-Arkil et al. (2010) *Assay and Drug Development Technologies* 8:542; Barascuk et al. (2010) *BMC Cardiovasc. Dis.* 10:19; Libby (2006) *Arterioscler. Thromb. Vasc. Biol.* 26:2181.

SUMMARY

[0008] The present disclosure provides methods of detecting an unstable arteriosclerotic plaque in an individual, involving detecting in a biological sample from the individual an enzymatic cleavage product of a protein component of an arteriosclerotic plaque. The present disclosure provides methods of assessing the risk that an individual will develop an occlusive vascular event. The present disclosure further provides kits for carrying out a subject method.

[0009] In a first embodiment, the present disclosure provides a method for detecting an unstable arteriosclerotic plaque in an individual, the method comprising detecting in a biological sample from the individual an enzymatic cleavage product of a protein component of an arteriosclerotic plaque. In some cases, the protein component is not collagen type III, elastin, decorin, biglycan, versican, apolipoprotein E, C-reactive protein, or lumican.

[0010] In the first embodiment of a subject method, the protein can be a structural protein, e.g., a non-enzymatic protein. In some cases, in the first and/or the second embodiment of a subject method, the individual is asymptomatic with respect to an arterial occlusive event and/or is an apparently healthy human subject. In some cases, in any of the above embodiments of a subject method, the individual has experienced one or more typical symptoms of cardiovascular disease. In some cases, in any of the above embodiments of a subject method, the individual has experienced an atypical symptom of cardiovascular disease. In any of the above embodiments, the biological sample is blood; or is a blood fraction (e.g., serum or plasma). In any of the above embodiments, level of the one or more enzymatic cleavage products is determined by an immunological method. In any of the above embodiments, the protein component is fibrillin, vitronectin, fibronectin, tenascin, prolargin, dermatopontin, vascular collagen, metalloproteinase inhibitor-1, galectin-1, or tenascin-X. For example, the collagen can be collagen alpha-1 (I) chain, collagen alpha-1 (II) chain, collagen alpha-1 (IV) chain, collagen alpha-1 (VI) chain, collagen alpha-1 (XII), collagen alpha-1 (XIV) chain, collagen alpha-1 (XV) chain, collagen alpha-1 (XVIII), collagen alpha-1 (XIX); collagen alpha-2 (I) chain, collagen alpha-3 (VI), collagen alpha-2 (IV), or collagen alpha-5 (IV). In any of the above embodiments, the enzymatic cleavage product has a molecular weight in a range of from about 0.5 kDa to about 50 kDa; for example, the enzymatic cleavage product can have a length in a range of from about 5 amino acids to about 500 amino acids.

[0011] In any of the above embodiments of a subject method for detecting an unstable arteriosclerotic plaque in an individual, the detecting step can comprise processing the enzymatic cleavage product in vitro. For example, in some cases, the processing comprises trypsin digestion.

[0012] In any of the above embodiments of a subject method for detecting an unstable arteriosclerotic plaque in an individual, the enzymatic cleavage product can be a cleavage product of a matrix metalloproteinase (MMP). For example, in some cases, the MMP is secreted by a macrophage. For example, in some cases, the MMP is MMP1, MMP2, MMP3, MMP7, MMP8, MMP9, MMP10, MMP11, MMP12, or MMP13.

[0013] In some cases, the enzymatic cleavage product is a cleavage product of a cathepsin.

[0014] In any of the above embodiments of a subject method for detecting an unstable arteriosclerotic plaque in an individual, the method can further comprise generating a report providing an indication of the risk that the individual will experience an occlusive vascular event.

[0015] In a second embodiment, the present disclosure provides a method for determining a risk that an individual will develop an occlusive vascular event, the method comprising determining the level, in a biological sample from the individual, of an enzymatic cleavage product of a protein component of an arteriosclerotic plaque, wherein a level of the enzymatic cleavage product that is higher than a normal control level indicates risk of developing an occlusive vascular event. For example, the protein component can be fibrillin, vitronectin, fibronectin, tenascin, prolargin, dermatopontin, vascular collagen, metalloproteinase inhibitor-1, galectin-1, or tenascin-X. In some cases, the level of the one or more enzymatic cleavage products is determined by an immunological method. In some cases, the protein component is not collagen type III, elastin, decorin, biglycan, versican, apolipoprotein E, C-reactive protein, or lumican.

[0016] In any of the above embodiments of a subject method for determining a risk that an individual will develop an occlusive vascular event, the biological sample can be blood, serum, or plasma. In any of the above embodiments of a subject method for determining a risk that an individual will develop an occlusive vascular event, the subject can be an apparently healthy human subject. In any of the above embodiments of a subject method for determining a risk that an individual will develop an occlusive vascular event, the individual can be one who does not have a history of having an occlusive vascular event.

[0017] In a third embodiment, the present disclosure provides a kit for detecting an unstable arteriosclerotic plaque in an individual, the kit comprising: a) a binding reagent that specifically binds an enzymatic cleavage product of a protein component of an arteriosclerotic plaque; and b) a control that provides for quantitation of the enzymatic product. In some cases, the protein component is not collagen type III, elastin, decorin, biglycan, versican, apolipoprotein E, C-reactive protein, or lumican.

[0018] In some embodiments of a subject kit, the reagent that specifically binds an enzymatic cleavage product of a protein component of an arteriosclerotic plaque is an antibody. For example, the antibody can be a monoclonal antibody, or an antigen-binding fragment. In some embodiments of a subject kit, the antibody is immobilized on an insoluble support. In some embodiments of a subject kit, the antibody comprises a detectable label; in some of these embodiments, the kit further comprises one or more reagents for developing a detectable label.

[0019] In a fourth embodiment, the present disclosure provides an assay device for use in detecting, in a liquid biological sample obtained from an individual, an enzymatic cleavage product of a protein component of an arteriosclerotic plaque, the device comprising a matrix defining an axial flow path, the matrix comprising: i) a sample receiving zone at an upstream end of the flow path that receives the liquid sample; ii) one or more test zones positioned within the flow path and downstream from the sample receiving zone, each of said one or more test zones comprising an antibody specific for an enzymatic cleavage product of a protein component of an arteriosclerotic plaque immobilized in each of said test zones, wherein each of said immobilized antibodies is capable of binding different enzymatic cleavage product present in said liquid sample, to form an immobilized antibody/enzymatic cleavage product complex; and iii) one or more control zones positioned within the flow path and downstream from the sample receiving zone. In some embodiments, the protein component is not collagen type III, elastin, decorin, biglycan, versican, apolipoprotein E, C-reactive protein, or lumican.

[0020] In some embodiments of a subject assay device, the one or more control zones are positioned between the test zones when two or more test zones are present. In some embodiments of a subject assay device, wherein the test zones and control zones are positioned in an alternating format within the flow path beginning with a test zone positioned upstream of any control zone. In some embodiments of a subject assay device, the assay device further comprises a label zone positioned upstream of a test zone, wherein the label zone comprises a labeled antibody specific for an enzymatic cleavage product of a protein component of an arteriosclerotic plaque, wherein the labeled antibody is capable of binding an enzymatic cleavage product present in an immobilized antibody/enzymatic cleavage product complex to form a labeled immobilized antibody/enzymatic cleavage product complex, and wherein the labeled antibody is mobilizable in the presence of the liquid sample.

[0021] In some embodiments of a subject assay device that include a labeled antibody, the labeled antibody comprises a label component selected from the group consisting of a chemiluminescent agent, a particulate label, a colorimetric agent, an energy transfer agent, an enzyme, a fluorescent agent, and a radioisotope. In some embodiments of a subject assay device, the matrix is positioned within a housing comprising a support and optionally a cover, wherein the housing contains an application aperture and one or more observation ports. In any of the embodiments of a subject assay device, the device can be a test strip or a dipstick assay device. In any of the embodiments of a subject assay device, the liquid sample can be blood, serum, or plasma.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] FIGS. **1**A-B provide an amino acid sequence of alpha-1 collagen (type I).

[0023] FIGS. **2**A-B provide an amino acid sequence of alpha-1 collagen (type II).

[0024] FIGS. **3**A-B provide an amino acid sequence of alpha-1 collagen (type III).

[0025] FIGS. **4**A-B provide an amino acid sequence of alpha-1 collagen (type IV).

[0026] FIG. **5** provides an amino acid sequence of alpha-1 collagen (type VI).

[0027] FIGS. **6**A-C provide an amino acid sequence of alpha-3 collagen (type VI).

[0028] FIGS. **7**A-C provide an amino acid sequence of alpha-1 collagen (type XII).

[0029] FIGS. **8**A-B provide an amino acid sequence of alpha-1 collagen (type XIV).

[0030] FIGS. **9**A-B provide an amino acid sequence of alpha-1 collagen (type XV).

[0031] FIGS. **10**A-B provide an amino acid sequence of alpha-1 collagen (type XVIII).

[0032] FIG. **11** provides an amino acid sequence of alpha-1 collagen (type XIX).

[0033] FIGS. **12**A-B provide an amino acid sequence of alpha-2 collagen (type I).

[0034] FIGS. **13**A-C provide an amino acid sequence of fibronectin.

[0035] FIGS. **14**A-C provide an amino acid sequence of fibrillin-1.

[0036] FIG. **15** provides an amino acid sequence of dermatopontin.

[0037] FIG. **16** provides an amino acid sequence of metalloproteinase inhibitor-1.

[0038] FIG. **17** provides an amino acid sequence of galectin-1.

[0039] FIG. **18** provides an amino acid sequence of lumican.

[0040] FIG. **19** provides an amino acid sequence of prolargin.

[0041] FIGS. **20**A and B provide an amino acid sequence of tenascin.

[0042] FIG. **21** provides an amino acid sequence of vitronectin.

[0043] FIGS. **22**A-D provide an amino acid sequence of tenascin-X.

[0044] FIGS. **23**A and **23**B provide an amino acid sequence of collagen alpha-2(IV).

[0045] FIGS. **24**A and **24**B provide an amino acid sequence of collagen alpha-5(IV).

[0046] FIG. **25** provides an amino acid sequence of elastin.

DEFINITIONS

[0047] The terms "polypeptide," "peptide" and "protein", used interchangeably herein, refer to a polymeric form of amino acids of any length, which can include coded and non-coded amino acids, chemically or biochemically modified or derivatized amino acids, and polypeptides having modified peptide backbones. The term includes fusion proteins, including, but not limited to, fusion proteins with a heterologous amino acid sequence, fusions with heterologous and homologous leader sequences, with or without N-terminal methionine residues; immunologically tagged proteins; and the like. NH_2 refers to the free amino group present at the amino terminus of a polypeptide. COOH refers to the free carboxyl group present at the carboxyl terminus of a polypeptide. In keeping with standard polypeptide nomenclature, *J. Biol. Chem.,* 243 (1969), 3552-59 is used.

[0048] A "biological sample" encompasses a variety of sample types obtained from an individual and can be used in a diagnostic or monitoring assay. The definition encompasses blood, blood products, and other liquid samples of biological origin; and solid tissue samples such as a biopsy specimen. The definition includes biological samples obtained via catheter during or as a result of coronary angiogram; and biological samples obtained during catheterization of a carotid artery, a femoral artery, or the aorta. The definition also includes samples that have been manipulated in any way after their procurement, such as by treatment with reagents, solubilization, or enrichment for certain components, such as peptides (e.g., enzymatic cleavage products of an arteriosclerotic plaque). The term "biological sample" encompasses a clinical sample, and also includes serum, plasma, biological fluid, and tissue samples. Enzymatic cleavage products of an arteriosclerotic plaque present in a biological sample can be eluted, monomerized, solubilized, etc., or otherwise treated in order to render the enzymatic cleavage products in a physical state suitable for analysis. Enzymatic cleavage products of an arteriosclerotic plaque present in a biological sample can be purified from the liquid sample, e.g., using immunoaffinity methods. For example, magnetic beads comprising an antibody specific for a given enzymatic cleavage product can be used to enrich the cleavage product from a biological sample.

[0049] The terms "individual," "subject," "host," and "patient," used interchangeably herein, refer to a mammal, including, e.g., humans and non-human primates.

[0050] "Conservative amino acid substitution" refers to a substitution of one amino acid residue for another sharing chemical and physical properties of the amino acid side chain (e.g., charge, size, hydrophobicity/hydrophilicity). "Conservative substitutions" are intended to include substitution within the following groups of amino acid residues: gly, ala; val, ile, leu; asp, glu; asn, gln; ser, thr; lys, arg; and phe, tyr. Guidance for such substitutions can be drawn from alignments of amino acid sequences of polypeptides.

[0051] "Isolated" refers to an entity of interest that is in an environment different from that in which the compound may naturally occur. "Isolated" is meant to include compounds that are within samples that are substantially enriched for the compound of interest and/or in which the compound of interest is partially or substantially purified.

[0052] By "purified" is meant a compound of interest (e.g., a polypeptide) has been separated from components that accompany it in nature. "Purified" can also be used to refer to a compound of interest separated from components that can accompany it during manufacture (e.g., in chemical synthesis). In some embodiments, a compound is substantially pure when it is at least 50% to 60%, by weight, free from organic molecules with which it is naturally associated or with which it is associated during manufacture. In some embodiments, the preparation is at least 75%, at least 90%, at least 95%, or at least 99%, by weight, of the compound of interest. A substantially pure compound can be obtained, for example, by extraction from a natural source (e.g., bacteria), by chemically synthesizing a compound, or by a combination of purification and chemical modification. A substantially pure compound can also be obtained by, for example, enriching a sample that contains the compound. Purity can be measured by any appropriate method, e.g., chromatography, mass spectroscopy, high performance liquid chromatography analysis, etc.

[0053] "Axial flow" as used herein refers to lateral, vertical or transverse flow through a particular matrix or material comprising one or more test and/or control zones. The type of flow contemplated in a particular device, assay or method varies according to the structure of the device. Without being bound by theory, lateral, vertical or transverse flow may refer to flow of a fluid sample from the point of fluid contact on one end or side of a particular matrix (the upstream or proximal end) to an area downstream (or distal) of this contact. The downstream area may be on the same side or on the opposite side of the matrix from the point of fluid contact. For example, in vertical flow devices of the present invention, axial flow may progress vertically from and through a first member (top to bottom) to a second member and from there on to an absorbent medium. By way of further example, and as will be appreciated by those of skill in the art, in a vertical flow device configured, for example, as a dipstick, a fluid sample may flow literally up the device, in which case however, the point of first contact of the fluid sample to the device is nonetheless considered the upstream (i.e., proximal) end and the point of termination of flow the downstream (i.e., distal) end.

[0054] As used herein the terms "upstream" and "downstream" refer to the direction of fluid sample flow subsequent to contact of the fluid sample with a representative device of the present disclosure, wherein, under normal operating conditions, the fluid sample flow direction runs from an upstream position to a downstream position. For example, when fluid sample is initially contacted with the sample receiving zone, the fluid sample then flows downstream through the label zone and so forth.

[0055] Before the present invention is further described, it is to be understood that this invention is not limited to particular embodiments described, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

[0056] Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

[0057] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited.

[0058] It must be noted that as used herein and in the appended claims, the singular forms “a,” “an,” and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “an enzymatic cleavage product” includes a plurality of such enzymatic cleavage products and reference to “the protease secreted by an inflammatory cell” includes reference to one or more such proteases and equivalents thereof known to those skilled in the art, and so forth. It is further noted that the claims may be drafted to exclude any optional element. As such, this statement is intended to serve as antecedent basis for use of such exclusive terminology as “solely,” “only” and the like in connection with the recitation of claim elements, or use of a “negative” limitation.

[0059] It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable sub-combination. All combinations of the embodiments pertaining to the invention are specifically embraced by the present invention and are disclosed herein just as if each and every combination was individually and explicitly disclosed, to the extent that such combinations embrace subject matter that are, for example, compounds that are stable compounds (i.e., compounds that can be made, isolated, characterized, and tested for biological activity). In addition, all sub-combinations of the various embodiments and elements thereof (e.g., elements of the chemical groups listed in the embodiments describing such variables) are also specifically embraced by the present invention and are disclosed herein just as if each and every such sub-combination was individually and explicitly disclosed herein.

[0060] The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed.

DETAILED DESCRIPTION

[0061] The present disclosure provides methods of detecting an unstable arteriosclerotic plaque in an individual, the methods generally involving detecting in a biological sample from the individual an enzymatic cleavage product of a protein component of an arteriosclerotic plaque. The present disclosure provides methods of assessing the risk that an individual will develop an occlusive vascular event. The present disclosure further provides kits for carrying out a subject method.

[0062] Stable arteriosclerotic plaques can comprise extracellular matrix (ECM) components. Under certain circumstances, inflammatory cells secrete enzymes that can break down a protein component of an arteriosclerotic plaque. As plaques become unstable, they erode or rupture, exposing prothrombotic stimuli to the blood, which in turn initiates thrombi. Thus, arterial plaque instability is a critical element in occlusive vascular disease events, including myocardial ischemia, myocardial infarction, stroke, and peripheral arterial disease. A hallmark of an unstable arteriosclerotic plaque (also referred to as an “unstable atherosclerotic plaque”) is the presence in an arteriosclerotic plaque of inflammatory cells, which cells secrete enzymes that proteolytically cleave protein components of the plaque, thereby destabilizing the plaque. The present disclosure provides methods of detecting an unstable arteriosclerotic plaque. Detection of an unstable arteriosclerotic plaque can provide an indication of an individual’s risk of developing an occlusive vascular event. Thus, the present disclosure provides methods of determining a risk that an individual will develop an occlusive vascular event. Based on detection an enzymatic cleavage product of a protein component of an arteriosclerotic plaque, a physician or other qualified medical personnel can determine whether appropriate medical intervention is advised, e.g., in order to reduce the risk that an occlusive vascular event will actually occur.

Methods of Detecting an Unstable Arteriosclerotic Plaque

[0063] The present disclosure provides methods of detecting an unstable arteriosclerotic plaque in an individual, the methods generally involving detecting in a biological sample from the individual an enzymatic cleavage product of a protein component of an arteriosclerotic plaque. The enzymatic cleavage products are generated in vivo by enzymes produced by cells in the vasculature.

[0064] Protein components of an arteriosclerotic plaque include non-enzymatic proteins. Protein components of an arteriosclerotic plaque include structural proteins.

[0065] Enzymatic cleavage products of a protein component of an arteriosclerotic plaque include cleavage products generated by an enzyme produced by a cell in the vasculature (e.g., cleavage products generated in vivo in the vasculature by enzyme(s) produced by a cell (e.g., an inflammatory cell) in the vasculature). Enzymatic cleavage products include unmodified polypeptides and covalently modified polypeptides. Covalently modified polypeptides include polypeptides comprising a covalently linked chemical adduct. For example, a covalently modified polypeptide can include a covalently linked Schiff base modification, such as a fatty aldehyde, a malondialdehyde, and the like.

Enzymes

[0066] An enzymatic cleavage product of a protein component of an arteriosclerotic plaque can be a cleavage product of an acid protease, a serine protease, a cysteine protease, an aspartic acid protease, a matrix metalloprotease (MMP), and the like. The enzymes are produced in vivo by a cell (e.g., an inflammatory cell) in the vasculature.

[0067] Proteolytic cleavage enzymes that may be present in the artery wall, and that can give rise to an enzymatic cleavage product of a protein component of an arteriosclerotic plaque, include, but are not limited to, acid proteases, serine proteases (e.g., elastase-like serine proteases; chymotrypsin-like serine proteases; cysteine proteases; aspartic acid proteases; MMPs; an ADAMTS (A Disintegrin And Metalloproteinase with Thrombospondin Motifs) protease (e.g., any one of ADAMTS-1 through ADAMTS-20); and the like. Proteolytic cleavage enzymes that may be present in the artery wall, and that can give rise to an enzymatic cleavage product of a protein component of an arteriosclerotic plaque, include, but are not limited to, cathepsins (e.g., cathepsin K, cathepsin S, cathepsin L, cathepsin B, cathepsin D, cathepsin H, and cystatin C); chymase; tryptase; macrophage metalloproteases; aggrecanases; protease-3; granzymes (e.g., granzyme A, granzyme B, granzyme H, granzyme K, etc.); and the like.

[0068] In some instances, an enzymatic cleavage product of a protein component of an arteriosclerotic plaque is a cleavage product of a matrix metalloproteinase (MMP), where MMPs include, e.g., secreted MMPs such as MMP1 (interstitial collagenase); MMP2 (72-kDa gelatinase, or gelatinase-A); MMP3 (stromelysin-1); MMP7 (matrilysin); MMP8 (neutrophil collagenase); MMP9 (92-kDa gelatinase or gelatinase-B); MMP10 (stromelysin-2); MMP11 (stromelysin-3); MMP12 (macrophage metalloprotease); MMP13 (collagenase-3); and MMP16. An enzymatic cleavage product of a protein component of an arteriosclerotic plaque can also be a cleavage product of a cathepsin. In some instances, cleavage products of a cathepsin are specifically excluded.

[0069] Enzymes that produce an enzymatic cleavage product of a protein component of an arteriosclerotic plaque can be produced by (e.g., secreted by) inflammatory cells, e.g., macrophages, neutrophils, monocytes, or transformed smooth muscle cells. Thus, in some embodiments, a subject method generally involves detecting in a biological sample from the individual an enzymatic cleavage product (e.g., an in vivo-generated enzymatic cleavage product) of a protein component of an arteriosclerotic plaque, where the enzymatic cleavage product is a product of cleavage by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature.

[0070] An enzymatic cleavage product of a protein component of an arteriosclerotic plaque can have a signature structure characteristic of cleavage by an enzyme(s) produced by an inflammatory cell in the vasculature.

Enzymatic Cleavage Products

[0071] Enzymatic cleavage products of a protein component of an arteriosclerotic plaque include enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by an inflammatory cell in the vasculature) of vascular collagen (where vascular collagen encompasses, e.g., collagen alpha-1 (I) chain; collagen alpha-1 (II) chain; collagen alpha-1 (III) chain; collagen alpha-1 (IV) chain; collagen alpha-1 (VI) chain; collagen alpha-1 (XII); collagen alpha-1 (XIV) chain; collagen alpha-1 (XV) chain; collagen alpha-1 (XVIII); collagen alpha-1 (XIX); collagen alpha-2 (I) chain; collagen alpha-3 (VI); collagen alpha-2 (IV); and collagen alpha-5 (IV)); fibrillin-1; fibronectin; vitronectin; metalloproteinase inhibitor 1; dermatopontin; galectin-1; prolargin; tenascin; and tenascin-X. Enzymatic cleavage products of a protein component of an arteriosclerotic plaque can also include enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by an inflammatory cell in the vasculature) of collagen type III, elastin, decorin, biglycan, versican, apolipoprotein E, C-reactive protein, or lumican. In some embodiments, enzymatic cleavage products of one or more of collagen type III, elastin, decorin, biglycan, versican, apolipoprotein E, C-reactive protein, and lumican are specifically excluded. Amino acid sequences of such proteins are known in the art. Exemplary sequences are provided in FIGS. **1-24**.

[0072] Enzymatic cleavage products to be detected according to a method of the present disclosure can include cleavage products of all, or a subset of, the above-listed proteins. For example, enzymatic cleavage products of a protein component of an arteriosclerotic plaque can include enzymatic cleavage products of all 23, or a subset of 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 19, 20, 21, or 22, of the following set of proteins: 1) fibrillin (fibrillin-1); 2) vitronectin; 3) fibronectin; 4) tenascin; 5) prolargin; 6) dermatopontin; 7) collagen alpha-1 (I) chain; 8) collagen alpha-1 (II) chain; 9) collagen alpha-1 (III) chain; 10) collagen alpha-1 (IV) chain; 11) collagen alpha-1 (VI) chain; 12) collagen alpha-1 (XII); 13) collagen alpha-1 (XIV) chain; 14) collagen alpha-1 (XV) chain; 15) collagen alpha-1 (XVIII); 16) collagen alpha-1 (XIX); 17) collagen alpha-2 (I) chain; 18) collagen alpha-3 (VI); 19) collagen alpha-2 (IV); 20) collagen alpha-5 (IV); 21) metalloproteinase inhibitor 1; 22) galectin-1; and 23) tenascin-X. As an example, enzymatic cleavage products of a protein component of an arteriosclerotic plaque can include enzymatic cleavage products of: collagen alpha-1 (I) chain; collagen alpha-1 (II) chain; collagen alpha-1 (IV) chain; collagen alpha-1 (VI) chain; collagen alpha-1 (XII); collagen alpha-1 (XIV) chain; collagen alpha-1 (XV) chain; collagen alpha-1 (XVIII); collagen alpha-1 (XIX); collagen alpha-2 (I) chain; collagen alpha-3 (VI); collagen alpha-2 (IV); collagen alpha-5 (IV); fibrillin-1; fibronectin; vitronectin; metalloproteinase inhibitor 1; dermatopontin; galectin-1; prolargin; tenascin; and tenascin-X.

[0073] Enzymatic cleavage products of one or more of the above-listed proteins can in certain instances be specifically excluded. For example, in some instances, an enzymatic cleavage product of collagen type III is specifically excluded. In some instances, an enzymatic cleavage product of lumican is specifically excluded. In some instances, an enzymatic cleavage product of elastin is specifically excluded. In some instances, an enzymatic cleavage product of one or more of versican, perlecan, decorin, and biglycan is specifically excluded. In some instances, an enzymatic cleavage product of versican, perlecan, decorin, and biglycan is specifically excluded. In some instances, an enzymatic cleavage product of C-reactive protein (CRP) is specifically excluded. In some instances, an enzymatic cleavage product of apolipoprotein-E is specifically excluded.

[0074] Enzymatic cleavage products of a protein component of an arteriosclerotic plaque can have a size in a range of from about 0.5 kDa to about 50 kDa, e.g., from about 0.5 kDa to about 1 kDa, from about 1 kDa to about 1.5 kDa, from about 1.5 kDa to about 2 kDa, from about 2 kDa to about 5 kDa, from about 5 kDa to about 7.5 kDa, from about 7.5 kDa to about 10 kDa, from about 10 kDa to about 15 kDa, from about 15 kDa to about 20 kDa, from about 20 kDa to about 25 kDa, from about 25 kDa to about 30 kDa, from about 30 kDa to about 35 kDa, from about 35 kDa to about 40 kDa, from about 40 kDa to about 45 kDa, or from about 45 kDa to about 50 kDa.

[0075] An enzymatic cleavage product of a protein component of an arteriosclerotic plaque can have a length of from about 5 amino acids to about 500 amino acids, e.g., from about 5 amino acids (aa) to about 10 aa, from about 10 aa to about 15 aa, from about 15 aa to about 20 aa, from about 20 aa to about 25 aa, from about 25 aa to about 30 aa, from about 30 aa to about 35 aa, from about 35 aa to about 40 aa, from about 40 aa to about 45 aa, from about 45 aa to about 50 aa, from about 50 aa to about 75 aa, from about 75 aa to about 100 aa, from about 100 aa to about 150 aa, from about 150 aa to about 200 aa, from about 200 aa to about 250 aa, from about 250 aa to about 300 aa, from about 300 aa to about 350 aa, from about 350 aa to about 400 aa, from about 400 aa to about 450 aa, or from about 450 aa to about 500 aa.

Collagens

[0076] Collagens are extracellular matrix proteins and have a triple-helical domain as their common structural element. Each collagen molecule includes three polypeptides referred to as alpha chains. For example, the basic structural unit of collagen VI is a heterotrimer of the alpha-1(VI), alpha-2(VI), and alpha-3(VI) chains.

[0077] Vascular collagens that are structural components of arteriosclerotic plaques include collagen alpha-1 (I) chain; collagen alpha-1 (II) chain; collagen alpha-1 (III) chain; collagen alpha-1 (IV) chain; collagen alpha-1 (VI) chain; collagen alpha-1 (XII); collagen alpha-1 (XIV) chain; collagen alpha-1 (XV) chain; collagen alpha-1 (XVIII); collagen alpha-1 (XIX); collagen alpha-2 (I) chain; and collagen alpha-3 (VI). Vascular collagen is present in the vasculature.

[0078] Exemplary amino acid sequences of collagen alpha-1 (I) chain; collagen alpha-1 (II) chain; collagen alpha-1 (III) chain; collagen alpha-1 (IV) chain; collagen alpha-1 (VI) chain; collagen alpha-1 (XII); collagen alpha-1 (XIV) chain; collagen alpha-1 (XV) chain; collagen alpha-1 (XVIII); collagen alpha-1 (XIX); collagen alpha-2 (I) chain; and collagen alpha-3 (VI) are provided in FIGS. **1-12**. Exemplary amino acid sequences of collagen alpha-2 (IV) and collagen alpha-5 (IV) are provided in FIGS. **23** and **24**.

[0079] An enzymatic cleavage product of a vascular collagen component of an arteriosclerotic plaque can be an enzymatic cleavage product of a collagen polypeptide having at least about 98%, at least about 99%, or 100%, amino acid sequence identity with an amino acid sequence of a collagen polypeptide depicted in one of FIGS. **1-12**, **23**, and **24**. An enzymatic cleavage product of a vascular collagen component of an arteriosclerotic plaque can be an enzymatic cleavage product of a naturally-occurring variant (polymorphism) of a collagen polypeptide depicted in one of FIGS. **1-12**, **23**, and **24**.

Collagen Alpha-1(I) Proteolytic Fragments

[0080] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-1(I) chain, listed in sequence order, include:

(SEQ ID NO: 26)
TGGISVPGPMGPSGPR;

(SEQ ID NO: 27)
GLPGPPGAPGPQG;

(SEQ ID NO: 28)
GLPGPPGAPGPQGF;

(SEQ ID NO: 29)
PGEPGEPGASGPMGPRGPPGPPGK;

(SEQ ID NO: 30)
GASGPMGPRGPPGPPGK;

(SEQ ID NO: 31)
KPGRPGERGPPGPQGAR;

(SEQ ID NO: 32)
GPPGPQGARGLPGTAGLPGM;

(SEQ ID NO: 33)
AGPQGPR;

(SEQ ID NO: 34)
GAPGIAGAPGFPGAR;

(SEQ ID NO: 35)
PGIAGAPGFPGARGPSGPQGPGGPPGPK;

(SEQ ID NO: 36)
IAGAPGFPGARGPSGPQGPGGPPGPK;

(SEQ ID NO: 37)
GFPGARGPSGPQGPGGPPGPK;

(SEQ ID NO: 38)
GPSGPQGPGG;

(SEQ ID NO: 39)
GDTGAKGEP;

(SEQ ID NO: 40)
VQGPPGPAGEEGK;

(SEQ ID NO: 41)
GEPGPTGLPGPPG;

(SEQ ID NO: 42)
GEPGPTGLPGPPGERGGPGS;

(SEQ ID NO: 43)
TGLPGPPGER;

(SEQ ID NO: 44)
LPGPPGER;

(SEQ ID NO: 45)
AGPKGPAGER;

(SEQ ID NO: 46)
GSPGPAGPKGSPGEAGRPGEAG;

(SEQ ID NO: 47)
PGEAGRPGEAGLPGAKGLTGSPGSPGPDGK;

(SEQ ID NO: 48)
LTGSPGSPGPDGK;

(SEQ ID NO: 49)
TGPPGPAGQDGRPGPPGPPGARG;

(SEQ ID NO: 50)
PGAVGPAGKDGEAGAQGPPGPAGPAGER;

(SEQ ID NO: 51)
GEAGAQGPPGPAGPAGER;

-continued

(SEQ ID NO: 52)
EAGAQGPPGPAGPAGER;

(SEQ ID NO: 53)
VQGPPGPAGPR;

(SEQ ID NO: 54)
QGPPGPAGPR*;

(SEQ ID NO: 55)
GPPGPAGPR;

(SEQ ID NO: 56)
ANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGER;

(SEQ ID NO: 57)
LQGMPGER*;

(SEQ ID NO: 58)
LTGPIGPPGPAGAPGDK;

(SEQ ID NO: 59)
IGPPGPAGAPGDK;

(SEQ ID NO: 60)
KGESGPSGPAGPTGAR;

(SEQ ID NO: 61)
PGDRGEPGPPGPAGFAGPPGADGQPGAK;

(SEQ ID NO: 62)
GEPGPPGPAGF;

(SEQ ID NO: 63)
FAGPPGADGQPGAK*;

(SEQ ID NO: 64)
AGPPGADGQPGAK*;

(SEQ ID NO: 65)
RVGPPGPSGNAGPPGPPGPAGK;

(SEQ ID NO: 66)
VGPPGPSGNAGPPGPPGPAGKEGG;

(SEQ ID NO: 67)
EVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR;

(SEQ ID NO: 68)
PGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR;

(SEQ ID NO: 69)
GSPGADGPAGAPGTPGPQG;

(SEQ ID NO: 70)
GPAGAPGTPGPQGIAGQR;

(SEQ ID NO: 71)
VVGLPGQR;

(SEQ ID NO: 72)
LAGPPGESGR;

(SEQ ID NO: 73)
ETGPAGPPGAPGAPGAPGPVGPAGKSGDR;

(SEQ ID NO: 74)
RGETGPAGPAGPVGPVGAR;

(SEQ ID NO: 75)
PAGPVGPVGAR;

(SEQ ID NO: 76)
PVGPVGAR;

(SEQ ID NO: 77)
SPGEQGPSGASGPAGPR;

-continued

(SEQ ID NO: 78)
PGEQGPSGASGPAGPR;

(SEQ ID NO: 79)
GPSGASGPAGPR;

(SEQ ID NO: 80)
ASGPAGPR;

(SEQ ID NO: 81)
GPPGSAGAPGKD;

(SEQ ID NO: 82)
PPGSAGAPGKDGLNGLPGPIGPPGPR;
and

(SEQ ID NO: 83)
LPQPPQEK*,

[0081] and naturally-occurring variants of any of the foregoing.

Collagen Alpha-2(I) Proteolytic Fragments

[0082] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-2(I) chain, listed in sequence order, include:

(SEQ ID NO: 84)
GLMGPRGPPGAAGAPGPQGFQGPAGEPGEPGQTGPAGAR;

(SEQ ID NO: 85)
FQGPAGEPGEPGQTGPAGAR;

(SEQ ID NO: 86)
QGPAGEPGEPGQTGPAGAR;

(SEQ ID NO: 87)
EDGHPGKPGRPGERGVVGPQGAR;

(SEQ ID NO: 88)
PAGARGSDGSVGPVGPAGPIGSAGPPGFPGAPGPK;

(SEQ ID NO: 89)
DGSVGPVGPAGPIGSAGPPGFPGAPGPK;

(SEQ ID NO: 90)
PGAPGPKGEIGAVGNAGPAGPAGPR;

(SEQ ID NO: 91)
GPAGPAGPR;

(SEQ ID NO: 92)
PAGPAGPR;

(SEQ ID NO: 93)
RGEVGLPGLSGPVGPPGNPGANGLTGAK;

(SEQ ID NO: 94)
GAPGLPGPR;

(SEQ ID NO: 95)
PNGEAGSAGPPGPPGLR;

(SEQ ID NO: 96)
GPRGLPGSPGNIGPAGK;

(SEQ ID NO: 97)
GRPGPIGPAGAR;

(SEQ ID NO: 98)
GPSGPPGPDG;

-continued

(SEQ ID NO: 99)
GPSGPPGPDGNKGEPGVVGAVGTAGPS;

(SEQ ID NO: 100)
GPSGLPGER;

(SEQ ID NO: 101)
GAVGAPGPAGATGDRGEAGAAGPAGPAGPR;

(SEQ ID NO: 102)
VGAPGPAGATGDRGEAGAAGPAGPAGPR;

(SEQ ID NO: 103)
PGPAGATGDRGEAGAAGPAGPAGPR;

(SEQ ID NO: 104)
NGVVGPTGPVGAAGPAGPNGPPGPAGSR;

(SEQ ID NO: 105)
GPPGPAGSR;

(SEQ ID NO: 106)
PGPAGSRGDGGPPGMTGFPGAAGR;

(SEQ ID NO: 107)
GDGGPPGMTGFPGAAGRTGPPGPSGISGPPGPPGPA;

(SEQ ID NO: 108)
ISGPPGPPGPAGK;

(SEQ ID NO: 109)
GPSGEAGTAGPPGTPGPQGL;

(SEQ ID NO: 110)
PGILGLPGSR;

(SEQ ID NO: 111)
IAGPPGAR;

(SEQ ID NO: 112)
PGNIGPVGAAGAPGPHGPVGPAGKHGNR;

(SEQ ID NO: 113)
VGPAGAVGPR;

(SEQ ID NO: 114)
QGAPGSVGPAGPR;

(SEQ ID NO: 115)
GPAGPSGPAGKD;
and

(SEQ ID NO: 116)
GTVGPAGIR,

[0083] and naturally-occurring variants of any of the foregoing.

Collagen Alpha-1(III) Proteolytic Fragments

[0084] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-1(III) chain, listed in sequence order, include:

(SEQ ID NO: 117)
GPQGPKGDPGPPGIPGR;

(SEQ ID NO: 118)
PGTSGHPGSPGSPGYQGPPGEPGQAGPSGPPGPPGAIGPSGPAGK;

(SEQ ID NO: 119)
GLPGPPGIKGPAG;

-continued

(SEQ ID NO: 120)
GEVGPAGSPGSNGAPGQRGEPGPQGHAG;

(SEQ ID NO: 121)
GEPGPQGHAGAQGPPGPPGINGSPGGKGEMGPAGIPG;

(SEQ ID NO: 122)
GEMGPAGIPGAPGLMGARGPPGPAG;

(SEQ ID NO: 123)
GIPGAPGLMGAR;

(SEQ ID NO: 124)
GAPGLMGARGPPGPAGANGAPGLR;

(SEQ ID NO: 125)
PAGERGAPGPAGPR;

(SEQ ID NO: 126)
GAPGPAGPRGAAGEP;

(SEQ ID NO: 127)
GEPGRDGVPGGPGMR;

(SEQ ID NO: 128)
DGKPGPPGSQGESGRPGPPGPSGPR;

(SEQ ID NO: 129)
GKPGPPGSQGESGRPGPPGPSGPR;

(SEQ ID NO: 130)
GRPGPPGPSGPR;

(SEQ ID NO: 131)
GPPGPSGPR;

(SEQ ID NO: 132)
QGPPGKNGETGPQGPPGPTGPGGDK;

(SEQ ID NO: 133)
GDAGAPGERGP;

(SEQ ID NO: 134)
LQGMPGER;

(SEQ ID NO: 135)
GEGGPPGVAGPPGGSGPAGPPGPQGV;

(SEQ ID NO: 136)
GSNGNPGPPGPSGSPGKDGPPGPAGNTGAPGSPGVSGPK;

(SEQ ID NO: 137)
NGNPGPPGPSGSPGK;

(SEQ ID NO: 138)
GSPGAQGPP;

(SEQ ID NO: 139)
GNPGSDGLPGR;

(SEQ ID NO: 140)
ENGSPGAPGAPGHPGPPGPVGPAGK;

(SEQ ID NO: 141)
PGAPGAPGHPGPPGPVGPAGK;

(SEQ ID NO: 142)
RGESGPAGPAGAPGPAGSR;

(SEQ ID NO: 143)
GESGPAGPAGAP;

(SEQ ID NO: 144)
PGAPGSPGPAGQQGAIGSPGPAGPR;

(SEQ ID NO: 145)
GQQGAIGSPGPAGPRGPVGPSGPPGK;

-continued

(SEQ ID NO: 146)
QGAIGSPGPAGPR;
and

(SEQ ID NO: 147)
GSEGSPGHPGQPGPPGPPGAPGPCCGGVGAAAIAGIGGEKAGGFAPYYG,

[0085] and naturally-occurring variants of any of the foregoing.

Collagen Alpha-1(II) Proteolytic Fragments

[0086] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-1(II) chain, listed in sequence order, include:

(SEQ ID NO: 148)
GPQGFQGNPGEPGEPGVSGPMGPRGPPGPPGKPGDDGEAGKPGK;

(SEQ ID NO: 149)
GAAGARGNDGQPGPAGPPGPVGPAGGPGFPGAPGAK;

(SEQ ID NO: 150)
AAGARGNDGQPGPAGPPGPVGPAGGPGFPGAPGAK;

(SEQ ID NO: 151)
PGAKGSAGAPGIAGAPGFPGPR;

(SEQ ID NO: 152)
GPRGPPGPQGATGPLGPK;

(SEQ ID NO: 153)
DGLAGPK;

(SEQ ID NO: 154)
PQGKVGPSGAPGEDGRPGPPGPQGAR;

(SEQ ID NO: 155)
GFPGPKGANGEPGK;

(SEQ ID NO: 156)
GLPGPPGPPGEGGKPGDQGVPGEAGAPGLVGPR;

(SEQ ID NO: 157)
GPPGEGGKPGDQGVPGEAGAPGLVGPR;

(SEQ ID NO: 158)
LQGMPGER;

(SEQ ID NO: 159)
GRGLTGPIGPPGPAGANGEK;

(SEQ ID NO: 160)
GLTGPIGPPGPAGANGEKGEVGPP;

(SEQ ID NO: 161)
GLTGPIGPPGPAGANGEKGEVGPPGPAGSAG;

(SEQ ID NO: 162)
LTGPIGPPGPAGANGEKGEVGPPGPAGSAGAR;

(SEQ ID NO: 163)
TGPIGPPGPAGANGEKGEVGPPGPAGSAGAR;

(SEQ ID NO: 164)
FAGPPGADGQPGAK*;

(SEQ ID NO: 165)
AGPPGADGQPGAK*;

(SEQ ID NO: 166)
SGPPGRAGEPGLQGPAGPPGEK;

-continued

(SEQ ID NO: 167)
GPPGRAGEPGLQGPAGPPGEK;

(SEQ ID NO: 168)
PPGLTGPAGEPGREGSPGADGPPGR;
and

(SEQ ID NO: 169)
PGPGIDMSAFAGLGPREK,

[0087] and naturally-occurring variants of any of the foregoing.

Collagen Alpha-1(XIV) Proteolytic Fragments

[0088] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-1(XIV) chain, listed in sequence order, include:

(SEQ ID NO: 170)
IEWHLNAF;

(SEQ ID NO: 171)
AITGPPTELITSEVTAR;

(SEQ ID NO: 172)
AIYAHTASEGLR;

(SEQ ID NO: 173)
LYDVTENSMR;

(SEQ ID NO: 174)
YLILYAPLTEGLAGDEKEMK;

(SEQ ID NO: 175)
YAPLTEGLAGDEK;

(SEQ ID NO: 176)
HVEMTSLCAH;

(SEQ ID NO: 177)
SIQGMPGMPGEKGEK;

(SEQ ID NO: 178)
QVCEQLIQSH;
and

(SEQ ID NO: 179)
EPGRPGSPGAPGEQGPPGTPGFPGNAGVPGTPGER,

[0089] and naturally-occurring variants of any of the foregoing.

Collagen Alpha-1(XII) Proteolytic Fragments

[0090] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-1(XII) chain, listed in sequence order, include:

(SEQ ID NO: 180)
GGSTNTGKAMTYVRE;

(SEQ ID NO: 181)
PKVMILITDGK;

(SEQ ID NO: 182)
PDDTHAYNVADFESLSR;

-continued

(SEQ ID NO: 183)
SVVEDEYSEPLK;

(SEQ ID NO: 184)
SETSTSLKD;

(SEQ ID NO: 185)
LKPDTPYTITVSSLYPDGEGGRMTG;

(SEQ ID NO: 186)
PGPAGGPGAK;

(SEQ ID NO: 187)
GRTGTPGLPGPPGPMGPPGDR;

(SEQ ID NO: 188)
TPGLPGPPGPMGPPGDRGFTGK;

(SEQ ID NO: 189)
GFPGTPGMQGPPGERGLPGEK;

(SEQ ID NO: 190)
QGPPGER;
and

(SEQ ID NO: 191)
PRGLPGPPGPQGESR,

[0091] and naturally-occurring variants of any of the foregoing.

Collagen Alpha-1(XVIII) Proteolytic Fragments

[0092] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-1(XVIII) chain, listed in sequence order, include:

(SEQ ID NO: 192)
PPSLGRPWAPLTGPSVPPPSSGR;

(SEQ ID NO: 193)
PGEDGKPGDTGPQGFPGTPGDVGPKGDK;

(SEQ ID NO: 194)
PGLPGEPGR;

(SEQ ID NO: 195)
GREGPPGFPGLPGPPGPPGR;

(SEQ ID NO: 196)
QDGSVLSVPGPEGRPGFAGFPGPAGPKGNLGSK;

(SEQ ID NO: 197)
AESSRPGPPGLPGNQGPPGPK;

(SEQ ID NO: 198)
GPPGPKGAK;

(SEQ ID NO: 199)
PGPPGPPGTMGASSGVR;

(SEQ ID NO: 200)
RLPEPQPYPGAPHHSSYVHLRPARPTSPPAHSHR;

(SEQ ID NO: 201)
LPEPQPYPGAPHHSSY;

(SEQ ID NO: 202)
NSPLSGGMR;
and

(SEQ ID NO: 203)
PSLGRPWAPLTGPSVPPPSSER,

[0093] and naturally-occurring variants of any of the foregoing.

Collagen Alpha-2(IV) Proteolytic Fragments

[0094] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-2(IV) chain, listed in sequence order, include:

(SEQ ID NO: 204)
GARGVSGFPGADGIPGHPGQGGPR;

(SEQ ID NO: 205)
GGPKGLPGLPGPPGPTGAK;

(SEQ ID NO: 206)
GPPGLHGFPGAPGQEGPLGLPGIPGREGLPGDR;

(SEQ ID NO: 207)
APGRPGSPGLPGMPGR;

(SEQ ID NO: 208)
LYCNPGDVCYYASR;
and

(SEQ ID NO: 209)
LMHTAAGDEGGGQSLVSPGSCLEDFR,

[0095] and naturally-occurring variants of any of the foregoing.

Collagen Alpha-1(IV) Proteolytic Fragments

[0096] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-1(IV) chain, listed in sequence order, include:

[0097] and naturally-occurring variants of any of the foregoing.

(SEQ ID NO: 210)
EPGPPGLPGSVGSPGVPGIGPPGAR;

(SEQ ID NO: 211)
PGVPGIGPPGARGPPGGQGPPGLSGPPGIK;

(SEQ ID NO: 212)
PPGGQGPPGLSGPPGIKGEK;

(SEQ ID NO: 213)
DPGFQGMPGIGGSPGITGSK;

(SEQ ID NO: 214)
KGQQGVTGLVGIPGPPGIPGFDGAPGQK;

(SEQ ID NO: 215)
SLLYVQGNER;

(SEQ ID NO: 216)
LFCNINNVCNFASR;

(SEQ ID NO: 217)
VMHTSAGAEGSGQALASPGSCLEEFR;

(SEQ ID NO: 218)
RSAPFIECHGR;

(SEQ ID NO: 219)
SFWLATIER;
and

(SEQ ID NO: 220)
WLATIER,

[0098] and naturally-occurring variants of any of the foregoing.

Collagen Alpha-5(IV) Proteolytic Fragments

[0099] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-5(IV) chain, listed in sequence order, include:

(SEQ ID NO: 221)
DGIPGPPGPK;

(SEQ ID NO: 222)
KGNPGYPGPPGIQGLPGPTGIPGPIGPPGPPGLMGPPGPPGLPGPK;

(SEQ ID NO: 223)
PHIPPSDEICEPGPPGPPGSPGDK;

(SEQ ID NO: 224)
GLPGLPGPPGSLGFPGQK;

(SEQ ID NO: 225)
PKGEPGGITFK;

(SEQ ID NO: 226)
TPGRIGLEGPPGPPGFPGPK;

(SEQ ID NO: 227)
GPPGRTGLDGLPGPK;

(SEQ ID NO: 228)
APGPIGPPGSPGLPGK;

(SEQ ID NO: 229)
KGEPGLPGPPGPMDPNLLGSK;

(SEQ ID NO: 230)
PGEPGPVGGGGHPGQPGPPGEK;

(SEQ ID NO: 231)
PALEGPKGNPGPQGPPGRPGPTGFQGLPGPEGPPGLPGNGGIK;
and

(SEQ ID NO: 232)
PPGPPGLPGPSGQSIIIK,

[0100] and naturally-occurring variants of any of the foregoing.

Collagen Alpha-1(XV) Proteolytic Fragments

[0101] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-1(XV) chain, listed in sequence order, include:

(SEQ ID NO: 233)
VDGATGLPGMK;

(SEQ ID NO: 234)
KGQAGPPGVMGPPGPPGPPGPPGPGCTMGLGFED;

(SEQ ID NO: 235)
KLQLGELIPIPADSPPPP;

(SEQ ID NO: 236)
AWRTADTAVTGLASPLSTGK;
and

(SEQ ID NO: 237)
AVTGLASPLSTGKILDQK,

[0102] and naturally-occurring variants of any of the foregoing.

Collagen Alpha-3(VI) Proteolytic Fragments

[0103] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-3(VI) chain, listed in sequence order, include:

(SEQ ID NO: 238)
GVEDADEGALKEIASEPLNMHMFNLENFTSLHDIVGNLVSCVHSSVSPER;

(SEQ ID NO: 239)
NNLFTSSAGYR;

(SEQ ID NO: 240)
AAPLQGMLPGLLAPLR;
and

(SEQ ID NO: 241)
IGDLHPQIVN,

[0104] and naturally-occurring variants thereof.

Collagen Alpha-1(VI) Proteolytic Fragments

[0105] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-1(VI) chain, listed in sequence order, include:

(SEQ ID NO: 242)
GPQGDQGR;

(SEQ ID NO: 243)
TDPAHDVR;

(SEQ ID NO: 244)
FSDGNSQGATPAAIEK;

(SEQ ID NO: 245)
QVNEPHIR;
and

(SEQ ID NO: 246)
GVFHQTVSR,

[0106] and naturally-occurring variants thereof.

Collagen Alpha-1(XIX) Proteolytic Fragments

[0107] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of a Collagen alpha-1(XIX) chain, include, e.g., NPGAPGPR (SEQ ID NO:355), and naturally-occurring variants thereof.

Fibronectin

[0108] An enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of fibronectin. For example, an enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of a fibronectin polypeptide having at least about 98%, at least about 99%, or 100%, amino acid sequence identity with an amino acid sequence of a fibronectin polypeptide depicted in FIGS. **13**A-C. An enzymatic cleavage product of a fibronectin component of an arteriosclerotic plaque can be an enzymatic cleavage product of a naturally-occurring variant (polymorphism) of a fibronectin polypeptide depicted in FIGS. **13**A-C.

[0109] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of fibronectin, listed in sequence order, include:

(SEQ ID NO: 247)
GPGLLLLAVQCLGTAVPSTGASK;

(SEQ ID NO: 248)
ALVCTCYGGSR;

(SEQ ID NO: 327)
ISCTIANR;

(SEQ ID NO: 249)
MVDCTCLGEGSGR;

(SEQ ID NO: 250)
AAHEEICTTNEGVMYR;

(SEQ ID NO: 251)
SHPIQWNAPQPSHISK;

(SEQ ID NO: 252)
VVSWVSASDTVSGFR;

(SEQ ID NO: 253)
SDTVPSPRDLQFVEVTDVK;

(SEQ ID NO: 254)
VDVIPVNLPGEHGQR;

(SEQ ID NO: 255)
VFAVSHGRESKPLTAQQTTK;

(SEQ ID NO: 256)
LGVRPSQGGEAPR;

(SEQ ID NO: 257)
DAPIVNKVVTPLSPPTNLH;

(SEQ ID NO: 258)
TPDITGYR;

(SEQ ID NO: 259)
PGTEYVVSVSSVYEQHESTPLR;

(SEQ ID NO: 260)
TGLDSPTGIDFSDITANSFTVH;

(SEQ ID NO: 261)
TVHWIAPR;

(SEQ ID NO: 262)
SPVQEFTVPGSK;

(SEQ ID NO: 263)
VVSVYAQNPSGESQPLVQTAVTNIDRPK;

(SEQ ID NO: 264)
RPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLK;

(SEQ ID NO: 265)
YEVSVYALK;

(SEQ ID NO: 266)
IYLYTLNDNAR;

(SEQ ID NO: 267)
SLLVSWQPPR;

(SEQ ID NO: 268)
YEKPGSPPR;

-continued

(SEQ ID NO: 269)
TPFVTHPG;

(SEQ ID NO: 270)
TPFVTHPGYDT;

(SEQ ID NO: 271)
TPFVTHPGYDTGNGIQLPGTSGQQPSVGQQM;

(SEQ ID NO: 272)
QDTSEYIISCHPVGTDEEPLQFR;

(SEQ ID NO: 273)
VPGTSTSATLTGLTRGATYNIIVEALK;

(SEQ ID NO: 274)
VREEVVTVGN;

(SEQ ID NO: 275)
SVNEGLNQPTDDSCFDPYTVSHYAVGDEWER;
and

(SEQ ID NO: 276)
LGFGSGHFR,

[0110] and naturally-occurring variants of any of the foregoing.

Fibrillin

[0111] An enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of fibrillin, e.g., fibrillin-1. For example, an enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of a fibrillin-1 polypeptide having at least about 98%, at least about 99%, or 100%, amino acid sequence identity with an amino acid sequence of a fibrillin-1 polypeptide depicted in FIGS. **14**A-C. An enzymatic cleavage product of a fibrillin-1 component of an arteriosclerotic plaque can be an enzymatic cleavage product of a naturally-occurring variant (polymorphism) of a fibrillin-1 polypeptide depicted in FIGS. **14**A-C.

[0112] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of fibrillin, listed in sequence order, include:

(SEQ ID NO: 277)
ACEDIDECSLPNICVFGTCHNLPGLFR;

(SEQ ID NO: 278)
TGLPVDIDECR;

(SEQ ID NO: 279)
PVDIDECR;

(SEQ ID NO: 280)
EIPGVCNGVCINHVGSFR;

(SEQ ID NO: 281)
EIPGVCENGVCINMVGSFR;

(SEQ ID NO: 282)
LLVCEDIDECQNGPVCQR;

(SEQ ID NO: 283)
TCVDINECLLEPR;

(SEQ ID NO: 284)
GEGWGDPCELCPTEPDEAFR,
and

[0113] and naturally-occurring variants thereof.

Vitronectin

[0114] An enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of vitronectin. For example, an enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of a vitronectin polypeptide having at least about 98%, at least about 99%, or 100%, amino acid sequence identity with an amino acid sequence of a vitronectin polypeptide depicted in FIG. **21**. An enzymatic cleavage product of a vitronectin component of an arteriosclerotic plaque can be an enzymatic cleavage product of a naturally-occurring variant (polymorphism) of a vitronectin polypeptide depicted in FIG. **21**.

[0115] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of vitronectin, listed in sequence order, include:

(SEQ ID NO: 285)
CTDYTAECKPQVTR;

(SEQ ID NO: 286)
IYISGMAPRPS;

(SEQ ID NO: 287)
TCEPIQSVFFFSGDK;

(SEQ ID NO: 288)
SIAQYWLGCPAPGH;
and

(SEQ ID NO: 289)
WLGCPAPGHL,

[0116] and naturally-occurring variants of any of the foregoing.

Metalloproteinase Inhibitor-1

[0117] An enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of metalloproteinase inhibitor-1. For example, an enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of a metalloproteinase inhibitor-1polypeptide having at least about 98%, at least about 99%, or 100%, amino acid sequence identity with an amino acid sequence of a metalloproteinase inhibitor-1polypeptide depicted in FIG. **16**. An enzymatic cleavage product of a metalloproteinase inhibitor-1component of an arteriosclerotic plaque can be an enzymatic cleavage product of a naturally-occurring variant (polymorphism) of a metalloproteinase inhibitor-1polypeptide depicted in FIG. **16**.

[0118] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of metalloproteinase inhibitor-1, listed in sequence order, include:

(SEQ ID NO: 290)
CNSDLVIR;

(SEQ ID NO: 291)
LQDGLLHITTC;
and

(SEQ ID NO: 292)
SFVAPWNSLSLAQR,

[0119] and naturally-occurring variants of any of the foregoing.

Dermatopontin

[0120] An enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of dermatopontin. For example, an enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of a dermatopontin polypeptide having at least about 98%, at least about 99%, or 100%, amino acid sequence identity with an amino acid sequence of a dermatopontin polypeptide depicted in FIG. **15**. An enzymatic cleavage product of a dermatopontin component of an arteriosclerotic plaque can be an enzymatic cleavage product of a naturally-occurring variant (polymorphism) of a dermatopontin polypeptide depicted in FIG. **15**.

[0121] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of dermatopontin, listed in sequence order, include:

(SEQ ID NO: 293)
SDDGWVNLNR;

(SEQ ID NO: 294)
SYQCPQGQVIVAVR;

(SEQ ID NO: 295)
SLGEPTECWWEEINR;
and

(SEQ ID NO: 296)
SNNGLVAGFQSR,

[0122] and naturally-occurring variants of any of the foregoing.

Galectin-1

[0123] An enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of galectin-1. For example, an enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of a galectin-1 polypeptide having at least about 98%, at least about 99%, or 100%, amino acid sequence identity with an amino acid sequence of a galectin-1 polypeptide depicted in FIG. **17**. An enzymatic cleavage product of a galectin-1 component of an arteriosclerotic plaque can be an enzymatic cleavage product of a naturally-occurring variant (polymorphism) of a galectin-1 polypeptide depicted in FIG. **17**.

[0124] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of galectin-1, listed in sequence order, include:

(SEQ ID NO: 297)
VASNLNLKPGECLR;

(SEQ ID NO: 298)
GDANTIVCNSK;
and

(SEQ ID NO: 299)
MAADGDFK,

[0125] and naturally-occurring variants of any of the foregoing.

Lumican

[0126] An enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of lumican. For example, an enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of a lumican polypeptide having at least about 98%, at least about 99%, or 100%, amino acid sequence identity with an amino acid sequence of a lumican polypeptide depicted in FIG. **18**. An enzymatic cleavage product of a lumican component of an arteriosclerotic plaque can be an enzymatic cleavage product of a naturally-occurring variant (polymorphism) of a lumican polypeptide depicted in FIG. **18**. In some cases, an enzymatic cleavage product of lumican is specifically excluded.

[0127] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of lumican, listed in sequence order, include:

(SEQ ID NO: 300)
CAPECNCPESYPSAMYCDELK;

(SEQ ID NO: 301)
RNNQIDHIDEK;

(SEQ ID NO: 302)
NNQIDHIDE;

(SEQ ID NO: 303)
ILDHNLLENSK;

(SEQ ID NO: 304)
SLEDLQLTH;

(SEQ ID NO: 305)
IHLQHNR;
and

(SEQ ID NO: 306)
CKILGPLSYSK,

[0128] and naturally-occurring variants of any of the foregoing.

Prolargin

[0129] An enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of prolargin. For example, an enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of a prolargin polypeptide having at least about 98%, at least about 99%, or 100%, amino acid sequence identity with an amino acid sequence of a prolargin polypeptide depicted in FIG. **19**. An enzymatic cleavage product of a prolargin component of an arteriosclerotic plaque can be an enzymatic cleavage product of a naturally-occurring variant (polymorphism) of a prolargin polypeptide depicted in FIG. **19**.

[0130] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of prolargin, listed in sequence order, include:

(SEQ ID NO: 307)
EVPSALPR;

(SEQ ID NO: 308)
RLSQNHISR;

-continued

(SEQ ID NO: 309)
RLSQNHISRIPPGVFSK;

(SEQ ID NO: 310)
LSDGVFKPDT;

(SEQ ID NO: 311)
NLAHNILR;

(SEQ ID NO: 312)
LAHNILR;

(SEQ ID NO: 313)
LDSNKIETIPNGYFKSFPNLAFIR;

(SEQ ID NO: 314)
IETIPNGYFKSFPNLA;

(SEQ ID NO: 315)
SFPNLAFIRLNYN;

(SEQ ID NO: 316)
LNNNSIEK;
and

(SEQ ID NO: 317)
DLVAFHDFSSDLENVPHLR,

[0131] and naturally-occurring variants of any of the foregoing.

Tenascin

[0132] An enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of tenascin. For example, an enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of a tenascin polypeptide having at least about 98%, at least about 99%, or 100%, amino acid sequence identity with an amino acid sequence of a tenascin polypeptide depicted in FIGS. **20**A and **20**B. An enzymatic cleavage product of a tenascin component of an arteriosclerotic plaque can be an enzymatic cleavage product of a naturally-occurring variant (polymorphism) of a tenascin polypeptide depicted in FIGS. **20**A and **20**B.

[0133] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of tenascin, listed in sequence order, include:

(SEQ ID NO: 318)
ELEPGVEYFIR;

(SEQ ID NO: 319)
TVSIYGVIQGYR;

(SEQ ID NO: 320)
TVTLHGEVR;
and

(SEQ ID NO: 321)
FRITYVPITGGTPSMVTVDGTK,

[0134] and naturally-occurring variants of any of the foregoing.

Tenascin-X

[0135] An enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of tenascin-X. For example, an enzymatic cleavage product of a structural component of an arteriosclerotic plaque includes an enzymatic cleavage product of a tenascin-X polypeptide having at least about 98%, at least about 99%, or 100%, amino acid sequence identity with an amino acid sequence of a tenascin-X polypeptide depicted in FIGS. **22**A-D. An enzymatic cleavage product of a tenascin-X component of an arteriosclerotic plaque can be an enzymatic cleavage product of a naturally-occurring variant (polymorphism) of a tenascin-X polypeptide depicted in FIGS. **22**A-D.

[0136] Non-limiting examples of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) of tenascin-X, listed in sequence order, include:

(SEQ ID NO: 322)
WRPQPPAEGPGGELTVPGTTRTVS;

(SEQ ID NO: 323)
FDSFTVQYK;

(SEQ ID NO: 324)
GEESEVTVGGLEPGR;

(SEQ ID NO: 325)
EPPNKPR;
and

(SEQ ID NO: 326)
GFEESEPLTGFLTTVPDGPTQ,

[0137] and naturally-occurring variants of any of the foregoing.

[0138] In some embodiments, any one or more of the above-listed fragments is specifically excluded.

Panels

[0139] The present disclosure provides a panel of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature). The panel can include 2, 3, 4, 5, 6, 7, 8, 9, 10, 10-15, 15-20, 20-25, 25-30, 30-35, 35-40, 40-45, 45-50, or more than 50, of the above-described enzymatic cleavage products. Thus, the panel can include 2, 3, 4, 5, 6, 7, 8, 9, 10, 10-15, 15-20, 20-25, 25-30, 30-35, 35-40, 40-45, 45-50, or more than 50, different enzymatic cleavage products (peptides), selected from the above-described enzymatic cleavage products. Enzymatic cleavage products in the panel can be purified.

[0140] As one non-limiting example, a subject peptide panel includes:

[0141] 1) one or more fibrillin fragments selected from:

(SEQ ID NO: 277)
ACEDIDECSLPNICVFGTCHNLPGLFR;

(SEQ ID NO: 278)
TGLPVDIDECR;

(SEQ ID NO: 279)
PVDIDECR;

(SEQ ID NO: 280)
EIPGVCNGVCINHVGSFR;

(SEQ ID NO: 281)
EIPGVCENGVCINMVGSFR;

-continued

(SEQ ID NO: 282)
LLVCEDIDECQNGPVCQR;

(SEQ ID NO: 283)
TCVDINECLLEPR;

(SEQ ID NO: 284)
GEGWGDPCELCPTEPDEAFR;
and

[0142] and naturally-occurring variants thereof;

[0143] 2) one or more vitronectin fragments selected from:

(SEQ ID NO: 285)
CTDYTAECKPQVTR;

(SEQ ID NO: 286)
IYISGMAPRPS;

(SEQ ID NO: 287)
TCEPIQSVFFFSGDK;

(SEQ ID NO: 288)
SIAQYWLGCPAPGH;
and

(SEQ ID NO: 289)
WLGCPAPGHL,

[0144] and naturally-occurring variants of any of the foregoing;

[0145] 3) one or more fibronectin fragments selected from:

(SEQ ID NO: 247)
GPGLLLLAVQCLGTAVPSTGASK;

(SEQ ID NO: 248)
ALVCTCYGGSR;

(SEQ ID NO: 327)
ISCTIANR;

(SEQ ID NO: 249)
MVDCTCLGEGSGR;

(SEQ ID NO: 250)
AAHEEICTTNEGVMYR;

(SEQ ID NO: 251)
SHPIQWNAPQPSHISK;

(SEQ ID NO: 252)
VVSWVSASDTVSGFR;

(SEQ ID NO: 253)
SDTVPSPRDLQFVEVTDVK;

(SEQ ID NO: 254)
VDVIPVNLPGEHGQR;

(SEQ ID NO: 255)
VFAVSHGRESKPLTAQQTTK;

(SEQ ID NO: 256)
LGVRPSQGGEAPR;

(SEQ ID NO: 257)
DAPIVNKVVTPLSPPTNLH;

(SEQ ID NO: 258)
TPDITGYR;

-continued

(SEQ ID NO: 259)
PGTEYVVSVSSVYEQHESTPLR;

(SEQ ID NO: 260)
TGLDSPTGIDFSDITANSFTVH;

(SEQ ID NO: 261)
TVHWIAPR;

(SEQ ID NO: 262)
SPVQEFTVPGSK;

(SEQ ID NO: 263)
VVSVYAQNPSGESQPLVQTAVTNIDRPK;

(SEQ ID NO: 264)
RPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLK;

(SEQ ID NO: 265)
YEVSVYALK;

(SEQ ID NO: 266)
IYLYTLNDNAR;

(SEQ ID NO: 267)
SLLVSWQPPR;

(SEQ ID NO: 268)
YEKPGSPPR;

(SEQ ID NO: 269)
TPFVTHPG;

(SEQ ID NO: 270)
TPFVTHPGYDT;

(SEQ ID NO: 271)
TPFVTHPGYDTGNGIQLPGTSGQQPSVGQQM;

(SEQ ID NO: 272)
QDTSEYIISCHPVGTDEEPLQFR;

(SEQ ID NO: 273)
VPGTSTSATLTGLTRGATYNIIVEALK;

(SEQ ID NO: 274)
VREEVVTVGN;

(SEQ ID NO: 275)
SVNEGLNQPTDDSCFDPYTVSHYAVGDEWER;
and

(SEQ ID NO: 276)
LGFGSGHFR,

[0146] and naturally-occurring variants of any of the foregoing.

[0147] A subject panel can further include:

[0148] 4) one or more tenascin peptides selected from:

(SEQ ID NO: 318)
ELEPGVEYFIR;

(SEQ ID NO: 319)
TVSIYGVIQGYR;

(SEQ ID NO: 320)
TVTLHGEVR;
and

(SEQ ID NO: 321)
FRITYVPITGGTPSMVTVDGTK,

[0149] and naturally-occurring variants of any of the foregoing;

[0150] 5) one or more prolargin peptides selected from:

(SEQ ID NO: 307)
EVPSALPR;

(SEQ ID NO: 308)
RLSQNHISR;

(SEQ ID NO: 309)
RLSQNHISRIPPGVFSK;

(SEQ ID NO: 310)
LSDGVFKPDT;

(SEQ ID NO: 311)
NLAHNILR;

(SEQ ID NO: 312)
LAHNILR;

(SEQ ID NO: 313)
LDSNKIETIPNGYFKSFPNLAFIR;

(SEQ ID NO: 314)
IETIPNGYFKSFPNLA;

(SEQ ID NO: 315)
SFPNLAFIRLNYN;

(SEQ ID NO: 316)
LNNNSIEK;
and

(SEQ ID NO: 317)
DLVAFHDFSSDLENVPHLR,

[0151] and naturally-occurring variants of any of the foregoing; and

[0152] 6) one or more dermatopontin peptides selected from:

(SEQ ID NO: 293)
SDDGWVNLNR;

(SEQ ID NO: 294)
SYQCPQGQVIVAVR;

(SEQ ID NO: 295)
SLGEPTECWWEEINR;
and

(SEQ ID NO: 296)
SNNGLVAGFQSR,

[0153] and naturally-occurring variants of any of the foregoing.

[0154] A subject method can involve detecting peptides present in a subject panel. In some embodiments, a subject panel can serve as a control.

[0155] In some embodiments, the enzymatic cleavage products of a subject panel are immobilized on an insoluble support. In some embodiments, the enzymatic cleavage products of a subject panel are detectably labeled.

Further Processing In Vitro

[0156] In some cases, an enzymatic cleavage product generated in the vasculature (e.g., in vivo) is further processed in vitro. In vitro processing of an in vivo-generated enzymatic cleavage product can include enzymatic digestion in vitro. Thus, in some cases, an enzymatic cleavage product generated in the vasculature (e.g., in vivo) is further cleaved enzymatically, e.g., in vitro. Such in vitro cleavage of a cleavage product produced in vivo may be undertaken in order to characterize an in vivo-generated cleavage product. As an example, an enzymatic cleavage product of a structural component of an unstable arteriosclerotic plaque, generated by an enzyme produced by an inflammatory cell in the vasculature, may be subjected to trypsin digestion or other enzymatic digestion in vitro before the cleavage product is analyzed by mass spectrometry (MS). In vitro enzymatic cleavage can include trypsinization.

[0157] Non-limiting examples of trypsin cleavage products of an enzymatic cleavage products of a collagen alpha-1 (VI) component of an arteriosclerotic plaque include:

1)
(SEQ ID NO: 328)
LFSDGNSQGATPAAIEKA;

2)
(SEQ ID NO: 329)
RGVFHQTVSRK;

3)
(SEQ ID NO: 330)
RQVNEPHIRV;
and

4)
(SEQ ID NO: 331)
RTDPAHDVRV,

[0158] and naturally-occurring variants of any of the foregoing.

[0159] A non-limiting example of enzymatic cleavage products of a collagen alpha-3(VI) component of an arteriosclerotic plaque include: IGDLHPQIVN (SEQ ID NO:241).

[0160] Non-limiting examples of enzymatic cleavage products of fibronectin include, e.g.:

1)
(SEQ ID NO: 332)
DAPIVNK;

2)
(SEQ ID NO: 333)
SEPLIGR;

3)
(SEQ ID NO: 334)
ATITGYR;

4)
(SEQ ID NO: 335)
AQITGYR;

5)
(SEQ ID NO: 336)
SDTVPSPR;

6)
(SEQ ID NO: 337)
VFAVSHGR;

7)
(SEQ ID NO: 338)
ISCTIANRC;

8)
(SEQ ID NO: 339)
PLTAQQTTK;

9)
(SEQ ID NO: 340)
YEVSVYALK;

-continued

10)
(SEQ ID NO: 341)
QYNVGPSVSK;

11)
(SEQ ID NO: 342)
GATYNIIVEALK;

12)
(SEQ ID NO: 343)
DLQFVEVTDVK;

13)
(SEQ ID NO: 344)
LGVRPSQGGEAPR;

14)
(SEQ ID NO: 345)
IYLYTLNDNAR;

15)
(SEQ ID NO: 346)
VPGTSTSATLTGLTR;
and

16)
(SEQ ID NO: 347)
VDVIPVNLPGEHGQR,

[0161] and naturally-occurring variants thereof.

[0162] Non-limiting examples of enzymatic cleavage products of fibrillin-1 include, e.g.:

1)
(SEQ ID NO: 348)
KACEDIDECSLPNICVFGTCHNLPGLFRC;

2)
(SEQ ID NO: 349)
YTGLPVDIDECRE;

3)
(SEQ ID NO: 350)
LPVDIDECRE;

4)
(SEQ ID NO: 351)
REIPGVCENGVCINMVGSFRC;

5)
(SEQ ID NO: 352)
KLLVCEDIDECQNGPVCQRN;

6)
(SEQ ID NO: 353)
RTCVDINECLLEPRK;
and

7)
(SEQ ID NO: 354)
KGEGWGDPCELCPTEPDEAFRQ,

[0163] and naturally-occurring variants thereof.

Detection Methods

[0164] An enzymatic cleavage product of a protein component of an arteriosclerotic plaque can be detected using any known method, where suitable methods include, e.g., immunological methods, gel electrophoresis methods, chromatographic methods, and mass spectrometric methods.

Immunological Methods

[0165] Suitable immunological methods include, e.g., enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and an immunofixation assay. Immunological assays involve use of antibody specific for an enzymatic cleavage product of a protein component of an arteriosclerotic plaque. In some instances, the primary antibody used an immunological assay is an antibody specific for an epitope that is exposed upon cleavage of a protein component of an arteriosclerotic plaque, e.g., an epitope that is not accessible to the antibody in the protein in its uncleaved state. For example, an immunological assay can involve use of antibody specific for an epitope that is exposed upon cleavage of a protein component of an arteriosclerotic plaque, e.g., an epitope comprising the newly-formed carboxyl-terminus or amino-terminus of an enzymatic cleavage product of a protein component of an arteriosclerotic plaque. For example, an enzyme(s) produced by an inflammatory cell in the vasculature can proteolytically cleave a protein component of an arteriosclerotic plaque; and the cleavage product would then present epitope(s) (e.g., linear epitopes; conformational epitopes) not presented by the uncleaved protein component, where such epitopes could include the C-terminal amino acids of the cleavage product, or the N-terminal amino acids of the cleavage product.

[0166] In some instances, the antibody used in an immunological assay is immobilized on an insoluble (e.g., a solid) support. Suitable supports are well known in the art and comprise, inter alia, commercially available column materials, polystyrene beads, latex beads, magnetic beads, colloid metal particles, glass and/or silicon chips and surfaces, nitrocellulose strips, nylon membranes, sheets, duracytes, wells of reaction trays (e.g., multi-well plates), test strips, plastic tubes, etc. A solid support can comprise any of a variety of substances, including, e.g., glass, polystyrene, polyvinyl chloride, polypropylene, polyethylene, polycarbonate, dextran, nylon, amylose, natural and modified celluloses, polyacrylamides, agaroses, and magnetite. Suitable methods for immobilizing an antibody onto a solid support are well known and include, but are not limited to ionic, hydrophobic, covalent interactions and the like. Solid supports can be soluble or insoluble, e.g., in aqueous solution. In some embodiments, a suitable solid support is generally insoluble in an aqueous solution.

[0167] In some instances, antibody used in an immunological assay comprises a detectable label. Suitable detectable labels include any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Suitable include, but are not limited to, magnetic beads (e.g. Dynabeads™), fluorescent dyes (e.g., fluorescein isothiocyanate, texas red, rhodamine, a green fluorescent protein, a red fluorescent protein, a yellow fluorescent protein, and the like), radiolabels (e.g., ^{3}H, ^{125}I, ^{35}S, ^{14}C, or ^{32}P), enzymes (e.g., horse radish peroxidase, alkaline phosphatase, luciferase, and others commonly used in an enzyme-linked immunosorbent assay (ELISA)), and colorimetric labels such as colloidal gold or colored glass or plastic (e.g. multistyrene, multipropylene, latex, etc.) beads.

Mass Spectrometric Methods

[0168] In some cases, a detection method provides size information about an enzymatic cleavage product. Detection methods that provide size information include, e.g., gel electrophoresis methods, and the like. In some cases, a detection method provides size information about an enzymatic cleavage product; and also involves use of an antibody specific for the enzymatic cleavage product.

[0169] In some instances, identification of cleavage products is carried out using mass spectrometry. For example, as discussed above, an in vivo-generated enzymatic cleavage product can be subjected to enzymatic digestion in vitro using a specific protease (e.g. trypsin), followed by detection and/or quantitation, of specific peptide products of the in vivo-generated enzymatic cleavage product. Mass spectrometric detection approaches include detection of peptide masses, detection of masses of fragments formed in the mass spectrometer, or a combination of the foregoing (e.g. Selective Reaction Monitoring).

Controls

[0170] Levels of an enzymatic cleavage product of a protein component of an arteriosclerotic plaque present in a biological sample obtained from a test subject are compared to a normal control value(s) or range of normal control values. The control value can be based on levels of the enzymatic cleavage product in comparable samples (e.g., blood, plasma, or serum sample, or other biological sample) obtained from a control population, e.g., the general population or a select population of human subjects. For example, the select population may be comprised of apparently healthy subjects, e.g., individuals who have not previously had any signs or symptoms of cardiovascular disease. Apparently healthy individuals also generally do not otherwise exhibit symptoms of disease. In other words, such individuals, if examined by a medical professional, would be characterized as healthy and free of symptoms of disease.

[0171] The control value can take a variety of forms. The control value can be a single cut-off value, such as a median or mean. A normal control value can be a normal control range. The control value can be established based on comparative groups such as where the risk in one defined group is double the risk in another defined group. The control values can be divided equally (or unequally) into groups, such as a low risk group, a medium risk group and a high-risk group, or into quadrants, the lowest quadrant being individuals with the lowest risk the highest quadrant being individuals with the highest risk, and the test subject's risk of having CVD can be based upon which group his or her test value falls.

Biological Samples

[0172] Suitable biological samples useful for predicting or monitoring cardiovascular disease in a subject or for assessing the effect of therapeutic agents on subjects with cardiovascular disease include, but are not limited to, whole blood samples, and blood fractions (also referred to as "blood products"), where suitable blood fractions include, but are not limited to, serum and plasma. The biological sample can be fresh blood or stored blood (e.g. in a blood bank) or blood fractions. The biological sample can be a blood sample expressly obtained for an assay of the present disclosure or a blood sample obtained for another purpose which can be subsampled for an assay of the present disclosure. A suitable biological sample can also be a biological sample obtained via catheter during or as a result of coronary angiogram. A suitable biological sample can also be a biological sample obtained during catheterization of a carotid artery.

[0173] In one embodiment, the biological sample is whole blood. Whole blood can be obtained from the subject using standard clinical procedures. In another embodiment, the biological sample is plasma. Plasma can be obtained from whole blood samples by centrifugation of anti-coagulated blood. Such process provides a buffy coat of white cell components and a supernatant of the plasma. In another embodiment, the biological sample is serum.

[0174] The sample can be pretreated as necessary by dilution in an appropriate buffer solution, heparinized, concentrated if desired, or fractionated by any number of methods including but not limited to ultracentrifugation, fractionation by fast performance liquid chromatography (FPLC), or precipitation. Any of a number of standard aqueous buffer solutions, employing one of a variety of buffers, such as phosphate, Tris, or the like, at physiological pH can be used.

Subjects

[0175] Subjects to be tested using a method of the present disclosure include individuals who have experienced one or more typical symptoms of cardiovascular disease; individuals who have experienced an atypical symptom of cardiovascular disease; smokers; non-smokers; individuals who have a body mass index greater than about 25 kg/m^2, or greater than about 30 kg/m^2; individuals aged 50 years or older; and apparently healthy individuals. An individual can be male or female. In some instances, the individual is a female who has experienced an atypical symptom of cardiovascular disease, e.g., a symptom not normally associated with cardiovascular disease. In some instances, the individual has a disorder or disease involving a pathological process that pre-disposes the individual to a vascular occlusive event, where such predisposing diseases include, but are not limited to, systemic lupus erythematosus. In some instances, the individual does not have a history of having an occlusive vascular event.

[0176] In some cases, the individual has a disorder of lipid metabolism that can lead to plaque formation, where such disorders include, e.g., familial hypercholesterolemia; familial combined hyperlipidemia; high-density lipoprotein (HDL) deficiency; and other primary and secondary causes of dyslipidemia.

Methods of Assessing Risk of an Occlusive Vascular Event

[0177] The present disclosure provides methods of determining a risk that an individual will develop an occlusive vascular event. The methods generally involve determining the level, in a biological sample from the individual, of an in vivo-generated enzymatic cleavage product of a protein component of an arteriosclerotic plaque. A level of the enzymatic cleavage product that is higher than a normal control level indicates risk of developing or experiencing an occlusive vascular event.

[0178] In some embodiments, a subject method for determining a risk that an individual will develop an occlusive vascular event comprises: a) assaying the level, in a biological sample from the individual, of an enzymatic cleavage product of a protein component of an arteriosclerotic plaque; and b) identifying the individual as being at risk of developing an occlusive vascular event when the level of the enzymatic cleavage product is higher than a normal control level. In some cases, as discussed below, a subject method for determining a risk that an individual will develop an occlusive vascular event further comprises outputting a report indicating a risk assessment based on said identifying to facilitate a treatment decision by a clinician.

[0179] Individuals to be subjected to a risk assessment method of the present disclosure include individuals who have experienced one or more typical symptoms of cardiovascular disease; individuals who have experienced an atypical symptom of cardiovascular disease; smokers; non-smokers; individuals who have a body mass index greater than about 25 kg/m^2, or greater than about 30 kg/m^2; individuals aged 50 years and older; and apparently healthy individuals. An individual can be male or female. In some instances, the individual is a female who has experienced an atypical symptom of cardiovascular disease, e.g., a symptom not normally associated with cardiovascular disease. In some instances, the individual is not otherwise known to be at an elevated risk of having an occlusive vascular event. In some instances, the individual does not have a history of having an occlusive vascular event. In some instances, the individual has a disease or disorder that predisposes the individual to having an occlusive vascular event. In some cases, the individual has a disorder of lipid metabolism that can lead to plaque formation, where such disorders include, e.g., familial hypercholesterolemia; familial combined hyperlipidemia; high-density lipoprotein (HDL) deficiency; and other primary and secondary causes of dyslipidemia.

[0180] Suitable biological samples are as described above, and include, but are not limited to, blood; a blood product, such as serum or plasma; a biological sample obtained from a catheter during or as a result of coronary angiogram; and biological samples obtained during catheterization of a carotid artery.

[0181] Enzymatic cleavage products of a protein component of an arteriosclerotic plaque, and suitable methods of detecting same, are as described above. Suitable normal controls are as described above.

[0182] Occlusive vascular disease events include, but are not limited to, peripheral artery disease, arterial thrombosis, arterial occlusion, occlusive coronary arteriosclerosis, etc.

Generating a Report

[0183] In some embodiments, a subject method of determining a risk that an individual will develop an occlusive vascular event further involves generating a report. Such a report can include information such as a predicted risk that the patient will experience an occlusive vascular event; a recommendation regarding further evaluation; a recommendation regarding therapeutic drug and/or device intervention; and the like.

[0184] For example, the methods disclosed herein can further include a step of generating or outputting a report providing the results of a subject risk assessment, which report can be provided in the form of an electronic medium (e.g., an electronic display on a computer monitor), or in the form of a tangible medium (e.g., a report printed on paper or other tangible medium). An assessment as to the likelihood can be referred to as a "risk report" or, simply, "risk score." A person or entity that prepares a report ("report generator") may also perform steps such as sample gathering, sample processing, and the like. Alternatively, an entity other than the report generator can perform steps such as sample gathering, sample processing, and the like. A risk assessment report can be provided to a user. A "user" can be a health professional (e.g., a clinician, a laboratory technician, a physician (e.g., a cardiologist), etc.).

Further Evaluation

[0185] Based on detection an enzymatic cleavage product of a protein component of an arteriosclerotic plaque, and/or based on a report (as described above), a physician or other qualified medical personnel can determine whether further evaluation of the test subject (the patient) is required. Further evaluation can include, e.g., angiogram; electrocardiogram; an echocardiogram; a test for blood (or blood product, such as plasma or serum) triglyceride levels; a test for blood (or blood product, such as plasma or serum) low density lipoprotein levels; a test for blood (or blood product, such as plasma or serum) high density lipoprotein levels; and the like.

Therapeutic Intervention

[0186] Based on detection of an enzymatic cleavage product of a protein component of an arteriosclerotic plaque, and/or based on a report (as described above), a physician or other qualified medical personnel can determine whether appropriate therapeutic intervention is advised, e.g., in order to reduce the risk that an occlusive vascular event will actually occur. Thus, in some embodiments, a subject method comprises detecting an unstable arteriosclerotic plaque in an individual (where the detection method comprises detecting in a biological sample from the individual an enzymatic cleavage product of a protein component of an arteriosclerotic plaque); and administering to the individual a therapeutic intervention for reducing an arteriosclerotic plaque.

[0187] Therapeutic intervention includes drug-based therapeutic intervention, device-based therapeutic intervention, and surgical intervention. Drug-based therapeutic intervention includes, an anti-inflammatory agent, an antithrombotic agent, an anti-platelet agent, a fibrinolytic agent, a lipid reducing agent, a direct thrombin inhibitor, a glycoprotein IIb/IIIa receptor inhibitor, an agent that binds to cellular adhesion molecules and inhibits the ability of white blood cells to attach to such molecules, a calcium channel blocker, a beta-adrenergic receptor blocker, a cyclooxygenase-2 inhibitor, and an angiotensin system inhibitor.

[0188] Device-based therapeutic intervention includes, e.g., installation of an intravascular stent; balloon angioplasty; and the like. Surgical intervention includes, e.g., arterial bypass surgery.

Kits and Assay Devices

[0189] The present disclosure provides a kit for carrying out a method of the present disclosure, e.g., a method of detecting, in a biological sample obtained from an individual, an enzymatic cleavage product of a protein component of an arteriosclerotic plaque. The present disclosure further provides an assay device for carrying out a method of the present disclosure, e.g., a method of detecting, in a biological sample obtained from an individual, an enzymatic cleavage product of a protein component of an arteriosclerotic plaque.

Kits

[0190] A subject kit can include: a) a binding reagent that specifically binds an enzymatic cleavage product of a protein component of an arteriosclerotic plaque; and b) a control that provides for quantitation of the enzymatic cleavage product.

[0191] In some embodiments, a subject kit includes standard enzymatic cleavage products of a protein component of an arteriosclerotic plaque, where the enzymatic cleavage product is of greater than 90% purity, greater than 95% purity, greater than 98% purity, or greater than 99% purity. The standard enzymatic cleavage product can be prepared synthetically, e.g., by incubating a protein component of an arteriosclerotic plaque with an enzyme (e.g., an enzyme that is secreted by an inflammatory cell, as described above); and isolating a fragment that corresponds to a fragment that is produced by an unstable arteriosclerotic plaque. The standard enzymatic cleavage product can be prepared synthetically, e.g., using standard chemical methods for peptide synthesis. Thus, in some embodiments, a subject kit includes purified enzymatic cleavage products of a protein component of an arteriosclerotic plaque, where the purified enzymatic cleavage products are suitable for generating a standard curve, e.g., for quantitating an enzymatic cleavage product of a protein component of an arteriosclerotic plaque detected in a test biological sample from a test individual.

[0192] In some embodiments, a subject kit includes a panel of purified enzymatic cleavage products of a protein component of an arteriosclerotic plaque, where the purified enzymatic cleavage products are suitable for generating a standard curve, e.g., for quantitating an enzymatic cleavage product of a protein component of an arteriosclerotic plaque detected in a test biological sample from a test individual.

[0193] A panel of enzymatic cleavage products (enzymatic cleavage products generated by an enzyme produced by a cell (e.g., an inflammatory cell) in the vasculature) suitable for inclusion in a subject kit can include 2, 3, 4, 5, 6, 7, 8, 9, 10, 10-15, 15-20, 20-25, 25-30, 30-35, 35-40, 40-45, 45-50, or more than 50, of the above-described enzymatic cleavage products.

[0194] As one non-limiting example, a suitable peptide panel includes:

[0195] 1) one or more fibrillin fragments selected from:

(SEQ ID NO: 277)
ACEDIDECSLPNICVFGTCHNLPGLFR;

(SEQ ID NO: 278)
TGLPVDIDECR;

(SEQ ID NO: 279)
PVDIDECR;

(SEQ ID NO: 280)
EIPGVCNGVCINHVGSFR;

(SEQ ID NO: 281)
EIPGVCENGVCINMVGSFR;

(SEQ ID NO: 282)
LLVCEDIDECQNGPVCQR;

(SEQ ID NO: 283)
TCVDINECLLEPR;

(SEQ ID NO: 284)
GEGWGDPCELCPTEPDEAFR;
and

[0196] and naturally-occurring variants thereof;

[0197] 2) one or more vitronectin fragments selected from:

(SEQ ID NO: 285)
CTDYTAECKPQVTR;

(SEQ ID NO: 286)
IYISGMAPRPS;

(SEQ ID NO: 287)
TCEPIQSVFFFSGDK;

-continued

(SEQ ID NO: 288)
SIAQYWLGCPAPGH;
and

(SEQ ID NO: 289)
WLGCPAPGHL,

[0198] and naturally-occurring variants of any of the foregoing;

[0199] 3) one or more fibronectin fragments selected from:

(SEQ ID NO: 247)
GPGLLLLAVQCLGTAVPSTGASK;

(SEQ ID NO: 248)
ALVCTCYGGSR;

(SEQ ID NO: 327)
ISCTIANR;

(SEQ ID NO: 249)
MVDCTCLGEGSGR;

(SEQ ID NO: 250)
AAHEEICTTNEGVMYR;

(SEQ ID NO: 251)
SHPIQWNAPQPSHISK;

(SEQ ID NO: 252)
VVSWVSASDTVSGFR;

(SEQ ID NO: 253)
SDTVPSPRDLQFVEVTDVK;

(SEQ ID NO: 254)
VDVIPVNLPGEHGQR;

(SEQ ID NO: 255)
VFAVSHGRESKPLTAQQTTK;

(SEQ ID NO: 256)
LGVRPSQGGEAPR;

(SEQ ID NO: 257)
DAPIVNKVVTPLSPPTNLH;

(SEQ ID NO: 258)
TPDITGYR;

(SEQ ID NO: 259)
PGTEYVVSVSSVYEQHESTPLR;

(SEQ ID NO: 260)
TGLDSPTGIDFSDITANSFTVH;

(SEQ ID NO: 261)
TVHWIAPR;

(SEQ ID NO: 262)
SPVQEFTVPGSK;

(SEQ ID NO: 263)
VVSVYAQNPSGESQPLVQTAVTNIDRPK;

(SEQ ID NO: 264)
RPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLK;

(SEQ ID NO: 265)
YEVSVYALK;

(SEQ ID NO: 266)
IYLYTLNDNAR;

(SEQ ID NO: 267)
SLLVSWQPPR;

-continued

(SEQ ID NO: 268)
YEKPGSPPR;

(SEQ ID NO: 269)
TPFVTHPG;

(SEQ ID NO: 270)
TPFVTHPGYDT;

(SEQ ID NO: 271)
TPFVTHPGYDTGNGIQLPGTSGQQPSVGQQM;

(SEQ ID NO: 272)
QDTSEYIISCHPVGTDEEPLQFR;

(SEQ ID NO: 273)
VPGTSTSATLTGLTRGATYNIIVEALK;

(SEQ ID NO: 274)
VREEVVTVGN;

(SEQ ID NO: 275)
SVNEGLNQPTDDSCFDPYTVSHYAVGDEWER;
and

(SEQ ID NO: 276)
LGFGSGHFR,

[0200] and naturally-occurring variants of any of the foregoing.

[0201] A subject panel can further include:

[0202] 4) one or more tenascin peptides selected from:

(SEQ ID NO: 318)
ELEPGVEYFIR;

(SEQ ID NO: 319)
TVSIYGVIQGYR;

(SEQ ID NO: 320)
TVTLHGEVR;
and

(SEQ ID NO: 321)
FRITYVPITGGTPSMVTVDGTK,

[0203] and naturally-occurring variants of any of the foregoing;

[0204] 5) one or more prolargin peptides selected from:

(SEQ ID NO: 307)
EVPSALPR;

(SEQ ID NO: 308)
RLSQNHISR;

(SEQ ID NO: 309)
RLSQNHISRIPPGVFSK;

(SEQ ID NO: 310)
LSDGVFKPDT;

(SEQ ID NO: 311)
NLAHNILR;

(SEQ ID NO: 312)
LAHNILR;

(SEQ ID NO: 313)
LDSNKIETIPNGYFKSFPNLAFIR;

-continued

(SEQ ID NO: 314)
IETIPNGYFKSFPNLA;

(SEQ ID NO: 315)
SFPNLAFIRLNYN;

(SEQ ID NO: 316)
LNNNSIEK;
and

(SEQ ID NO: 317)
DLVAFHDFSSDLENVPHLR,

[0205] and naturally-occurring variants of any of the foregoing; and

[0206] 6) one or more dermatopontin peptides selected from:

(SEQ ID NO: 293)
SDDGWVNLNR;

(SEQ ID NO: 294)
SYQCPQGQVIVAVR;

(SEQ ID NO: 295)
SLGEPTECWWEEINR;
and

(SEQ ID NO: 296)
SNNGLVAGFQSR,

[0207] and naturally-occurring variants of any of the foregoing.

[0208] In some cases, the reagent that specifically binds an enzymatic cleavage product of a protein component of an arteriosclerotic plaque is an antibody. Suitable antibodies include monoclonal antibodies, and antigen-binding fragments (e.g., a Fv, scFv, Fab, F(ab')2, or Fab' fragment). Where the binding reagent is an antibody, the antibody can be immobilized on an insoluble support (e.g., a test strip, a well of a multi-well plate, beads, etc.). Where the binding reagent is an antibody, the antibody can comprise a detectable label. Where the antibody comprises a detectable label, a subject kit can include one or more reagents for developing the detectable label. A labeled antibody can comprise a label such as a chemiluminescent agent, a particulate label, a colorimetric agent, an energy transfer agent, an enzyme, a fluorescent agent, or a radioisotope.

[0209] In some cases, a subject kit includes a plurality of antibodies, where each member of the plurality is specific for a different enzymatic cleavage product of a protein component of an arteriosclerotic plaque. For example, the plurality of antibodies can include individual member antibodies, each of which is specific for a different enzymatic cleavage product of a protein component of an arteriosclerotic plaque present in a panel of such enzymatic cleavage products.

[0210] A suitable antibody includes an antibody specific for an epitope that is exposed upon cleavage of a protein component of an arteriosclerotic plaque, e.g., an epitope comprising the newly-formed carboxyl-terminus or amino-terminus of an enzymatic cleavage product of a protein component of an arteriosclerotic plaque. For example, an enzyme(s) produced by an inflammatory cell in the vasculature can proteolytically cleave a protein component of an arteriosclerotic plaque; and the cleavage product would then present epitope (s) (e.g., linear epitopes; conformational epitopes) not presented by the uncleaved protein component, where such epitopes could include the C-terminal amino acids of the cleavage product, or the N-terminal amino acids of the cleavage product.

[0211] Other optional components of the kit include: a buffer; a protease inhibitor; a detectable label; etc. The various components of the kit may be present in separate containers or certain compatible components may be pre-combined into a single container, as desired.

[0212] In addition to above-mentioned components, a subject kit can include instructions for using the components of the kit to practice a subject method. The instructions for practicing a subject method are generally recorded on a suitable recording medium. For example, the instructions may be printed on a substrate, such as paper or plastic, etc. As such, the instructions may be present in the kits as a package insert, in the labeling of the container of the kit or components thereof (i.e., associated with the packaging or subpackaging) etc. In other embodiments, the instructions are present as an electronic storage data file present on a suitable computer readable storage medium, e.g. compact disc-read only memory (CD-ROM), digital versatile disk (DVD), diskette, etc. In yet other embodiments, the actual instructions are not present in the kit, but means for obtaining the instructions from a remote source, e.g. via the internet, are provided. An example of this embodiment is a kit that includes a web address where the instructions can be viewed and/or from which the instructions can be downloaded. As with the instructions, this means for obtaining the instructions is recorded on a suitable substrate.

Assay Device

[0213] The present disclosure further provides an assay device for use in detecting, in a liquid biological sample obtained from an individual, an enzymatic cleavage product of an arteriosclerotic plaque. The device can include a matrix defining an axial flow path. The matrix can comprise: i) a sample receiving zone at an upstream end of the flow path that receives the liquid sample; ii) one or more test zones positioned within the flow path and downstream from the sample receiving zone, each of the one or more test zones comprising an antibody specific for an enzymatic cleavage product of an arteriosclerotic plaque in each of the test zones, where each of the immobilized antibodies is capable of binding a different enzymatic cleavage product present in the liquid sample, to form an immobilized enzymatic cleavage product; and iii) one or more control zones positioned within the flow path and downstream from the sample receiving zone, where the one or more control zones can include positive and/or negative controls. The test zones and control zones can be positioned in an alternating format within the flow path beginning with a test zone positioned upstream of any control zone.

[0214] In using such an assay device, in some embodiments, a labeled antibody specific for an enzymatic cleavage product of an arteriosclerotic plaque can first be mixed with a liquid sample before the liquid sample is applied to the sample receiving zone of the device, where such mixing results in a labeled antibody/enzymatic cleavage product complex. In these embodiments, the liquid sample comprising the labeled antibody/enzymatic cleavage product complex is applied to the sample receiving zone of the assay device. The liquid sample flows along the device until the liquid sample reaches a test zone. Antibody present in the test zone binds an enzymatic cleavage product present in the labeled antibody/enzymatic cleavage product complex; and can then be detected.

[0215] The assay device can further include a label zone comprising a labeled antibody specific for an enzymatic cleavage product of an arteriosclerotic plaque, where the labeled antibody is capable of binding a cleavage product present in an immobilized cleavage product complex, to form a labeled enzymatic cleavage product complex, where the labeled antibody is mobilizable in the presence of liquid sample. In using such an assay device, a liquid sample comprising an enzymatic cleavage product of an arteriosclerotic plaque is applied to the sample receiving zone of the device; antibody present in the label zone binds the enzymatic cleavage product, forming labeled antibody/enzymatic cleavage product complex, which, like the labeled antibody, is mobilizable; and the labeled antibody/enzymatic cleavage product complex flows alone the device until the liquid sample reaches a test zone. Antibody present in the test zone binds an enzymatic cleavage product present in the labeled antibody/enzymatic cleavage product complex; and can then be detected.

[0216] The labeled antibody can comprise a label such as a chemiluminescent agent, a particulate label, a colorimetric agent, an energy transfer agent, an enzyme, a fluorescent agent, or a radioisotope.

[0217] Control zones include positive control zones and negative control zones.

[0218] The matrix is generally an insoluble support, where suitable insoluble supports include, but are not limited to, polyvinyl difluoride (PVDF), cellulose, nitrocellulose, nylon, and the like. The matrix can be flexible, or can be relatively inflexible. The matrix can be positioned within a housing comprising a support and optionally a cover, where the housing contains an application aperture and one or more observation ports. The assay device can be in any of a variety of formats, e.g., a test strip, a dipstick; etc.

EXAMPLES

[0219] The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Celsius, and pressure is at or near atmospheric. Standard abbreviations may be used, e.g., bp, base pair(s); kb, kilobase(s); pl, picoliter(s); s or sec, second(s); min, minute(s); h or hr, hour(s); aa, amino acid(s); kb, kilobase(s); bp, base pair(s); nt, nucleotide(s); i.m., intramuscular(ly); i.p., intraperitoneal(ly); s.c., subcutaneous(ly); and the like.

Example 1

Identification of Enzymatic Cleavage Products in Unstable Arteriosclerotic Plaques

[0220] Arteriosclerotic plaques that appeared unstable by visual inspection were incubated in buffer. Proteins released from the plaque into the buffer, including any enzymatic cleavage products, were isolated. To facilitate mass spectrometry analysis, the isolated enzymatic cleavage products were trypsinized. The trypsinization products were then subjected to mass spectrometry analysis.

[0221] Enzymatic cleavage products that were not solely the result of trypsin digestion (non-tryptic peptides) were identified. Examples of non-tryptic fragments of proteins present in the plaque are listed below. These represent in vivo-generated enzymatic cleavage products from the arteriosclerotic plaques. The peptides are listed in sequence order within each protein. Peptides denoted with an asterisk were detected in more than one protein.

Collagen alpha-1(I)chain fragments

(SEQ ID NO: 26)
TGGISVPGPMGPSGPR

(SEQ ID NO: 27)
GLPGPPGAPGPQG

(SEQ ID NO: 28)
GLPGPPGAPGPQGF

(SEQ ID NO: 29)
PGEPGEPGASGPMGPRGPPGPPGK

(SEQ ID NO: 30)
GASGPMGPRGPPGPPGK

(SEQ ID NO: 31)
KPGRPGERGPPGPQGAR

(SEQ ID NO: 32)
GPPGPQGARGLPGTAGLPGM

(SEQ ID NO: 33)
AGPQGPR

(SEQ ID NO: 34)
GAPGIAGAPGFPGAR

(SEQ ID NO: 35)
PGIAGAPGFPGARGPSGPQGPGGPPGPK

(SEQ ID NO: 36)
IAGAPGFPGARGPSGPQGPGGPPGPK

(SEQ ID NO: 37)
GFPGARGPSGPQGPGGPPGPK

(SEQ ID NO: 38)
GPSGPQGPGG

(SEQ ID NO: 39)
GDTGAKGEP

(SEQ ID NO: 40)
VQGPPGPAGEEGK

(SEQ ID NO: 41)
GEPGPTGLPGPPG

(SEQ ID NO: 42)
GEPGPTGLPGPPGERGGPGS

(SEQ ID NO: 43)
TGLPGPPGER

(SEQ ID NO: 44)
LPGPPGER

(SEQ ID NO: 45)
AGPKGPAGER

-continued

(SEQ ID NO: 46)
GSPGPAGPKGSPGEAGRPGEAG

(SEQ ID NO: 47)
PGEAGRPGEAGLPGAKGLTGSPGSPGPDGK

(SEQ ID NO: 48)
LTGSPGSPGPDGK

(SEQ ID NO: 49)
TGPPGPAGQDGRPGPPGPPGARG

(SEQ ID NO: 50)
PGAVGPAGKDGEAGAQGPPGPAGPAGER

(SEQ ID NO: 51)
GEAGAQGPPGPAGPAGER

(SEQ ID NO: 52)
EAGAQGPPGPAGPAGER

(SEQ ID NO: 53)
VQGPPGPAGPR

(SEQ ID NO: 54)
QGPPGPAGPR*

(SEQ ID NO: 55)
GPPGPAGPR

(SEQ ID NO: 56)
ANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGER

(SEQ ID NO: 57)
LQGMPGER*

(SEQ ID NO: 58)
LTGPIGPPGPAGAPGDK

(SEQ ID NO: 59)
IGPPGPAGAPGDK

(SEQ ID NO: 60)
KGESGPSGPAGPTGAR

(SEQ ID NO: 61)
PGDRGEPGPPGPAGFAGPPGADGQPGAK

(SEQ ID NO: 62)
GEPGPPGPAGF

(SEQ ID NO: 63)
FAGPPGADGQPGAK*

(SEQ ID NO: 64)
AGPPGADGQPGAK*

(SEQ ID NO: 65)
RVGPPGPSGNAGPPGPPGPAGK

(SEQ ID NO: 66)
VGPPGPSGNAGPPGPPGPAGKEGG

(SEQ ID NO: 67)
EVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR

(SEQ ID NO: 68)
PGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR

(SEQ ID NO: 69)
GSPGADGPAGAPGTPGPQG

(SEQ ID NO: 70)
GPAGAPGTPGPQGIAGQR

(SEQ ID NO: 71)
VVGLPGQR

-continued

(SEQ ID NO: 72)
LAGPPGESGR

(SEQ ID NO: 73)
ETGPAGPPGAPGAPGAPGPVGPAGKSGDR

(SEQ ID NO: 74)
RGETGPAGPAGPVGPVGAR

(SEQ ID NO: 75)
PAGPVGPVGAR

(SEQ ID NO: 76)
PVGPVGAR

(SEQ ID NO: 77)
SPGEQGPSGASGPAGPR

(SEQ ID NO: 78)
PGEQGPSGASGPAGPR

(SEQ ID NO: 79)
GPSGASGPAGPR

(SEQ ID NO: 80)
ASGPAGPR

(SEQ ID NO: 81)
GPPGSAGAPGKD

(SEQ ID NO: 82)
PPGSAGAPGKDGLNGLPGPIGPPGPR
and

(SEQ ID NO: 83)
LP QPPQEK*

Collagen alpha-2(I)chain fragments
(SEQ ID NO: 84)
GLMGPRGPPGAAGAPGPQGFQGPAGEPGEPGQTGPAGAR

(SEQ ID NO: 85)
FQGPAGEPGEPGQTGPAGAR

(SEQ ID NO: 86)
QGPAGEPGEPGQTGPAGAR

(SEQ ID NO: 87)
EDGHPGKPGRPGERGVVGPQGAR

(SEQ ID NO: 88)
PAGARGSDGSVGPVGPAGPIGSAGPPGFPGAPGPK

(SEQ ID NO: 89)
DGSVGPVGPAGPIGSAGPPGFPGAPGPK

(SEQ ID NO: 90)
PGAPGPKGEIGAVGNAGPAGPAGPR

(SEQ ID NO: 91)
GPAGPAGPR

(SEQ ID NO: 92)
PAGPAGPR

(SEQ ID NO: 93)
RGEVGLPGLSGPVGPPGNPGANGLTGAK

(SEQ ID NO: 94)
GAPGLPGPR

(SEQ ID NO: 95)
PNGEAGSAGPPGPPGLR

(SEQ ID NO: 96)
GPRGLPGSPGNIGPAGK

-continued

(SEQ ID NO: 97)
GRPGPIGPAGAR

(SEQ ID NO: 98)
GPSGPPGPDG

(SEQ ID NO: 99)
GPSGPPGPDGNKGEPGVVGAVGTAGPS

(SEQ ID NO: 100)
GPSGLPGER

(SEQ ID NO: 101)
GAVGAPGPAGATGDRGEAGAAGPAGPAGPR

(SEQ ID NO: 102)
VGAPGPAGATGDRGEAGAAGPAGPAGPR

(SEQ ID NO: 103)
PGPAGATGDRGEAGAAGPAGPAGPR

(SEQ ID NO: 104)
NGVVGPTGPVGAAGPAGPNGPPGPAGSR

(SEQ ID NO: 105)
GPPGPAGSR

(SEQ ID NO: 106)
PGPAGSRGDGGPPGMTGFPGAAGR

(SEQ ID NO: 107)
GDGGPPGMTGFPGAAGRTGPPGPSGISGPPGPPGPA

(SEQ ID NO: 108)
ISGPPGPPGPAGK

(SEQ ID NO: 109)
GPSGEAGTAGPPGTPGPQGL

(SEQ ID NO: 110)
PGILGLPGSR

(SEQ ID NO: 111)
IAGPPGAR

(SEQ ID NO: 112)
PGNIGPVGAAGAPGPHGPVGPAGKHGNR

(SEQ ID NO: 113)
VGPAGAVGPR

(SEQ ID NO: 114)
QGAPGSVGPAGPR

(SEQ ID NO: 115)
GPAGPSGPAGKD

(SEQ ID NO: 116)
GTVGPAGIR

Collagen alpha-1(III)chain fragments

(SEQ ID NO: 117)
GPQGPKGDPGPPGIPGR

(SEQ ID NO: 118)
PGTSGHPGSPGSPGYQGPPGEPGQAGPSGPPGPPGAIGPSGPAGK

(SEQ ID NO: 119)
GLPGPPGIKGPAG

(SEQ ID NO: 120)
GEVGPAGSPGSNGAPGQRGEPGPQGHAG

(SEQ ID NO: 121)
GEPGPQGHAGAQGPPGPPGINGSPGGKGEMGPAGIPG

(SEQ ID NO: 122)
GEMGPAGIPGAPGLMGARGPPGPAG

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(SEQ ID NO: 123)
GIPGAPGLMGAR

(SEQ ID NO: 124)
GAPGLMGARGPPGPAGANGAPGLR

(SEQ ID NO: 125)
PAGERGAPGPAGPR

(SEQ ID NO: 126)
GAPGPAGPRGAAGEP

(SEQ ID NO: 127)
GEPGRDGVPGGPGMR

(SEQ ID NO: 128)
DGKPGPPGSQGESGRPGPPGPSGPR

(SEQ ID NO: 129)
GKPGPPGSQGESGRPGPPGPSGPR

(SEQ ID NO: 130)
GRPGPPGPSGPR

(SEQ ID NO: 131)
GPPGPSGPR

(SEQ ID NO: 132)
QGPPGKNGETGPQGPPGPTGPGGDK

(SEQ ID NO: 133)
GDAGAPGERGP

(SEQ ID NO: 134)
LQGMPGER

(SEQ ID NO: 135)
GEGGPPGVAGPPGGSGPAGPPGPQGV

(SEQ ID NO: 136)
GSNGNPGPPGPSGSPGKDGPPGPAGNTGAPGSPGVSGPK

(SEQ ID NO: 137)
NGNPGPPGPSGSPGK

(SEQ ID NO: 138)
GSPGAQGPP

(SEQ ID NO: 139)
GNPGSDGLPGR

(SEQ ID NO: 140)
ENGSPGAPGAPGHPGPPGPVGPAGK

(SEQ ID NO: 141)
PGAPGAPGHPGPPGPVGPAGK

(SEQ ID NO: 142)
RGESGPAGPAGAPGPAGSR

(SEQ ID NO: 143)
GESGPAGPAGAP

(SEQ ID NO: 144)
PGAPGSPGPAGQQGAIGSPGPAGPR

(SEQ ID NO: 145)
GQQGAIGSPGPAGPRGPVGPSGPPGK

(SEQ ID NO: 146)
QGAIGSPGPAGPR
and

(SEQ ID NO: 147)
GSEGSPGHPGQPGPPGPPGAPGPCCGGVGAAAIAGIGGEKAGGFAPYYG

-continued

Collagen alpha-1(II)chain fragments

(SEQ ID NO: 148)
GPQGFQGNPGEPGEPGVSGPMGPRGPPGPPGKPGDDGEAGKPGK

(SEQ ID NO: 149)
GAAGARGNDGQPGPAGPPGPVGPAGGPGFPGAPGAK

(SEQ ID NO: 150)
AAGARGNDGQPGPAGPPGPVGPAGGPGFPGAPGAK

(SEQ ID NO: 151)
PGAKGSAGAPGIAGAPGFPGPR

(SEQ ID NO: 152)
GPRGPPGPQGATGPLGPK

(SEQ ID NO: 153)
DGLAGPK

(SEQ ID NO: 154)
PQGKVGPSGAPGEDGRPGPPGPQGAR

(SEQ ID NO: 155)
GFPGPKGANGEPGK

(SEQ ID NO: 156)
GLPGPPGPPGEGGKPGDQGVPGEAGAPGLVGPR

(SEQ ID NO: 157)
GPPGEGGKPGDQGVPGEAGAPGLVGPR

(SEQ ID NO: 158)
LQGMPGER

(SEQ ID NO: 159)
GRGLTGPIGPPGPAGANGEK

(SEQ ID NO: 160)
GLTGPIGPPGPAGANGEKGEVGPP

(SEQ ID NO: 161)
GLTGPIGPPGPAGANGEKGEVGPPGPAGSAG

(SEQ ID NO: 162)
LTGPIGPPGPAGANGEKGEVGPPGPAGSAGAR

(SEQ ID NO: 163)
TGPIGPPGPAGANGEKGEVGPPGPAGSAGAR

(SEQ ID NO: 164)
FAGPPGADGQPGAK*

(SEQ ID NO: 165)
AGPPGADGQPGAK*

(SEQ ID NO: 166)
SGPPGRAGEPGLQGPAGPPGEK

(SEQ ID NO: 167)
GPPGRAGEPGLQGPAGPPGEK

(SEQ ID NO: 168)
PPGLTGPAGEPGREGSPGADGPPGR

(SEQ ID NO: 169)
PGPGIDMSAFAGLGPREK

Collagen alpha-1(XIV)chain fragments

(SEQ ID NO: 170)
IEWHLNAF

(SEQ ID NO: 171)
AITGPPTELITSEVTAR

(SEQ ID NO: 172)
AIYAHTASEGLR

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(SEQ ID NO: 173)
LYDVTENSMR

(SEQ ID NO: 174)
YLILYAPLTEGLAGDEKEMK

(SEQ ID NO: 175)
YAPLTEGLAGDEK

(SEQ ID NO: 176)
HVEMTSLCAH

(SEQ ID NO: 177)
SIQGMPGMPGEKGEK

(SEQ ID NO: 178)
QVCEQLIQSH

(SEQ ID NO: 179)
EPGRPGSPGAPGEQGPPGTPGFPGNAGVPGTPGER

Collagen alpha-1(XII)chain fragments

(SEQ ID NO: 180)
GGSTNTGKAMTYVRE

(SEQ ID NO: 181)
PKVMILITDGK

(SEQ ID NO: 182)
PDDTHAYNVADFESLSR

(SEQ ID NO: 183)
SVVEDEYSEPLK

(SEQ ID NO: 184)
SETSTSLKD

(SEQ ID NO: 185)
LKPDTPYTITVSSLYPDGEGGRMTG

(SEQ ID NO: 186)
PGPAGGPGAK

(SEQ ID NO: 187)
GRTGTPGLPGPPGPMGPPGDR

(SEQ ID NO: 188)
TPGLPGPPGPMGPPGDRGFTGK

(SEQ ID NO: 189)
GFPGTPGMQGPPGERGLPGEK

(SEQ ID NO: 190)
QGPPGER

(SEQ ID NO: 191)
PRGLPGPPGPQGESR

Collagen alpha-1(XVIII)chain fragments

(SEQ ID NO: 192)
PPSLGRPWAPLTGPSVPPPSSGR

(SEQ ID NO: 193)
PGEDGKPGDTGPQGFPGTPGDVGPKGDK

(SEQ ID NO: 194)
PGLPGEPGR

(SEQ ID NO: 195)
GREGPPGFPGLPGPPGPPGR

(SEQ ID NO: 196)
QDGSVLSVPGPEGRPGFAGFPGPAGPKGNLGSK

(SEQ ID NO: 197)
AESSRPGPPGLPGNQGPPGPK

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(SEQ ID NO: 198)
GPPGPKGAK

(SEQ ID NO: 199)
PGPPGPPGTMGASSGVR

(SEQ ID NO: 200)
RLPEPQPYPGAPHHSSYVHLRPARPTSPPAHSHR

(SEQ ID NO: 201)
LPEPQPYPGAPHHSSY

(SEQ ID NO: 202)
NSPLSGGMR

(SEQ ID NO: 203)
PSLGRPWAPLTGPSVPPPSSER

Collagen alpha-2(IV)chain fragments
(SEQ ID NO: 204)
GARGVSGFPGADGIPGHPGQGGPR

(SEQ ID NO: 205)
GGPKGLPGLPGPPGPTGAK

(SEQ ID NO: 206)
GPPGLHGFPGAPGQEGPLGLPGIPGREGLPGDR

(SEQ ID NO: 207)
APGRPGSPGLPGMPGR

(SEQ ID NO: 208)
LYCNPGDVCYYASR

(SEQ ID NO: 209)
LMHTAAGDEGGGQSLVSPGSCLEDFR

Collagen alpha-1(IV)chain fragments
(SEQ ID NO: 210)
EPGPPGLPGSVGSPGVPGIGPPGAR

(SEQ ID NO: 211)
PGVPGIGPPGARGPPGGQGPPGLSGPPGIK

(SEQ ID NO: 212)
PPGGQGPPGLSGPPGIKGEK

(SEQ ID NO: 213)
DPGFQGMPGIGGSPGITGSK

(SEQ ID NO: 214)
KGQQGVTGLVGIPGPPGIPGFDGAPGQK

(SEQ ID NO: 215)
SLLYVQGNER

(SEQ ID NO: 216)
LFCNINNVCNFASR

(SEQ ID NO: 217)
VMHTSAGAEGSGQALASPGSCLEEFR

(SEQ ID NO: 218)
RSAPFIECHGR

(SEQ ID NO: 219)
SFWLATIER

(SEQ ID NO: 220)
WLATIER

Collagen alpha-5(IV)chain fragments
(SEQ ID NO: 221)
DGIPGPPGPK

(SEQ ID NO: 222)
KGNPGYPGPPGIQGLPGPTGIPGPIGPPGPPGLMGPPGPPGLPGPK

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(SEQ ID NO: 223)
PHIPPSDEICEPGPPGPPGSPGDK

(SEQ ID NO: 224)
GLPGLPGPPGSLGFPGQK

(SEQ ID NO: 225)
PKGEPGGITFK

(SEQ ID NO: 226)
TPGRIGLEGPPGPPGFPGPK

(SEQ ID NO: 227)
GPPGRTGLDGLPGPK

(SEQ ID NO: 228)
APGPIGPPGSPGLPGK

(SEQ ID NO: 229)
KGEPGLPGPPGPMDPNLLGSK

(SEQ ID NO: 230)
PGEPGPVGGGGHPGQPGPPGEK

(SEQ ID NO: 231)
PALEGPKGNPGPQGPPGRPGPTGFQGLPGPEGPPGLPGNGGIK

(SEQ ID NO: 232)
GPPGPPGLPGPSGQSIIIK

Collagen alpha-1(XV)chain fragments
(SEQ ID NO: 233)
VDGATGLPGMK

(SEQ ID NO: 234)
KGQAGPPGVMGPPGPPGPPGPPGPGCTMGLGFED

(SEQ ID NO: 235)
KLQLGELIPIPADSPPPP

(SEQ ID NO: 236)
AWRTADTAVTGLASPLSTGK

(SEQ ID NO: 237)
AVTGLASPLSTGKILDQK

Collagen alpha-3(VI)chain fragments
(SEQ ID NO: 238)
GVEDADEGALKEIASEPLNMHMFNLENFTSLHDIVGNLVSCVHSSVSPER

(SEQ ID NO: 241)
IGDLHPQIVN

Collagen alpha-1(VI)chain fragments
(SEQ ID NO: 242)
GPQGDQGR

(SEQ ID NO: 244)
FSDGNSQGATPAAIEK

Collagen alpha-1(XIX)chain fragment
(SEQ ID NO: 355)
NPGAPGPR

Fibronectin fragments
(SEQ ID NO: 247)
GPGLLLLAVQCLGTAVPSTGASK

(SEQ ID NO: 248)
ALVCTCYGGSR

(SEQ ID NO: 327)
ISCTIANR

(SEQ ID NO: 249)
MVDCTCLGEGSGR

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(SEQ ID NO: 250)
AAHEEICTTNEGVMYR

(SEQ ID NO: 251)
SHPIQWNAPQPSHISK

(SEQ ID NO: 252)
VVSWVSASDTVSGFR

(SEQ ID NO: 253)
SDTVPSPRDLQFVEVTDVK

(SEQ ID NO: 254)
VDVIPVNLPGEHGQR

(SEQ ID NO: 255)
VFAVSHGRESKPLTAQQTTK

(SEQ ID NO: 256)
LGVRPSQGGEAPR

(SEQ ID NO: 257)
DAPIVNKVVTPLSPPTNLH

(SEQ ID NO: 258)
TPDITGYR

(SEQ ID NO: 259)
PGTEYVVSVSSVYEQHESTPLR

(SEQ ID NO: 260)
TGLDSPTGIDFSDITANSFTVH

(SEQ ID NO: 261)
TVHWIAPR

(SEQ ID NO: 262)
SPVQEFTVPGSK

(SEQ ID NO: 263)
VVSVYAQNPSGESQPLVQTAVTNIDRPK

(SEQ ID NO: 264)
RPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLK

(SEQ ID NO: 265)
YEVSVYALK

(SEQ ID NO: 266)
IYLYTLNDNAR

(SEQ ID NO: 267)
SLLVSWQPPR

(SEQ ID NO: 268)
YEKPGSPPR

(SEQ ID NO: 269)
TPFVTHPG

(SEQ ID NO: 270)
TPFVTHPGYDT

(SEQ ID NO: 271)
TPFVTHPGYDTGNGIQLPGTSGQQPSVGQQM

(SEQ ID NO: 272)
QDTSEYIISCHPVGTDEEPLQFR

(SEQ ID NO: 273)
VPGTSTSATLTGLTRGATYNIIVEALK

(SEQ ID NO: 274)
VREEVVTVGN

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(SEQ ID NO: 275)
SVNEGLNQPTDDSCFDPYTVSHYAVGDEWER

(SEQ ID NO: 276)
LGFGSGHFR

Fibrillin fragments

(SEQ ID NO: 278)
TGLPVDIDECR

(SEQ ID NO: 279)
PVDIDECR

Vitronectin fragments

(SEQ ID NO: 285)
CTDYTAECKPQVTR

(SEQ ID NO: 286)
IYISGMAPRPS

(SEQ ID NO: 287)
TCEPIQSVFFFSGDK

(SEQ ID NO: 288)
SIAQYWLGCPAPGH

(SEQ ID NO: 289)
WLGCPAPGHL

Metalloproteinase inhibitor 1 fragments

(SEQ ID NO: 290)
CNSDLVIR

(SEQ ID NO: 291)
LQDGLLHITTC

(SEQ ID NO: 292)
SFVAPWNSLSLAQR

Dermatopontin fragments

(SEQ ID NO: 293)
SDDGWVNLNR

(SEQ ID NO: 294)
SYQCPQGQVIVAVR

(SEQ ID NO: 295)
SLGEPTECWWEEINR

(SEQ ID NO: 296)
SNNGLVAGFQSR

Galectin-1 fragments

(SEQ ID NO: 297)
VASNLNLKPGECLR

(SEQ ID NO: 298)
GDANTIVCNSK

(SEQ ID NO: 299)
MAADGDFK

Lumican fragments

(SEQ ID NO: 300)
CAPECNCPESYPSAMYCDELK

(SEQ ID NO: 301)
RNNQIDHIDEK

(SEQ ID NO: 302)
NNQIDHIDE

(SEQ ID NO: 303)
ILDHNLLENSK

(SEQ ID NO: 304)
SLEDLQLTH

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(SEQ ID NO: 305)
IHLQHNR

(SEQ ID NO: 306)
CKILGPLSYSK

Prolargin fragments

(SEQ ID NO: 307)
EVPSALPR

(SEQ ID NO: 308)
RLSQNHISR

(SEQ ID NO: 309)
RLSQNHISRIPPGVFSK

(SEQ ID NO: 310)
LSDGVFKPDT

(SEQ ID NO: 311)
NLAHNILR

(SEQ ID NO: 312)
LAHNILR

(SEQ ID NO: 313)
LDSNKIETIPNGYFKSFPNLAFIR

(SEQ ID NO: 314)
IETIPNGYFKSFPNLA

(SEQ ID NO: 315)
SFPNLAFIRLNYN

(SEQ ID NO: 316)
LNNNSIEK

(SEQ ID NO: 317)
DLVAFHDFSSDLENVPHLR

Tenascin fragments

(SEQ ID NO: 318)
ELEPGVEYFIR

(SEQ ID NO: 319)
TVSIYGVIQGYR

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(SEQ ID NO: 320)
TVTLHGEVR

(SEQ ID NO: 321)
FRITYVPITGGTPSMVTVDGTK

Tenascin-X fragments

(SEQ ID NO: 322)
WRPQPPAEGPGGELTVPGTTRTVS

(SEQ ID NO: 323)
FDSFTVQYK

(SEQ ID NO: 324)
GEESEVTVGGLEPGR

(SEQ ID NO: 325)
EPPNKPR

(SEQ ID NO: 326)
GFEESEPLTGFLTTVPDGPTQ.

Example 2

Detecting Enzymatic Cleavage Products of an Arteriosclerotic Plaque

[0222] Blood is drawn into tubes containing buffered ethylenediamine tetraacetic acid (EDTA). Plasma is separated by centrifugation. Target protein fragments are monomerized by addition of 0.005% Tween 20 in 0.005 M phosphate buffer, pH 7.4.

[0223] Target peptide fragments are quantitated by ELISA using monovalent antibodies. Synthetic peptides are used as standards. The contents of target peptides are reported in mass units per mL.

[0224] While the present invention has been described with reference to the specific embodiments thereof, it should be understood by those skilled in the art that various changes may be made and equivalents may be substituted without departing from the true spirit and scope of the invention. In addition, many modifications may be made to adapt a particular situation, material, composition of matter, process, process step or steps, to the objective, spirit and scope of the present invention. All such modifications are intended to be within the scope of the claims appended hereto.

SEQUENCE LISTING

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

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Ala Leu Leu Thr His Gly Gln Glu Glu Gly Gln Val Glu Gly Gln Asp
            20                  25                  30

Glu Asp Ile Pro Pro Ile Thr Cys Val Gln Asn Gly Leu Arg Tyr His
        35                  40                  45

Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Arg Ile Cys Val Cys Asp
    50                  55                  60

Asn Gly Lys Val Leu Cys Asp Asp Val Ile Cys Asp Glu Thr Lys Asn
65                  70                  75                  80
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Cys Pro Gly Ala Glu Val Pro Glu Gly Glu Cys Cys Pro Val Cys Pro
                85                  90                  95

Asp Gly Ser Glu Ser Pro Thr Asp Gln Glu Thr Thr Gly Val Glu Gly
            100                 105                 110

Pro Lys Gly Asp Thr Gly Pro Arg Gly Pro Arg Gly Pro Ala Gly Pro
        115                 120                 125

Pro Gly Arg Asp Gly Ile Pro Gly Gln Pro Gly Leu Pro Gly Pro Pro
    130                 135                 140

Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala
145                 150                 155                 160

Pro Gln Leu Ser Tyr Gly Tyr Asp Glu Lys Ser Thr Gly Gly Ile Ser
                165                 170                 175

Val Pro Gly Pro Met Gly Pro Ser Gly Pro Arg Gly Leu Pro Gly Pro
            180                 185                 190

Pro Gly Ala Pro Gly Pro Gln Gly Phe Gln Gly Pro Pro Gly Glu Pro
        195                 200                 205

Gly Glu Pro Gly Ala Ser Gly Pro Met Gly Pro Arg Gly Pro Pro Gly
    210                 215                 220

Pro Pro Gly Lys Asn Gly Asp Asp Gly Glu Ala Gly Lys Pro Gly Arg
225                 230                 235                 240

Pro Gly Glu Arg Gly Pro Pro Gly Pro Gln Gly Ala Arg Gly Leu Pro
                245                 250                 255

Gly Thr Ala Gly Leu Pro Gly Met Lys Gly His Arg Gly Phe Ser Gly
            260                 265                 270

Leu Asp Gly Ala Lys Gly Asp Ala Gly Pro Ala Gly Pro Lys Gly Glu
        275                 280                 285

Pro Gly Ser Pro Gly Glu Asn Gly Ala Pro Gly Gln Met Gly Pro Arg
    290                 295                 300

Gly Leu Pro Gly Glu Arg Gly Arg Pro Gly Ala Pro Gly Pro Ala Gly
305                 310                 315                 320

Ala Arg Gly Asn Asp Gly Ala Thr Gly Ala Ala Gly Pro Pro Gly Pro
                325                 330                 335

Thr Gly Pro Ala Gly Pro Pro Gly Phe Pro Gly Ala Val Gly Ala Lys
            340                 345                 350

Gly Glu Ala Gly Pro Gln Gly Pro Arg Gly Ser Glu Gly Pro Gln Gly
        355                 360                 365

Val Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Ala Ala Gly Pro
    370                 375                 380

Ala Gly Asn Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys Gly Ala Asn
385                 390                 395                 400

Gly Ala Pro Gly Ile Ala Gly Ala Pro Gly Phe Pro Gly Ala Arg Gly
                405                 410                 415

Pro Ser Gly Pro Gln Gly Pro Gly Gly Pro Pro Gly Pro Lys Gly Asn
            420                 425                 430

Ser Gly Glu Pro Gly Ala Pro Gly Ser Lys Gly Asp Thr Gly Ala Lys
        435                 440                 445

Gly Glu Pro Gly Pro Val Gly Val Gln Gly Pro Pro Gly Pro Ala Gly
    450                 455                 460

Glu Glu Gly Lys Arg Gly Ala Arg Gly Glu Pro Gly Pro Thr Gly Leu
465                 470                 475                 480
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Pro Gly Pro Pro Gly Glu Arg Gly Gly Pro Gly Ser Arg Gly Phe Pro
                485                 490                 495

Gly Ala Asp Gly Val Ala Gly Pro Lys Gly Pro Ala Gly Glu Arg Gly
            500                 505                 510

Ser Pro Gly Pro Ala Gly Pro Lys Gly Ser Pro Gly Glu Ala Gly Arg
        515                 520                 525

Pro Gly Glu Ala Gly Leu Pro Gly Ala Lys Gly Leu Thr Gly Ser Pro
    530                 535                 540

Gly Ser Pro Gly Pro Asp Gly Lys Thr Gly Pro Pro Gly Pro Ala Gly
545                 550                 555                 560

Gln Asp Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Ala Arg Gly Gln
                565                 570                 575

Ala Gly Val Met Gly Phe Pro Gly Pro Lys Gly Ala Ala Gly Glu Pro
            580                 585                 590

Gly Lys Ala Gly Glu Arg Gly Val Pro Gly Pro Pro Gly Ala Val Gly
        595                 600                 605

Pro Ala Gly Lys Asp Gly Glu Ala Gly Ala Gln Gly Pro Pro Gly Pro
    610                 615                 620

Ala Gly Pro Ala Gly Glu Arg Gly Glu Gln Gly Pro Ala Gly Ser Pro
625                 630                 635                 640

Gly Phe Gln Gly Leu Pro Gly Pro Ala Gly Pro Pro Gly Glu Ala Gly
                645                 650                 655

Lys Pro Gly Glu Gln Gly Val Pro Gly Asp Leu Gly Ala Pro Gly Pro
            660                 665                 670

Ser Gly Ala Arg Gly Glu Arg Gly Phe Pro Gly Glu Arg Gly Val Gln
        675                 680                 685

Gly Pro Pro Gly Pro Ala Gly Pro Arg Gly Ala Asn Gly Ala Pro Gly
    690                 695                 700

Asn Asp Gly Ala Lys Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly Ser
705                 710                 715                 720

Gln Gly Ala Pro Gly Leu Gln Gly Met Pro Gly Glu Arg Gly Ala Ala
                725                 730                 735

Gly Leu Pro Gly Pro Lys Gly Asp Arg Gly Asp Ala Gly Pro Lys Gly
            740                 745                 750

Ala Asp Gly Ser Pro Gly Lys Asp Gly Val Arg Gly Leu Thr Gly Pro
        755                 760                 765

Ile Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Asp Lys Gly Glu Ser
    770                 775                 780

Gly Pro Ser Gly Pro Ala Gly Pro Thr Gly Ala Arg Gly Ala Pro Gly
785                 790                 795                 800

Asp Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Phe Ala Gly Pro
                805                 810                 815

Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys Gly Glu Pro Gly Asp Ala
            820                 825                 830

Gly Ala Lys Gly Asp Ala Gly Pro Pro Gly Pro Ala Gly Pro Ala Gly
        835                 840                 845

Pro Pro Gly Pro Ile Gly Asn Val Gly Ala Pro Gly Ala Lys Gly Ala
    850                 855                 860

Arg Gly Ser Ala Gly Pro Pro Gly Ala Thr Gly Phe Pro Gly Ala Ala
865                 870                 875                 880

Gly Arg Val Gly Pro Pro Gly Pro Ser Gly Asn Ala Gly Pro Pro Gly
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                885                 890                 895

Pro Pro Gly Pro Ala Gly Lys Glu Gly Gly Lys Gly Pro Arg Gly Glu
            900                 905                 910

Thr Gly Pro Ala Gly Arg Pro Gly Glu Val Gly Pro Pro Gly Pro Pro
        915                 920                 925

Gly Pro Ala Gly Glu Lys Gly Ser Pro Gly Ala Asp Gly Pro Ala Gly
    930                 935                 940

Ala Pro Gly Thr Pro Gly Pro Gln Gly Ile Ala Gly Gln Arg Gly Val
945                 950                 955                 960

Val Gly Leu Pro Gly Gln Arg Gly Glu Arg Gly Phe Pro Gly Leu Pro
                965                 970                 975

Gly Pro Ser Gly Glu Pro Gly Lys Gln Gly Pro Ser Gly Ala Ser Gly
            980                 985                 990

Glu Arg Gly Pro Pro Gly Pro Met  Gly Pro Pro Gly Leu  Ala Gly Pro
        995                 1000                 1005

Pro Gly  Glu Ser Gly Arg Glu  Gly Ala Pro Gly Ala  Glu Gly Ser
    1010                 1015                 1020

Pro Gly  Arg Asp Gly Ser Pro  Gly Ala Lys Gly Asp  Arg Gly Glu
    1025                 1030                 1035

Thr Gly  Pro Ala Gly Pro Pro  Gly Ala Pro Gly Ala  Pro Gly Ala
    1040                 1045                 1050

Pro Gly  Pro Val Gly Pro Ala  Gly Lys Ser Gly Asp  Arg Gly Glu
    1055                 1060                 1065

Thr Gly  Pro Ala Gly Pro Ala  Gly Pro Val Gly Pro  Val Gly Ala
    1070                 1075                 1080

Arg Gly  Pro Ala Gly Pro Gln  Gly Pro Arg Gly Asp  Lys Gly Glu
    1085                 1090                 1095

Thr Gly  Glu Gln Gly Asp Arg  Gly Ile Lys Gly His  Arg Gly Phe
    1100                 1105                 1110

Ser Gly  Leu Gln Gly Pro Pro  Gly Pro Pro Gly Ser  Pro Gly Glu
    1115                 1120                 1125

Gln Gly  Pro Ser Gly Ala Ser  Gly Pro Ala Gly Pro  Arg Gly Pro
    1130                 1135                 1140

Pro Gly  Ser Ala Gly Ala Pro  Gly Lys Asp Gly Leu  Asn Gly Leu
    1145                 1150                 1155

Pro Gly  Pro Ile Gly Pro Pro  Gly Pro Arg Gly Arg  Thr Gly Asp
    1160                 1165                 1170

Ala Gly  Pro Val Gly Pro Pro  Gly Pro Pro Gly Pro  Pro Gly Pro
    1175                 1180                 1185

Pro Gly  Pro Pro Ser Ala Gly  Phe Asp Phe Ser Phe  Leu Pro Gln
    1190                 1195                 1200

Pro Pro  Gln Glu Lys Ala His  Asp Gly Gly Arg Tyr  Tyr Arg Ala
    1205                 1210                 1215

Asp Asp  Ala Asn Val Val Arg  Asp Arg Asp Leu Glu  Val Asp Thr
    1220                 1225                 1230

Thr Leu  Lys Ser Leu Ser Gln  Gln Ile Glu Asn Ile  Arg Ser Pro
    1235                 1240                 1245

Glu Gly  Ser Arg Lys Asn Pro  Ala Arg Thr Cys Arg  Asp Leu Lys
    1250                 1255                 1260

Met Cys  His Ser Asp Trp Lys  Ser Gly Glu Tyr Trp  Ile Asp Pro
    1265                 1270                 1275
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Asn Gln  Gly Cys Asn Leu Asp  Ala Ile Lys Val Phe  Cys Asn Met
    1280                 1285                 1290

Glu Thr  Gly Glu Thr Cys Val  Tyr Pro Thr Gln Pro  Ser Val Ala
    1295                 1300                 1305

Gln Lys  Asn Trp Tyr Ile Ser  Lys Asn Pro Lys Asp  Lys Arg His
    1310                 1315                 1320

Val Trp  Phe Gly Glu Ser Met  Thr Asp Gly Phe Gln  Phe Glu Tyr
    1325                 1330                 1335

Gly Gly  Gln Gly Ser Asp Pro  Ala Asp Val Ala Ile  Gln Leu Thr
    1340                 1345                 1350

Phe Leu  Arg Leu Met Ser Thr  Glu Ala Ser Gln Asn  Ile Thr Tyr
    1355                 1360                 1365

His Cys  Lys Asn Ser Val Ala  Tyr Met Asp Gln Gln  Thr Gly Asn
    1370                 1375                 1380

Leu Lys  Lys Ala Leu Leu Leu  Lys Gly Ser Asn Glu  Ile Glu Ile
    1385                 1390                 1395

Arg Ala  Glu Gly Asn Ser Arg  Phe Thr Tyr Ser Val  Thr Val Asp
    1400                 1405                 1410

Gly Cys  Thr Ser His Thr Gly  Ala Trp Gly Lys Thr  Val Ile Glu
    1415                 1420                 1425

Tyr Lys  Thr Thr Lys Thr Ser  Arg Leu Pro Ile Ile  Asp Val Ala
    1430                 1435                 1440

Pro Leu  Asp Val Gly Ala Pro  Asp Gln Glu Phe Gly  Phe Asp Val
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Gly Pro  Val Cys Phe Leu
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Met Ile Arg Leu Gly Ala Pro Gln Ser Leu Val Leu Leu Thr Leu Leu
1               5                   10                  15

Val Ala Ala Val Leu Arg Cys Gln Gly Gln Asp Val Gln Glu Ala Gly
            20                  25                  30

Ser Cys Val Gln Asp Gly Gln Arg Tyr Asn Asp Lys Asp Val Trp Lys
        35                  40                  45

Pro Glu Pro Cys Arg Ile Cys Val Cys Asp Thr Gly Thr Val Leu Cys
    50                  55                  60

Asp Asp Ile Ile Cys Glu Asp Val Lys Asp Cys Leu Ser Pro Glu Ile
65                  70                  75                  80

Pro Phe Gly Glu Cys Cys Pro Ile Cys Pro Thr Asp Leu Ala Thr Ala
                85                  90                  95

Ser Gly Gln Pro Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Asp Ile
            100                 105                 110

Lys Asp Ile Val Gly Pro Lys Gly Pro Pro Gly Pro Gln Gly Pro Ala
        115                 120                 125

Gly Glu Gln Gly Pro Arg Gly Asp Arg Gly Asp Lys Gly Glu Lys Gly
    130                 135                 140

Ala Pro Gly Pro Arg Gly Arg Asp Gly Glu Pro Gly Thr Pro Gly Asn
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145                 150                 155                 160

Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly
                165                 170                 175

Gly Asn Phe Ala Ala Gln Met Ala Gly Gly Phe Asp Glu Lys Ala Gly
            180                 185                 190

Gly Ala Gln Leu Gly Val Met Gln Gly Pro Met Gly Pro Met Gly Pro
        195                 200                 205

Arg Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Pro Gln Gly Phe Gln
    210                 215                 220

Gly Asn Pro Gly Glu Pro Gly Glu Pro Gly Val Ser Gly Pro Met Gly
225                 230                 235                 240

Pro Arg Gly Pro Pro Gly Pro Pro Gly Lys Pro Gly Asp Asp Gly Glu
                245                 250                 255

Ala Gly Lys Pro Gly Lys Ala Gly Glu Arg Gly Pro Pro Gly Pro Gln
            260                 265                 270

Gly Ala Arg Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Val Lys Gly
        275                 280                 285

His Arg Gly Tyr Pro Gly Leu Asp Gly Ala Lys Gly Glu Ala Gly Ala
    290                 295                 300

Pro Gly Val Lys Gly Glu Ser Gly Ser Pro Gly Glu Asn Gly Ser Pro
305                 310                 315                 320

Gly Pro Met Gly Pro Arg Gly Leu Pro Gly Glu Arg Gly Arg Thr Gly
                325                 330                 335

Pro Ala Gly Ala Ala Gly Ala Arg Gly Asn Asp Gly Gln Pro Gly Pro
            340                 345                 350

Ala Gly Pro Pro Gly Pro Val Gly Pro Ala Gly Gly Pro Gly Phe Pro
        355                 360                 365

Gly Ala Pro Gly Ala Lys Gly Glu Ala Gly Pro Thr Gly Ala Arg Gly
    370                 375                 380

Pro Glu Gly Ala Gln Gly Pro Arg Gly Glu Pro Gly Thr Pro Gly Ser
385                 390                 395                 400

Pro Gly Pro Ala Gly Ala Ser Gly Asn Pro Gly Thr Asp Gly Ile Pro
                405                 410                 415

Gly Ala Lys Gly Ser Ala Gly Ala Pro Gly Ile Ala Gly Ala Pro Gly
            420                 425                 430

Phe Pro Gly Pro Arg Gly Pro Pro Gly Pro Gln Gly Ala Thr Gly Pro
        435                 440                 445

Leu Gly Pro Lys Gly Gln Thr Gly Glu Pro Gly Ile Ala Gly Phe Lys
    450                 455                 460

Gly Glu Gln Gly Pro Lys Gly Glu Pro Gly Pro Ala Gly Pro Gln Gly
465                 470                 475                 480

Ala Pro Gly Pro Ala Gly Glu Glu Gly Lys Arg Gly Ala Arg Gly Glu
                485                 490                 495

Pro Gly Gly Val Gly Pro Ile Gly Pro Pro Gly Glu Arg Gly Ala Pro
            500                 505                 510

Gly Asn Arg Gly Phe Pro Gly Gln Asp Gly Leu Ala Gly Pro Lys Gly
        515                 520                 525

Ala Pro Gly Glu Arg Gly Pro Ser Gly Leu Ala Gly Pro Lys Gly Ala
    530                 535                 540

Asn Gly Asp Pro Gly Arg Pro Gly Glu Pro Gly Leu Pro Gly Ala Arg
545                 550                 555                 560
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Gly Leu Thr Gly Arg Pro Gly Asp Ala Gly Pro Gln Gly Lys Val Gly
                565                 570                 575

Pro Ser Gly Ala Pro Gly Glu Asp Gly Arg Pro Gly Pro Pro Gly Pro
            580                 585                 590

Gln Gly Ala Arg Gly Gln Pro Gly Val Met Gly Phe Pro Gly Pro Lys
        595                 600                 605

Gly Ala Asn Gly Glu Pro Gly Lys Ala Gly Glu Lys Gly Leu Pro Gly
    610                 615                 620

Ala Pro Gly Leu Arg Gly Leu Pro Gly Lys Asp Gly Glu Thr Gly Ala
625                 630                 635                 640

Ala Gly Pro Pro Gly Pro Ala Gly Pro Ala Gly Glu Arg Gly Glu Gln
                645                 650                 655

Gly Ala Pro Gly Pro Ser Gly Phe Gln Gly Leu Pro Gly Pro Pro Gly
            660                 665                 670

Pro Pro Gly Glu Gly Gly Lys Pro Gly Asp Gln Gly Val Pro Gly Glu
        675                 680                 685

Ala Gly Ala Pro Gly Leu Val Gly Pro Arg Gly Glu Arg Gly Phe Pro
    690                 695                 700

Gly Glu Arg Gly Ser Pro Gly Ala Gln Gly Leu Gln Gly Pro Arg Gly
705                 710                 715                 720

Leu Pro Gly Thr Pro Gly Thr Asp Gly Pro Lys Gly Ala Ser Gly Pro
                725                 730                 735

Ala Gly Pro Pro Gly Ala Gln Gly Pro Pro Gly Leu Gln Gly Met Pro
            740                 745                 750

Gly Glu Arg Gly Ala Ala Gly Ile Ala Gly Pro Lys Gly Asp Arg Gly
        755                 760                 765

Asp Val Gly Glu Lys Gly Pro Glu Gly Ala Pro Gly Lys Asp Gly Gly
    770                 775                 780

Arg Gly Leu Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly Ala Asn
785                 790                 795                 800

Gly Glu Lys Gly Glu Val Gly Pro Pro Gly Pro Ala Gly Ser Ala Gly
                805                 810                 815

Ala Arg Gly Ala Pro Gly Glu Arg Gly Glu Thr Gly Pro Pro Gly Pro
            820                 825                 830

Ala Gly Phe Ala Gly Pro Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys
        835                 840                 845

Gly Glu Gln Gly Glu Ala Gly Gln Lys Gly Asp Ala Gly Ala Pro Gly
    850                 855                 860

Pro Gln Gly Pro Ser Gly Ala Pro Gly Pro Gln Gly Pro Thr Gly Val
865                 870                 875                 880

Thr Gly Pro Lys Gly Ala Arg Gly Ala Gln Gly Pro Pro Gly Ala Thr
                885                 890                 895

Gly Phe Pro Gly Ala Ala Gly Arg Val Gly Pro Pro Gly Ser Asn Gly
            900                 905                 910

Asn Pro Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Lys Asp Gly Pro
        915                 920                 925

Lys Gly Ala Arg Gly Asp Ser Gly Pro Pro Gly Arg Ala Gly Glu Pro
    930                 935                 940

Gly Leu Gln Gly Pro Ala Gly Pro Pro Gly Glu Lys Gly Glu Pro Gly
945                 950                 955                 960
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Asp Asp Gly Pro Ser Gly Ala Glu Gly Pro Pro Gly Pro Gln Gly Leu
                965                 970                 975

Ala Gly Gln Arg Gly Ile Val Gly Leu Pro Gly Gln Arg Gly Glu Arg
            980                 985                 990

Gly Phe Pro Gly Leu Pro Gly Pro  Ser Gly Glu Pro Gly  Lys Gln Gly
        995                 1000                 1005

Ala Pro  Gly Ala Ser Gly Asp  Arg Gly Pro Pro Gly  Pro Val Gly
    1010                 1015                 1020

Pro Pro  Gly Leu Thr Gly Pro  Ala Gly Glu Pro Gly  Arg Glu Gly
    1025                 1030                 1035

Ser Pro  Gly Ala Asp Gly Pro  Pro Gly Arg Asp Gly  Ala Ala Gly
    1040                 1045                 1050

Val Lys  Gly Asp Arg Gly Glu  Thr Gly Ala Val Gly  Ala Pro Gly
    1055                 1060                 1065

Ala Pro  Gly Pro Pro Gly Ser  Pro Gly Pro Ala Gly  Pro Thr Gly
    1070                 1075                 1080

Lys Gln  Gly Asp Arg Gly Glu  Ala Gly Ala Gln Gly  Pro Met Gly
    1085                 1090                 1095

Pro Ser  Gly Pro Ala Gly Ala  Arg Gly Ile Gln Gly  Pro Gln Gly
    1100                 1105                 1110

Pro Arg  Gly Asp Lys Gly Glu  Ala Gly Glu Pro Gly  Glu Arg Gly
    1115                 1120                 1125

Leu Lys  Gly His Arg Gly Phe  Thr Gly Leu Gln Gly  Leu Pro Gly
    1130                 1135                 1140

Pro Pro  Gly Pro Ser Gly Asp  Gln Gly Ala Ser Gly  Pro Ala Gly
    1145                 1150                 1155

Pro Ser  Gly Pro Arg Gly Pro  Pro Gly Pro Val Gly  Pro Ser Gly
    1160                 1165                 1170

Lys Asp  Gly Ala Asn Gly Ile  Pro Gly Pro Ile Gly  Pro Pro Gly
    1175                 1180                 1185

Pro Arg  Gly Arg Ser Gly Glu  Thr Gly Pro Ala Gly  Pro Pro Gly
    1190                 1195                 1200

Asn Pro  Gly Pro Pro Gly Pro  Pro Gly Pro Pro Gly  Pro Gly Ile
    1205                 1210                 1215

Asp Met  Ser Ala Phe Ala Gly  Leu Gly Pro Arg Glu  Lys Gly Pro
    1220                 1225                 1230

Asp Pro  Leu Gln Tyr Met Arg  Ala Asp Gln Ala Ala  Gly Gly Leu
    1235                 1240                 1245

Arg Gln  His Asp Ala Glu Val  Asp Ala Thr Leu Lys  Ser Leu Asn
    1250                 1255                 1260

Asn Gln  Ile Glu Ser Ile Arg  Ser Pro Glu Gly Ser  Arg Lys Asn
    1265                 1270                 1275

Pro Ala  Arg Thr Cys Arg Asp  Leu Lys Leu Cys His  Pro Glu Trp
    1280                 1285                 1290

Lys Ser  Gly Asp Tyr Trp Ile  Asp Pro Asn Gln Gly  Cys Thr Leu
    1295                 1300                 1305

Asp Ala  Met Lys Val Phe Cys  Asn Met Glu Thr Gly  Glu Thr Cys
    1310                 1315                 1320

Val Tyr  Pro Asn Pro Ala Asn  Val Pro Lys Lys Asn  Trp Trp Ser
    1325                 1330                 1335

Ser Lys  Ser Lys Glu Lys Lys  His Ile Trp Phe Gly  Glu Thr Ile
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    1340                 1345                 1350

Asn Gly  Gly Phe His Phe Ser  Tyr Gly Asp Asp Asn  Leu Ala Pro
    1355                 1360                 1365

Asn Thr  Ala Asn Val Gln Met  Thr Phe Leu Arg Leu  Leu Ser Thr
    1370                 1375                 1380

Glu Gly  Ser Gln Asn Ile Thr  Tyr His Cys Lys Asn  Ser Ile Ala
    1385                 1390                 1395

Tyr Leu  Asp Glu Ala Ala Gly  Asn Leu Lys Lys Ala  Leu Leu Ile
    1400                 1405                 1410

Gln Gly  Ser Asn Asp Val Glu  Ile Arg Ala Glu Gly  Asn Ser Arg
    1415                 1420                 1425

Phe Thr  Tyr Thr Ala Leu Lys  Asp Gly Cys Thr Lys  His Thr Gly
    1430                 1435                 1440

Lys Trp  Gly Lys Thr Val Ile  Glu Tyr Arg Ser Gln  Lys Thr Ser
    1445                 1450                 1455

Arg Leu  Pro Ile Ile Asp Ile  Ala Pro Met Asp Ile  Gly Gly Pro
    1460                 1465                 1470

Glu Gln  Glu Phe Gly Val Asp  Ile Gly Pro Val Cys  Phe Leu
    1475                 1480                 1485


<210> SEQ ID NO 3
<211> LENGTH: 1466
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

Met Met Ser Phe Val Gln Lys Gly Ser Trp Leu Leu Leu Ala Leu Leu
1               5                   10                  15

His Pro Thr Ile Ile Leu Ala Gln Gln Glu Ala Val Glu Gly Gly Cys
            20                  25                  30

Ser His Leu Gly Gln Ser Tyr Ala Asp Arg Asp Val Trp Lys Pro Glu
        35                  40                  45

Pro Cys Gln Ile Cys Val Cys Asp Ser Gly Ser Val Leu Cys Asp Asp
    50                  55                  60

Ile Ile Cys Asp Asp Gln Glu Leu Asp Cys Pro Asn Pro Glu Ile Pro
65                  70                  75                  80

Phe Gly Glu Cys Cys Ala Val Cys Pro Gln Pro Pro Thr Ala Pro Thr
                85                  90                  95

Arg Pro Pro Asn Gly Gln Gly Pro Gln Gly Pro Lys Gly Asp Pro Gly
            100                 105                 110

Pro Pro Gly Ile Pro Gly Arg Asn Gly Asp Pro Gly Ile Pro Gly Gln
        115                 120                 125

Pro Gly Ser Pro Gly Ser Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys
    130                 135                 140

Pro Thr Gly Pro Gln Asn Tyr Ser Pro Gln Tyr Asp Ser Tyr Asp Val
145                 150                 155                 160

Lys Ser Gly Val Ala Val Gly Gly Leu Ala Gly Tyr Pro Gly Pro Ala
                165                 170                 175

Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Thr Ser Gly His Pro Gly
            180                 185                 190

Ser Pro Gly Ser Pro Gly Tyr Gln Gly Pro Pro Gly Glu Pro Gly Gln
        195                 200                 205
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```
Ala Gly Pro Ser Gly Pro Pro Gly Pro Pro Gly Ala Ile Gly Pro Ser
    210                 215                 220

Gly Pro Ala Gly Lys Asp Gly Glu Ser Gly Arg Pro Gly Arg Pro Gly
225                 230                 235                 240

Glu Arg Gly Leu Pro Gly Pro Pro Gly Ile Lys Gly Pro Ala Gly Ile
                245                 250                 255

Pro Gly Phe Pro Gly Met Lys Gly His Arg Gly Phe Asp Gly Arg Asn
            260                 265                 270

Gly Glu Lys Gly Glu Thr Gly Ala Pro Gly Leu Lys Gly Glu Asn Gly
        275                 280                 285

Leu Pro Gly Glu Asn Gly Ala Pro Gly Pro Met Gly Pro Arg Gly Ala
    290                 295                 300

Pro Gly Glu Arg Gly Arg Pro Gly Leu Pro Gly Ala Ala Gly Ala Arg
305                 310                 315                 320

Gly Asn Asp Gly Ala Arg Gly Ser Asp Gly Gln Pro Gly Pro Pro Gly
                325                 330                 335

Pro Pro Gly Thr Ala Gly Phe Pro Gly Ser Pro Gly Ala Lys Gly Glu
            340                 345                 350

Val Gly Pro Ala Gly Ser Pro Gly Ser Asn Gly Ala Pro Gly Gln Arg
        355                 360                 365

Gly Glu Pro Gly Pro Gln Gly His Ala Gly Ala Gln Gly Pro Pro Gly
    370                 375                 380

Pro Pro Gly Ile Asn Gly Ser Pro Gly Gly Lys Gly Glu Met Gly Pro
385                 390                 395                 400

Ala Gly Ile Pro Gly Ala Pro Gly Leu Met Gly Ala Arg Gly Pro Pro
                405                 410                 415

Gly Pro Ala Gly Ala Asn Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly
            420                 425                 430

Glu Pro Gly Lys Asn Gly Ala Lys Gly Glu Pro Gly Pro Arg Gly Glu
        435                 440                 445

Arg Gly Glu Ala Gly Ile Pro Gly Val Pro Gly Ala Lys Gly Glu Asp
    450                 455                 460

Gly Lys Asp Gly Ser Pro Gly Glu Pro Gly Ala Asn Gly Leu Pro Gly
465                 470                 475                 480

Ala Ala Gly Glu Arg Gly Ala Pro Gly Phe Arg Gly Pro Ala Gly Pro
                485                 490                 495

Asn Gly Ile Pro Gly Glu Lys Gly Pro Ala Gly Glu Arg Gly Ala Pro
            500                 505                 510

Gly Pro Ala Gly Pro Arg Gly Ala Ala Gly Glu Pro Gly Arg Asp Gly
        515                 520                 525

Val Pro Gly Gly Pro Gly Met Arg Gly Met Pro Gly Ser Pro Gly Gly
    530                 535                 540

Pro Gly Ser Asp Gly Lys Pro Gly Pro Pro Gly Ser Gln Gly Glu Ser
545                 550                 555                 560

Gly Arg Pro Gly Pro Pro Gly Pro Ser Gly Pro Arg Gly Gln Pro Gly
                565                 570                 575

Val Met Gly Phe Pro Gly Pro Lys Gly Asn Asp Gly Ala Pro Gly Lys
            580                 585                 590

Asn Gly Glu Arg Gly Gly Pro Gly Gly Pro Gly Pro Gln Gly Pro Pro
        595                 600                 605

Gly Lys Asn Gly Glu Thr Gly Pro Gln Gly Pro Pro Gly Pro Thr Gly
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    610                 615                 620

Pro Gly Gly Asp Lys Gly Asp Thr Gly Pro Pro Gly Pro Gln Gly Leu
625                 630                 635                 640

Gln Gly Leu Pro Gly Thr Gly Gly Pro Pro Gly Glu Asn Gly Lys Pro
                645                 650                 655

Gly Glu Pro Gly Pro Lys Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly
            660                 665                 670

Gly Lys Gly Asp Ala Gly Ala Pro Gly Glu Arg Gly Pro Pro Gly Leu
        675                 680                 685

Ala Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly Pro Pro Gly Pro Glu
    690                 695                 700

Gly Gly Lys Gly Ala Ala Gly Pro Pro Gly Pro Pro Gly Ala Ala Gly
705                 710                 715                 720

Thr Pro Gly Leu Gln Gly Met Pro Gly Glu Arg Gly Gly Leu Gly Ser
                725                 730                 735

Pro Gly Pro Lys Gly Asp Lys Gly Glu Pro Gly Gly Pro Gly Ala Asp
            740                 745                 750

Gly Val Pro Gly Lys Asp Gly Pro Arg Gly Pro Thr Gly Pro Ile Gly
        755                 760                 765

Pro Pro Gly Pro Ala Gly Gln Pro Gly Asp Lys Gly Glu Gly Gly Ala
    770                 775                 780

Pro Gly Leu Pro Gly Ile Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg
785                 790                 795                 800

Gly Glu Thr Gly Pro Pro Gly Pro Ala Gly Phe Pro Gly Ala Pro Gly
                805                 810                 815

Gln Asn Gly Glu Pro Gly Gly Lys Gly Glu Arg Gly Ala Pro Gly Glu
            820                 825                 830

Lys Gly Glu Gly Gly Pro Pro Gly Val Ala Gly Pro Pro Gly Gly Ser
        835                 840                 845

Gly Pro Ala Gly Pro Pro Gly Pro Gln Gly Val Lys Gly Glu Arg Gly
    850                 855                 860

Ser Pro Gly Gly Pro Gly Ala Ala Gly Phe Pro Gly Ala Arg Gly Leu
865                 870                 875                 880

Pro Gly Pro Pro Gly Ser Asn Gly Asn Pro Gly Pro Pro Gly Pro Ser
                885                 890                 895

Gly Ser Pro Gly Lys Asp Gly Pro Pro Gly Pro Ala Gly Asn Thr Gly
            900                 905                 910

Ala Pro Gly Ser Pro Gly Val Ser Gly Pro Lys Gly Asp Ala Gly Gln
        915                 920                 925

Pro Gly Glu Lys Gly Ser Pro Gly Ala Gln Gly Pro Pro Gly Ala Pro
    930                 935                 940

Gly Pro Leu Gly Ile Ala Gly Ile Thr Gly Ala Arg Gly Leu Ala Gly
945                 950                 955                 960

Pro Pro Gly Met Pro Gly Pro Arg Gly Ser Pro Gly Pro Gln Gly Val
                965                 970                 975

Lys Gly Glu Ser Gly Lys Pro Gly Ala Asn Gly Leu Ser Gly Glu Arg
            980                 985                 990

Gly Pro Pro Gly Pro Gln Gly Leu  Pro Gly Leu Ala Gly  Thr Ala Gly
        995                 1000                1005

Glu Pro  Gly Arg Asp Gly Asn  Pro Gly Ser Asp Gly  Leu Pro Gly
    1010                 1015                1020
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Arg Asp  Gly Ser Pro Gly Gly  Lys Gly Asp Arg Gly  Glu Asn Gly
    1025                1030                1035

Ser Pro  Gly Ala Pro Gly Ala  Pro Gly His Pro Gly  Pro Pro Gly
    1040                1045                1050

Pro Val  Gly Pro Ala Gly Lys  Ser Gly Asp Arg Gly  Glu Ser Gly
    1055                1060                1065

Pro Ala  Gly Pro Ala Gly Ala  Pro Gly Pro Ala Gly  Ser Arg Gly
    1070                1075                1080

Ala Pro  Gly Pro Gln Gly Pro  Arg Gly Asp Lys Gly  Glu Thr Gly
    1085                1090                1095

Glu Arg  Gly Ala Ala Gly Ile  Lys Gly His Arg Gly  Phe Pro Gly
    1100                1105                1110

Asn Pro  Gly Ala Pro Gly Ser  Pro Gly Pro Ala Gly  Gln Gln Gly
    1115                1120                1125

Ala Ile  Gly Ser Pro Gly Pro  Ala Gly Pro Arg Gly  Pro Val Gly
    1130                1135                1140

Pro Ser  Gly Pro Pro Gly Lys  Asp Gly Thr Ser Gly  His Pro Gly
    1145                1150                1155

Pro Ile  Gly Pro Pro Gly Pro  Arg Gly Asn Arg Gly  Glu Arg Gly
    1160                1165                1170

Ser Glu  Gly Ser Pro Gly His  Pro Gly Gln Pro Gly  Pro Pro Gly
    1175                1180                1185

Pro Pro  Gly Ala Pro Gly Pro  Cys Cys Gly Gly Val  Gly Ala Ala
    1190                1195                1200

Ala Ile  Ala Gly Ile Gly Gly  Glu Lys Ala Gly Gly  Phe Ala Pro
    1205                1210                1215

Tyr Tyr  Gly Asp Glu Pro Met  Asp Phe Lys Ile Asn  Thr Asp Glu
    1220                1225                1230

Ile Met  Thr Ser Leu Lys Ser  Val Asn Gly Gln Ile  Glu Ser Leu
    1235                1240                1245

Ile Ser  Pro Asp Gly Ser Arg  Lys Asn Pro Ala Arg  Asn Cys Arg
    1250                1255                1260

Asp Leu  Lys Phe Cys His Pro  Glu Leu Lys Ser Gly  Glu Tyr Trp
    1265                1270                1275

Val Asp  Pro Asn Gln Gly Cys  Lys Leu Asp Ala Ile  Lys Val Phe
    1280                1285                1290

Cys Asn  Met Glu Thr Gly Glu  Thr Cys Ile Ser Ala  Asn Pro Leu
    1295                1300                1305

Asn Val  Pro Arg Lys His Trp  Trp Thr Asp Ser Ser  Ala Glu Lys
    1310                1315                1320

Lys His  Val Trp Phe Gly Glu  Ser Met Asp Gly Gly  Phe Gln Phe
    1325                1330                1335

Ser Tyr  Gly Asn Pro Glu Leu  Pro Glu Asp Val Leu  Asp Val Gln
    1340                1345                1350

Leu Ala  Phe Leu Arg Leu Leu  Ser Ser Arg Ala Ser  Gln Asn Ile
    1355                1360                1365

Thr Tyr  His Cys Lys Asn Ser  Ile Ala Tyr Met Asp  Gln Ala Ser
    1370                1375                1380

Gly Asn  Val Lys Lys Ala Leu  Lys Leu Met Gly Ser  Asn Glu Gly
    1385                1390                1395
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Glu Phe  Lys Ala Glu Gly Asn  Ser Lys Phe Thr Tyr  Thr Val Leu
    1400                 1405                 1410

Glu Asp  Gly Cys Thr Lys His  Thr Gly Glu Trp Ser  Lys Thr Val
    1415                 1420                 1425

Phe Glu  Tyr Arg Thr Arg Lys  Ala Val Arg Leu Pro  Ile Val Asp
    1430                 1435                 1440

Ile Ala  Pro Tyr Asp Ile Gly  Gly Pro Asp Gln Glu  Phe Gly Val
    1445                 1450                 1455

Asp Val  Gly Pro Val Cys Phe  Leu
    1460                 1465


<210> SEQ ID NO 4
<211> LENGTH: 1669
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

Met Gly Pro Arg Leu Ser Val Trp Leu Leu Leu Leu Pro Ala Ala Leu
1               5                   10                  15

Leu Leu His Glu Glu His Ser Arg Ala Ala Ala Lys Gly Gly Cys Ala
            20                  25                  30

Gly Ser Gly Cys Gly Lys Cys Asp Cys His Gly Val Lys Gly Gln Lys
        35                  40                  45

Gly Glu Arg Gly Leu Pro Gly Leu Gln Gly Val Ile Gly Phe Pro Gly
    50                  55                  60

Met Gln Gly Pro Glu Gly Pro Gln Gly Pro Pro Gly Gln Lys Gly Asp
65                  70                  75                  80

Thr Gly Glu Pro Gly Leu Pro Gly Thr Lys Gly Thr Arg Gly Pro Pro
                85                  90                  95

Gly Ala Ser Gly Tyr Pro Gly Asn Pro Gly Leu Pro Gly Ile Pro Gly
            100                 105                 110

Gln Asp Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly Cys Asn Gly Thr
        115                 120                 125

Lys Gly Glu Arg Gly Pro Leu Gly Pro Pro Gly Leu Pro Gly Phe Ala
    130                 135                 140

Gly Asn Pro Gly Pro Pro Gly Leu Pro Gly Met Lys Gly Asp Pro Gly
145                 150                 155                 160

Glu Ile Leu Gly His Val Pro Gly Met Leu Leu Lys Gly Glu Arg Gly
                165                 170                 175

Phe Pro Gly Ile Pro Gly Thr Pro Gly Pro Pro Gly Leu Pro Gly Leu
            180                 185                 190

Gln Gly Pro Val Gly Pro Pro Gly Phe Thr Gly Pro Pro Gly Pro Pro
        195                 200                 205

Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Gln Met Gly Leu Ser Phe
    210                 215                 220

Gln Gly Pro Lys Gly Asp Lys Gly Asp Gln Gly Val Ser Gly Pro Pro
225                 230                 235                 240

Gly Val Pro Gly Gln Ala Gln Val Gln Glu Lys Gly Asp Phe Ala Thr
                245                 250                 255

Lys Gly Glu Lys Gly Gln Lys Gly Glu Pro Gly Phe Gln Gly Met Pro
            260                 265                 270

Gly Val Gly Glu Lys Gly Glu Pro Gly Lys Pro Gly Pro Arg Gly Lys
        275                 280                 285
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```
Pro Gly Lys Asp Gly Asp Lys Gly Glu Lys Gly Ser Pro Gly Phe Pro
    290                 295                 300

Gly Glu Pro Gly Tyr Pro Gly Leu Ile Gly Arg Gln Gly Pro Gln Gly
305                 310                 315                 320

Glu Lys Gly Glu Ala Gly Pro Pro Gly Pro Pro Gly Ile Val Ile Gly
                325                 330                 335

Thr Gly Pro Leu Gly Glu Lys Gly Glu Arg Gly Tyr Pro Gly Thr Pro
            340                 345                 350

Gly Pro Arg Gly Glu Pro Gly Pro Lys Gly Phe Pro Gly Leu Pro Gly
        355                 360                 365

Gln Pro Gly Pro Pro Gly Leu Pro Val Pro Gly Gln Ala Gly Ala Pro
    370                 375                 380

Gly Phe Pro Gly Glu Arg Gly Glu Lys Gly Asp Arg Gly Phe Pro Gly
385                 390                 395                 400

Thr Ser Leu Pro Gly Pro Ser Gly Arg Asp Gly Leu Pro Gly Pro Pro
                405                 410                 415

Gly Ser Pro Gly Pro Pro Gly Gln Pro Gly Tyr Thr Asn Gly Ile Val
            420                 425                 430

Glu Cys Gln Pro Gly Pro Pro Gly Asp Gln Gly Pro Pro Gly Ile Pro
        435                 440                 445

Gly Gln Pro Gly Phe Ile Gly Glu Ile Gly Glu Lys Gly Gln Lys Gly
    450                 455                 460

Glu Ser Cys Leu Ile Cys Asp Ile Asp Gly Tyr Arg Gly Pro Pro Gly
465                 470                 475                 480

Pro Gln Gly Pro Pro Gly Glu Ile Gly Phe Pro Gly Gln Pro Gly Ala
                485                 490                 495

Lys Gly Asp Arg Gly Leu Pro Gly Arg Asp Gly Val Ala Gly Val Pro
            500                 505                 510

Gly Pro Gln Gly Thr Pro Gly Leu Ile Gly Gln Pro Gly Ala Lys Gly
        515                 520                 525

Glu Pro Gly Glu Phe Tyr Phe Asp Leu Arg Leu Lys Gly Asp Lys Gly
    530                 535                 540

Asp Pro Gly Phe Pro Gly Gln Pro Gly Met Pro Gly Arg Ala Gly Ser
545                 550                 555                 560

Pro Gly Arg Asp Gly His Pro Gly Leu Pro Gly Pro Lys Gly Ser Pro
                565                 570                 575

Gly Ser Val Gly Leu Lys Gly Glu Arg Gly Pro Pro Gly Gly Val Gly
            580                 585                 590

Phe Pro Gly Ser Arg Gly Asp Thr Gly Pro Pro Gly Pro Pro Gly Tyr
        595                 600                 605

Gly Pro Ala Gly Pro Ile Gly Asp Lys Gly Gln Ala Gly Phe Pro Gly
    610                 615                 620

Gly Pro Gly Ser Pro Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Lys
625                 630                 635                 640

Ile Val Pro Leu Pro Gly Pro Pro Gly Ala Glu Gly Leu Pro Gly Ser
                645                 650                 655

Pro Gly Phe Pro Gly Pro Gln Gly Asp Arg Gly Phe Pro Gly Thr Pro
            660                 665                 670

Gly Arg Pro Gly Leu Pro Gly Glu Lys Gly Ala Val Gly Gln Pro Gly
        675                 680                 685
```

-continued

```
Ile Gly Phe Pro Gly Pro Pro Gly Pro Lys Gly Val Asp Gly Leu Pro
    690                 695                 700

Gly Asp Met Gly Pro Pro Gly Thr Pro Gly Arg Pro Gly Phe Asn Gly
705                 710                 715                 720

Leu Pro Gly Asn Pro Gly Val Gln Gly Gln Lys Gly Glu Pro Gly Val
                725                 730                 735

Gly Leu Pro Gly Leu Lys Gly Leu Pro Gly Leu Pro Gly Ile Pro Gly
            740                 745                 750

Thr Pro Gly Glu Lys Gly Ser Ile Gly Val Pro Gly Val Pro Gly Glu
        755                 760                 765

His Gly Ala Ile Gly Pro Pro Gly Leu Gln Gly Ile Arg Gly Glu Pro
    770                 775                 780

Gly Pro Pro Gly Leu Pro Gly Ser Val Gly Ser Pro Gly Val Pro Gly
785                 790                 795                 800

Ile Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Gly Gln Gly Pro Pro
                805                 810                 815

Gly Leu Ser Gly Pro Pro Gly Ile Lys Gly Glu Lys Gly Phe Pro Gly
            820                 825                 830

Phe Pro Gly Leu Asp Met Pro Gly Pro Lys Gly Asp Lys Gly Ala Gln
        835                 840                 845

Gly Leu Pro Gly Ile Thr Gly Gln Ser Gly Leu Pro Gly Leu Pro Gly
    850                 855                 860

Gln Gln Gly Ala Pro Gly Ile Pro Gly Phe Pro Gly Ser Lys Gly Glu
865                 870                 875                 880

Met Gly Val Met Gly Thr Pro Gly Gln Pro Gly Ser Pro Gly Pro Val
                885                 890                 895

Gly Ala Pro Gly Leu Pro Gly Glu Lys Gly Asp His Gly Phe Pro Gly
            900                 905                 910

Ser Ser Gly Pro Arg Gly Asp Pro Gly Leu Lys Gly Asp Lys Gly Asp
        915                 920                 925

Val Gly Leu Pro Gly Lys Pro Gly Ser Met Asp Lys Val Asp Met Gly
    930                 935                 940

Ser Met Lys Gly Gln Lys Gly Asp Gln Gly Glu Lys Gly Gln Ile Gly
945                 950                 955                 960

Pro Ile Gly Glu Lys Gly Ser Arg Gly Asp Pro Gly Thr Pro Gly Val
                965                 970                 975

Pro Gly Lys Asp Gly Gln Ala Gly Gln Pro Gly Gln Pro Gly Pro Lys
            980                 985                 990

Gly Asp Pro Gly Ile Ser Gly Thr  Pro Gly Ala Pro Gly  Leu Pro Gly
        995                 1000                 1005

Pro Lys  Gly Ser Val Gly Gly  Met Gly Leu Pro Gly  Thr Pro Gly
    1010                 1015                 1020

Glu Lys  Gly Val Pro Gly Ile  Pro Gly Pro Gln Gly  Ser Pro Gly
    1025                 1030                 1035

Leu Pro  Gly Asp Lys Gly Ala  Lys Gly Glu Lys Gly  Gln Ala Gly
    1040                 1045                 1050

Pro Pro  Gly Ile Gly Ile Pro  Gly Leu Arg Gly Glu  Lys Gly Asp
    1055                 1060                 1065

Gln Gly  Ile Ala Gly Phe Pro  Gly Ser Pro Gly Glu  Lys Gly Glu
    1070                 1075                 1080

Lys Gly  Ser Ile Gly Ile Pro  Gly Met Pro Gly Ser  Pro Gly Leu
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    1085                1090                1095

Lys Gly  Ser Pro Gly Ser Val  Gly Tyr Pro Gly Ser  Pro Gly Leu
    1100                1105                1110

Pro Gly  Glu Lys Gly Asp Lys  Gly Leu Pro Gly Leu  Asp Gly Ile
    1115                1120                1125

Pro Gly  Val Lys Gly Glu Ala  Gly Leu Pro Gly Thr  Pro Gly Pro
    1130                1135                1140

Thr Gly  Pro Ala Gly Gln Lys  Gly Glu Pro Gly Ser  Asp Gly Ile
    1145                1150                1155

Pro Gly  Ser Ala Gly Glu Lys  Gly Glu Pro Gly Leu  Pro Gly Arg
    1160                1165                1170

Gly Phe  Pro Gly Phe Pro Gly  Ala Lys Gly Asp Lys  Gly Ser Lys
    1175                1180                1185

Gly Glu  Val Gly Phe Pro Gly  Leu Ala Gly Ser Pro  Gly Ile Pro
    1190                1195                1200

Gly Ser  Lys Gly Glu Gln Gly  Phe Met Gly Pro Pro  Gly Pro Gln
    1205                1210                1215

Gly Gln  Pro Gly Leu Pro Gly  Ser Pro Gly His Ala  Thr Glu Gly
    1220                1225                1230

Pro Lys  Gly Asp Arg Gly Pro  Gln Gly Gln Pro Gly  Leu Pro Gly
    1235                1240                1245

Leu Pro  Gly Pro Met Gly Pro  Pro Gly Leu Pro Gly  Ile Asp Gly
    1250                1255                1260

Val Lys  Gly Asp Lys Gly Asn  Pro Gly Trp Pro Gly  Ala Pro Gly
    1265                1270                1275

Val Pro  Gly Pro Lys Gly Asp  Pro Gly Phe Gln Gly  Met Pro Gly
    1280                1285                1290

Ile Gly  Gly Ser Pro Gly Ile  Thr Gly Ser Lys Gly  Asp Met Gly
    1295                1300                1305

Pro Pro  Gly Val Pro Gly Phe  Gln Gly Pro Lys Gly  Leu Pro Gly
    1310                1315                1320

Leu Gln  Gly Ile Lys Gly Asp  Gln Gly Asp Gln Gly  Val Pro Gly
    1325                1330                1335

Ala Lys  Gly Leu Pro Gly Pro  Pro Gly Pro Pro Gly  Pro Tyr Asp
    1340                1345                1350

Ile Ile  Lys Gly Glu Pro Gly  Leu Pro Gly Pro Glu  Gly Pro Pro
    1355                1360                1365

Gly Leu  Lys Gly Leu Gln Gly  Leu Pro Gly Pro Lys  Gly Gln Gln
    1370                1375                1380

Gly Val  Thr Gly Leu Val Gly  Ile Pro Gly Pro Pro  Gly Ile Pro
    1385                1390                1395

Gly Phe  Asp Gly Ala Pro Gly  Gln Lys Gly Glu Met  Gly Pro Ala
    1400                1405                1410

Gly Pro  Thr Gly Pro Arg Gly  Phe Pro Gly Pro Pro  Gly Pro Asp
    1415                1420                1425

Gly Leu  Pro Gly Ser Met Gly  Pro Pro Gly Thr Pro  Ser Val Asp
    1430                1435                1440

His Gly  Phe Leu Val Thr Arg  His Ser Gln Thr Ile  Asp Asp Pro
    1445                1450                1455

Gln Cys  Pro Ser Gly Thr Lys  Ile Leu Tyr His Gly  Tyr Ser Leu
    1460                1465                1470
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Leu Tyr  Val Gln Gly Asn Glu  Arg Ala His Gly Gln  Asp Leu Gly
    1475                 1480                 1485

Thr Ala  Gly Ser Cys Leu Arg  Lys Phe Ser Thr Met  Pro Phe Leu
    1490                 1495                 1500

Phe Cys  Asn Ile Asn Asn Val  Cys Asn Phe Ala Ser  Arg Asn Asp
    1505                 1510                 1515

Tyr Ser  Tyr Trp Leu Ser Thr  Pro Glu Pro Met Pro  Met Ser Met
    1520                 1525                 1530

Ala Pro  Ile Thr Gly Glu Asn  Ile Arg Pro Phe Ile  Ser Arg Cys
    1535                 1540                 1545

Ala Val  Cys Glu Ala Pro Ala  Met Val Met Ala Val  His Ser Gln
    1550                 1555                 1560

Thr Ile  Gln Ile Pro Pro Cys  Pro Ser Gly Trp Ser  Ser Leu Trp
    1565                 1570                 1575

Ile Gly  Tyr Ser Phe Val Met  His Thr Ser Ala Gly  Ala Glu Gly
    1580                 1585                 1590

Ser Gly  Gln Ala Leu Ala Ser  Pro Gly Ser Cys Leu  Glu Glu Phe
    1595                 1600                 1605

Arg Ser  Ala Pro Phe Ile Glu  Cys His Gly Arg Gly  Thr Cys Asn
    1610                 1615                 1620

Tyr Tyr  Ala Asn Ala Tyr Ser  Phe Trp Leu Ala Thr  Ile Glu Arg
    1625                 1630                 1635

Ser Glu  Met Phe Lys Lys Pro  Thr Pro Ser Thr Leu  Lys Ala Gly
    1640                 1645                 1650

Glu Leu  Arg Thr His Val Ser  Arg Cys Gln Val Cys  Met Arg Arg
    1655                 1660                 1665

Thr


<210> SEQ ID NO 5
<211> LENGTH: 1028
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

Met Arg Ala Ala Arg Ala Leu Leu Pro Leu Leu Leu Gln Ala Cys Trp
1               5                   10                  15

Thr Ala Ala Gln Asp Glu Pro Glu Thr Pro Arg Ala Val Ala Phe Gln
            20                  25                  30

Asp Cys Pro Val Asp Leu Phe Phe Val Leu Asp Thr Ser Glu Ser Val
        35                  40                  45

Ala Leu Arg Leu Lys Pro Tyr Gly Ala Leu Val Asp Lys Val Lys Ser
    50                  55                  60

Phe Thr Lys Arg Phe Ile Asp Asn Leu Arg Asp Arg Tyr Tyr Arg Cys
65                  70                  75                  80

Asp Arg Asn Leu Val Trp Asn Ala Gly Ala Leu His Tyr Ser Asp Glu
                85                  90                  95

Val Glu Ile Ile Gln Gly Leu Thr Arg Met Pro Gly Gly Arg Asp Ala
            100                 105                 110

Leu Lys Ser Ser Val Asp Ala Val Lys Tyr Phe Gly Lys Gly Thr Tyr
        115                 120                 125

Thr Asp Cys Ala Ile Lys Lys Gly Leu Glu Gln Leu Leu Val Gly Gly
    130                 135                 140
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Ser His Leu Lys Glu Asn Lys Tyr Leu Ile Val Val Thr Asp Gly His
145                 150                 155                 160

Pro Leu Glu Gly Tyr Lys Glu Pro Cys Gly Gly Leu Glu Asp Ala Val
                165                 170                 175

Asn Glu Ala Lys His Leu Gly Val Lys Val Phe Ser Val Ala Ile Thr
            180                 185                 190

Pro Asp His Leu Glu Pro Arg Leu Ser Ile Ile Ala Thr Asp His Thr
        195                 200                 205

Tyr Arg Arg Asn Phe Thr Ala Ala Asp Trp Gly Gln Ser Arg Asp Ala
    210                 215                 220

Glu Glu Ala Ile Ser Gln Thr Ile Asp Thr Ile Val Asp Met Ile Lys
225                 230                 235                 240

Asn Asn Val Glu Gln Val Cys Cys Ser Phe Glu Cys Gln Pro Ala Arg
                245                 250                 255

Gly Pro Pro Gly Leu Arg Gly Asp Pro Gly Phe Glu Gly Glu Arg Gly
            260                 265                 270

Lys Pro Gly Leu Pro Gly Glu Lys Gly Glu Ala Gly Asp Pro Gly Arg
        275                 280                 285

Pro Gly Asp Leu Gly Pro Val Gly Tyr Gln Gly Met Lys Gly Glu Lys
    290                 295                 300

Gly Ser Arg Gly Glu Lys Gly Ser Arg Gly Pro Lys Gly Tyr Lys Gly
305                 310                 315                 320

Glu Lys Gly Lys Arg Gly Ile Asp Gly Val Asp Gly Val Lys Gly Glu
                325                 330                 335

Met Gly Tyr Pro Gly Leu Pro Gly Cys Lys Gly Ser Pro Gly Phe Asp
            340                 345                 350

Gly Ile Gln Gly Pro Pro Gly Pro Lys Gly Asp Pro Gly Ala Phe Gly
        355                 360                 365

Leu Lys Gly Glu Lys Gly Glu Pro Gly Ala Asp Gly Glu Ala Gly Arg
    370                 375                 380

Pro Gly Ser Ser Gly Pro Ser Gly Asp Glu Gly Gln Pro Gly Glu Pro
385                 390                 395                 400

Gly Pro Pro Gly Glu Lys Gly Glu Ala Gly Asp Glu Gly Asn Pro Gly
                405                 410                 415

Pro Asp Gly Ala Pro Gly Glu Arg Gly Gly Pro Gly Glu Arg Gly Pro
            420                 425                 430

Arg Gly Thr Pro Gly Thr Arg Gly Pro Arg Gly Asp Pro Gly Glu Ala
        435                 440                 445

Gly Pro Gln Gly Asp Gln Gly Arg Glu Gly Pro Val Gly Val Pro Gly
    450                 455                 460

Asp Pro Gly Glu Ala Gly Pro Ile Gly Pro Lys Gly Tyr Arg Gly Asp
465                 470                 475                 480

Glu Gly Pro Pro Gly Ser Glu Gly Ala Arg Gly Ala Pro Gly Pro Ala
                485                 490                 495

Gly Pro Pro Gly Asp Pro Gly Leu Met Gly Glu Arg Gly Glu Asp Gly
            500                 505                 510

Pro Ala Gly Asn Gly Thr Glu Gly Phe Pro Gly Phe Pro Gly Tyr Pro
        515                 520                 525

Gly Asn Arg Gly Ala Pro Gly Ile Asn Gly Thr Lys Gly Tyr Pro Gly
    530                 535                 540
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Leu Lys Gly Asp Glu Gly Glu Ala Gly Asp Pro Gly Asp Asp Asn Asn
545                 550                 555                 560

Asp Ile Ala Pro Arg Gly Val Lys Gly Ala Lys Gly Tyr Arg Gly Pro
                565                 570                 575

Glu Gly Pro Gln Gly Pro Pro Gly His Gln Gly Pro Pro Gly Pro Asp
            580                 585                 590

Glu Cys Glu Ile Leu Asp Ile Ile Met Lys Met Cys Ser Cys Cys Glu
        595                 600                 605

Cys Lys Cys Gly Pro Ile Asp Leu Leu Phe Val Leu Asp Ser Ser Glu
    610                 615                 620

Ser Ile Gly Leu Gln Asn Phe Glu Ile Ala Lys Asp Phe Val Val Lys
625                 630                 635                 640

Val Ile Asp Arg Leu Ser Arg Asp Glu Leu Val Lys Phe Glu Pro Gly
                645                 650                 655

Gln Ser Tyr Ala Gly Val Val Gln Tyr Ser His Ser Gln Met Gln Glu
            660                 665                 670

His Val Ser Leu Arg Ser Pro Ser Ile Arg Asn Val Gln Glu Leu Lys
        675                 680                 685

Glu Ala Ile Lys Ser Leu Gln Trp Met Ala Gly Gly Thr Phe Thr Gly
    690                 695                 700

Glu Ala Leu Gln Tyr Thr Arg Asp Gln Leu Leu Pro Pro Ser Pro Asn
705                 710                 715                 720

Asn Arg Ile Ala Leu Val Ile Thr Asp Gly Arg Ser Asp Thr Gln Arg
                725                 730                 735

Asp Thr Thr Pro Leu Asn Val Leu Cys Ser Pro Gly Ile Gln Val Val
            740                 745                 750

Ser Val Gly Ile Lys Asp Val Phe Asp Phe Ile Pro Gly Ser Asp Gln
        755                 760                 765

Leu Asn Val Ile Ser Cys Gln Gly Leu Ala Pro Ser Gln Gly Arg Pro
    770                 775                 780

Gly Leu Ser Leu Val Lys Glu Asn Tyr Ala Glu Leu Leu Glu Asp Ala
785                 790                 795                 800

Phe Leu Lys Asn Val Thr Ala Gln Ile Cys Ile Asp Lys Lys Cys Pro
                805                 810                 815

Asp Tyr Thr Cys Pro Ile Thr Phe Ser Ser Pro Ala Asp Ile Thr Ile
            820                 825                 830

Leu Leu Asp Gly Ser Ala Ser Val Gly Ser His Asn Phe Asp Thr Thr
        835                 840                 845

Lys Arg Phe Ala Lys Arg Leu Ala Glu Arg Phe Leu Thr Ala Gly Arg
    850                 855                 860

Thr Asp Pro Ala His Asp Val Arg Val Ala Val Val Gln Tyr Ser Gly
865                 870                 875                 880

Thr Gly Gln Gln Arg Pro Glu Arg Ala Ser Leu Gln Phe Leu Gln Asn
                885                 890                 895

Tyr Thr Ala Leu Ala Ser Ala Val Asp Ala Met Asp Phe Ile Asn Asp
            900                 905                 910

Ala Thr Asp Val Asn Asp Ala Leu Gly Tyr Val Thr Arg Phe Tyr Arg
        915                 920                 925

Glu Ala Ser Ser Gly Ala Ala Lys Lys Arg Leu Leu Leu Phe Ser Asp
    930                 935                 940

Gly Asn Ser Gln Gly Ala Thr Pro Ala Ala Ile Glu Lys Ala Val Gln
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945                 950                 955                 960

Glu Ala Gln Arg Ala Gly Ile Glu Ile Phe Val Val Val Val Gly Arg
                965                 970                 975

Gln Val Asn Glu Pro His Ile Arg Val Leu Val Thr Gly Lys Thr Ala
            980                 985                 990

Glu Tyr Asp Val Ala Tyr Gly Glu  Ser His Leu Phe Arg  Val Pro Ser
        995                 1000                 1005

Tyr Gln  Ala Leu Leu Arg Gly  Val Phe His Gln Thr  Val Ser Arg
    1010                 1015                 1020

Lys Val  Ala Leu Gly
    1025


<210> SEQ ID NO 6
<211> LENGTH: 3177
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

Met Arg Lys His Arg His Leu Pro Leu Val Ala Val Phe Cys Leu Phe
1               5                   10                  15

Leu Ser Gly Phe Pro Thr Thr His Ala Gln Gln Gln Gln Ala Asp Val
            20                  25                  30

Lys Asn Gly Ala Ala Ala Asp Ile Ile Phe Leu Val Asp Ser Ser Trp
        35                  40                  45

Thr Ile Gly Glu Glu His Phe Gln Leu Val Arg Glu Phe Leu Tyr Asp
    50                  55                  60

Val Val Lys Ser Leu Ala Val Gly Glu Asn Asp Phe His Phe Ala Leu
65                  70                  75                  80

Val Gln Phe Asn Gly Asn Pro His Thr Glu Phe Leu Leu Asn Thr Tyr
                85                  90                  95

Arg Thr Lys Gln Glu Val Leu Ser His Ile Ser Asn Met Ser Tyr Ile
            100                 105                 110

Gly Gly Thr Asn Gln Thr Gly Lys Gly Leu Glu Tyr Ile Met Gln Ser
        115                 120                 125

His Leu Thr Lys Ala Ala Gly Ser Arg Ala Gly Asp Gly Val Pro Gln
    130                 135                 140

Val Ile Val Val Leu Thr Asp Gly His Ser Lys Asp Gly Leu Ala Leu
145                 150                 155                 160

Pro Ser Ala Glu Leu Lys Ser Ala Asp Val Asn Val Phe Ala Ile Gly
                165                 170                 175

Val Glu Asp Ala Asp Glu Gly Ala Leu Lys Glu Ile Ala Ser Glu Pro
            180                 185                 190

Leu Asn Met His Met Phe Asn Leu Glu Asn Phe Thr Ser Leu His Asp
        195                 200                 205

Ile Val Gly Asn Leu Val Ser Cys Val His Ser Ser Val Ser Pro Glu
    210                 215                 220

Arg Ala Gly Asp Thr Glu Thr Leu Lys Asp Ile Thr Ala Gln Asp Ser
225                 230                 235                 240

Ala Asp Ile Ile Phe Leu Ile Asp Gly Ser Asn Asn Thr Gly Ser Val
                245                 250                 255

Asn Phe Ala Val Ile Leu Asp Phe Leu Val Asn Leu Leu Glu Lys Leu
            260                 265                 270
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Pro Ile Gly Thr Gln Gln Ile Arg Val Gly Val Val Gln Phe Ser Asp
        275                 280                 285

Glu Pro Arg Thr Met Phe Ser Leu Asp Thr Tyr Ser Thr Lys Ala Gln
    290                 295                 300

Val Leu Gly Ala Val Lys Ala Leu Gly Phe Ala Gly Gly Glu Leu Ala
305                 310                 315                 320

Asn Ile Gly Leu Ala Leu Asp Phe Val Val Glu Asn His Phe Thr Arg
                325                 330                 335

Ala Gly Gly Ser Arg Val Glu Glu Gly Val Pro Gln Val Leu Val Leu
            340                 345                 350

Ile Ser Ala Gly Pro Ser Ser Asp Glu Ile Arg Tyr Gly Val Val Ala
        355                 360                 365

Leu Lys Gln Ala Ser Val Phe Ser Phe Gly Leu Gly Ala Gln Ala Ala
    370                 375                 380

Ser Arg Ala Glu Leu Gln His Ile Ala Thr Asp Asp Asn Leu Val Phe
385                 390                 395                 400

Thr Val Pro Glu Phe Arg Ser Phe Gly Asp Leu Gln Glu Lys Leu Leu
                405                 410                 415

Pro Tyr Ile Val Gly Val Ala Gln Arg His Ile Val Leu Lys Pro Pro
            420                 425                 430

Thr Ile Val Thr Gln Val Ile Glu Val Asn Lys Arg Asp Ile Val Phe
        435                 440                 445

Leu Val Asp Gly Ser Ser Ala Leu Gly Leu Ala Asn Phe Asn Ala Ile
    450                 455                 460

Arg Asp Phe Ile Ala Lys Val Ile Gln Arg Leu Glu Ile Gly Gln Asp
465                 470                 475                 480

Leu Ile Gln Val Ala Val Ala Gln Tyr Ala Asp Thr Val Arg Pro Glu
                485                 490                 495

Phe Tyr Phe Asn Thr His Pro Thr Lys Arg Glu Val Ile Thr Ala Val
            500                 505                 510

Arg Lys Met Lys Pro Leu Asp Gly Ser Ala Leu Tyr Thr Gly Ser Ala
        515                 520                 525

Leu Asp Phe Val Arg Asn Asn Leu Phe Thr Ser Ser Ala Gly Tyr Arg
    530                 535                 540

Ala Ala Glu Gly Ile Pro Lys Leu Leu Val Leu Ile Thr Gly Gly Lys
545                 550                 555                 560

Ser Leu Asp Glu Ile Ser Gln Pro Ala Gln Glu Leu Lys Arg Ser Ser
                565                 570                 575

Ile Met Ala Phe Ala Ile Gly Asn Lys Gly Ala Asp Gln Ala Glu Leu
            580                 585                 590

Glu Glu Ile Ala Phe Asp Ser Ser Leu Val Phe Ile Pro Ala Glu Phe
        595                 600                 605

Arg Ala Ala Pro Leu Gln Gly Met Leu Pro Gly Leu Leu Ala Pro Leu
    610                 615                 620

Arg Thr Leu Ser Gly Thr Pro Glu Val His Ser Asn Lys Arg Asp Ile
625                 630                 635                 640

Ile Phe Leu Leu Asp Gly Ser Ala Asn Val Gly Lys Thr Asn Phe Pro
                645                 650                 655

Tyr Val Arg Asp Phe Val Met Asn Leu Val Asn Ser Leu Asp Ile Gly
            660                 665                 670

Asn Asp Asn Ile Arg Val Gly Leu Val Gln Phe Ser Asp Thr Pro Val
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        675                 680                 685

Thr Glu Phe Ser Leu Asn Thr Tyr Gln Thr Lys Ser Asp Ile Leu Gly
    690                 695                 700

His Leu Arg Gln Leu Gln Leu Gln Gly Gly Ser Gly Leu Asn Thr Gly
705                 710                 715                 720

Ser Ala Leu Ser Tyr Val Tyr Ala Asn His Phe Thr Glu Ala Gly Gly
                725                 730                 735

Ser Arg Ile Arg Glu His Val Pro Gln Leu Leu Leu Leu Leu Thr Ala
            740                 745                 750

Gly Gln Ser Glu Asp Ser Tyr Leu Gln Ala Ala Asn Ala Leu Thr Arg
        755                 760                 765

Ala Gly Ile Leu Thr Phe Cys Val Gly Ala Ser Gln Ala Asn Lys Ala
    770                 775                 780

Glu Leu Glu Gln Ile Ala Phe Asn Pro Ser Leu Val Tyr Leu Met Asp
785                 790                 795                 800

Asp Phe Ser Ser Leu Pro Ala Leu Pro Gln Gln Leu Ile Gln Pro Leu
                805                 810                 815

Thr Thr Tyr Val Ser Gly Gly Val Glu Glu Val Pro Leu Ala Gln Pro
            820                 825                 830

Glu Ser Lys Arg Asp Ile Leu Phe Leu Phe Asp Gly Ser Ala Asn Leu
        835                 840                 845

Val Gly Gln Phe Pro Val Val Arg Asp Phe Leu Tyr Lys Ile Ile Asp
    850                 855                 860

Glu Leu Asn Val Lys Pro Glu Gly Thr Arg Ile Ala Val Ala Gln Tyr
865                 870                 875                 880

Ser Asp Asp Val Lys Val Glu Ser Arg Phe Asp Glu His Gln Ser Lys
                885                 890                 895

Pro Glu Ile Leu Asn Leu Val Lys Arg Met Lys Ile Lys Thr Gly Lys
            900                 905                 910

Ala Leu Asn Leu Gly Tyr Ala Leu Asp Tyr Ala Gln Arg Tyr Ile Phe
        915                 920                 925

Val Lys Ser Ala Gly Ser Arg Ile Glu Asp Gly Val Leu Gln Phe Leu
    930                 935                 940

Val Leu Leu Val Ala Gly Arg Ser Ser Asp Arg Val Asp Gly Pro Ala
945                 950                 955                 960

Ser Asn Leu Lys Gln Ser Gly Val Val Pro Phe Ile Phe Gln Ala Lys
                965                 970                 975

Asn Ala Asp Pro Ala Glu Leu Glu Gln Ile Val Leu Ser Pro Ala Phe
            980                 985                 990

Ile Leu Ala Ala Glu Ser Leu Pro  Lys Ile Gly Asp Leu  His Pro Gln
        995                 1000                 1005

Ile Val  Asn Leu Leu Lys Ser  Val His Asn Gly Ala  Pro Ala Pro
    1010                 1015                 1020

Val Ser  Gly Glu Lys Asp Val  Val Phe Leu Leu Asp  Gly Ser Glu
    1025                 1030                 1035

Gly Val  Arg Ser Gly Phe Pro  Leu Leu Lys Glu Phe  Val Gln Arg
    1040                 1045                 1050

Val Val  Glu Ser Leu Asp Val  Gly Gln Asp Arg Val  Arg Val Ala
    1055                 1060                 1065

Val Val  Gln Tyr Ser Asp Arg  Thr Arg Pro Glu Phe  Tyr Leu Asn
    1070                 1075                 1080
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Ser Tyr  Met Asn Lys Gln Asp  Val Val Asn Ala Val  Arg Gln Leu
    1085                 1090                 1095

Thr Leu  Leu Gly Gly Pro Thr  Pro Asn Thr Gly Ala  Ala Leu Glu
    1100                 1105                 1110

Phe Val  Leu Arg Asn Ile Leu  Val Ser Ser Ala Gly  Ser Arg Ile
    1115                 1120                 1125

Thr Glu  Gly Val Pro Gln Leu  Leu Ile Val Leu Thr  Ala Asp Arg
    1130                 1135                 1140

Ser Gly  Asp Asp Val Arg Asn  Pro Ser Val Val Val  Lys Arg Gly
    1145                 1150                 1155

Gly Ala  Val Pro Ile Gly Ile  Gly Ile Gly Asn Ala  Asp Ile Thr
    1160                 1165                 1170

Glu Met  Gln Thr Ile Ser Phe  Ile Pro Asp Phe Ala  Val Ala Ile
    1175                 1180                 1185

Pro Thr  Phe Arg Gln Leu Gly  Thr Val Gln Gln Val  Ile Ser Glu
    1190                 1195                 1200

Arg Val  Thr Gln Leu Thr Arg  Glu Glu Leu Ser Arg  Leu Gln Pro
    1205                 1210                 1215

Val Leu  Gln Pro Leu Pro Ser  Pro Gly Val Gly Gly  Lys Arg Asp
    1220                 1225                 1230

Val Val  Phe Leu Ile Asp Gly  Ser Gln Ser Ala Gly  Pro Glu Phe
    1235                 1240                 1245

Gln Tyr  Val Arg Thr Leu Ile  Glu Arg Leu Val Asp  Tyr Leu Asp
    1250                 1255                 1260

Val Gly  Phe Asp Thr Thr Arg  Val Ala Val Ile Gln  Phe Ser Asp
    1265                 1270                 1275

Asp Pro  Lys Val Glu Phe Leu  Leu Asn Ala His Ser  Ser Lys Asp
    1280                 1285                 1290

Glu Val  Gln Asn Ala Val Gln  Arg Leu Arg Pro Lys  Gly Gly Arg
    1295                 1300                 1305

Gln Ile  Asn Val Gly Asn Ala  Leu Glu Tyr Val Ser  Arg Asn Ile
    1310                 1315                 1320

Phe Lys  Arg Pro Leu Gly Ser  Arg Ile Glu Glu Gly  Val Pro Gln
    1325                 1330                 1335

Phe Leu  Val Leu Ile Ser Ser  Gly Lys Ser Asp Asp  Glu Val Asp
    1340                 1345                 1350

Asp Pro  Ala Val Glu Leu Lys  Gln Phe Gly Val Ala  Pro Phe Thr
    1355                 1360                 1365

Ile Ala  Arg Asn Ala Asp Gln  Glu Glu Leu Val Lys  Ile Ser Leu
    1370                 1375                 1380

Ser Pro  Glu Tyr Val Phe Ser  Val Ser Thr Phe Arg  Glu Leu Pro
    1385                 1390                 1395

Ser Leu  Glu Gln Lys Leu Leu  Thr Pro Ile Thr Thr  Leu Thr Ser
    1400                 1405                 1410

Glu Gln  Ile Gln Lys Leu Leu  Ala Ser Thr Arg Tyr  Pro Pro Pro
    1415                 1420                 1425

Ala Val  Glu Ser Asp Ala Ala  Asp Ile Val Phe Leu  Ile Asp Ser
    1430                 1435                 1440

Ser Glu  Gly Val Arg Pro Asp  Gly Phe Ala His Ile  Arg Asp Phe
    1445                 1450                 1455
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Val Ser  Arg Ile Val Arg Arg  Leu Asn Ile Gly Pro  Ser Lys Val
    1460                 1465                 1470

Arg Val  Gly Val Val Gln Phe  Ser Asn Asp Val Phe  Pro Glu Phe
    1475                 1480                 1485

Tyr Leu  Lys Thr Tyr Arg Ser  Gln Ala Pro Val Leu  Asp Ala Ile
    1490                 1495                 1500

Arg Arg  Leu Arg Leu Arg Gly  Gly Ser Pro Leu Asn  Thr Gly Lys
    1505                 1510                 1515

Ala Leu  Glu Phe Val Ala Arg  Asn Leu Phe Val Lys  Ser Ala Gly
    1520                 1525                 1530

Ser Arg  Ile Glu Asp Gly Val  Pro Gln His Leu Val  Leu Val Leu
    1535                 1540                 1545

Gly Gly  Lys Ser Gln Asp Asp  Val Ser Arg Phe Ala  Gln Val Ile
    1550                 1555                 1560

Arg Ser  Ser Gly Ile Val Ser  Leu Gly Val Gly Asp  Arg Asn Ile
    1565                 1570                 1575

Asp Arg  Thr Glu Leu Gln Thr  Ile Thr Asn Asp Pro  Arg Leu Val
    1580                 1585                 1590

Phe Thr  Val Arg Glu Phe Arg  Glu Leu Pro Asn Ile  Glu Glu Arg
    1595                 1600                 1605

Ile Met  Asn Ser Phe Gly Pro  Ser Ala Ala Thr Pro  Ala Pro Pro
    1610                 1615                 1620

Gly Val  Asp Thr Pro Pro Pro  Ser Arg Pro Glu Lys  Lys Lys Ala
    1625                 1630                 1635

Asp Ile  Val Phe Leu Leu Asp  Gly Ser Ile Asn Phe  Arg Arg Asp
    1640                 1645                 1650

Ser Phe  Gln Glu Val Leu Arg  Phe Val Ser Glu Ile  Val Asp Thr
    1655                 1660                 1665

Val Tyr  Glu Asp Gly Asp Ser  Ile Gln Val Gly Leu  Val Gln Tyr
    1670                 1675                 1680

Asn Ser  Asp Pro Thr Asp Glu  Phe Phe Leu Lys Asp  Phe Ser Thr
    1685                 1690                 1695

Lys Arg  Gln Ile Ile Asp Ala  Ile Asn Lys Val Val  Tyr Lys Gly
    1700                 1705                 1710

Gly Arg  His Ala Asn Thr Lys  Val Gly Leu Glu His  Leu Arg Val
    1715                 1720                 1725

Asn His  Phe Val Pro Glu Ala  Gly Ser Arg Leu Asp  Gln Arg Val
    1730                 1735                 1740

Pro Gln  Ile Ala Phe Val Ile  Thr Gly Gly Lys Ser  Val Glu Asp
    1745                 1750                 1755

Ala Gln  Asp Val Ser Leu Ala  Leu Thr Gln Arg Gly  Val Lys Val
    1760                 1765                 1770

Phe Ala  Val Gly Val Arg Asn  Ile Asp Ser Glu Glu  Val Gly Lys
    1775                 1780                 1785

Ile Ala  Ser Asn Ser Ala Thr  Ala Phe Arg Val Gly  Asn Val Gln
    1790                 1795                 1800

Glu Leu  Ser Glu Leu Ser Glu  Gln Val Leu Glu Thr  Leu His Asp
    1805                 1810                 1815

Ala Met  His Glu Thr Leu Cys  Pro Gly Val Thr Asp  Ala Ala Lys
    1820                 1825                 1830

Ala Cys  Asn Leu Asp Val Ile  Leu Gly Phe Asp Gly  Ser Arg Asp
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    1835                1840                1845

Gln Asn  Val Phe Val Ala Gln  Lys Gly Phe Glu Ser  Lys Val Asp
    1850                1855                1860

Ala Ile  Leu Asn Arg Ile Ser  Gln Met His Arg Val  Ser Cys Ser
    1865                1870                1875

Gly Gly  Arg Ser Pro Thr Val  Arg Val Ser Val Val  Ala Asn Thr
    1880                1885                1890

Pro Ser  Gly Pro Val Glu Ala  Phe Asp Phe Asp Glu  Tyr Gln Pro
    1895                1900                1905

Glu Met  Leu Glu Lys Phe Arg  Asn Met Arg Ser Gln  His Pro Tyr
    1910                1915                1920

Val Leu  Thr Glu Asp Thr Leu  Lys Val Tyr Leu Asn  Lys Phe Arg
    1925                1930                1935

Gln Ser  Ser Pro Asp Ser Val  Lys Val Val Ile His  Phe Thr Asp
    1940                1945                1950

Gly Ala  Asp Gly Asp Leu Ala  Asp Leu His Arg Ala  Ser Glu Asn
    1955                1960                1965

Leu Arg  Gln Glu Gly Val Arg  Ala Leu Ile Leu Val  Gly Leu Glu
    1970                1975                1980

Arg Val  Val Asn Leu Glu Arg  Leu Met His Leu Glu  Phe Gly Arg
    1985                1990                1995

Gly Phe  Met Tyr Asp Arg Pro  Leu Arg Leu Asn Leu  Leu Asp Leu
    2000                2005                2010

Asp Tyr  Glu Leu Ala Glu Gln  Leu Asp Asn Ile Ala  Glu Lys Ala
    2015                2020                2025

Cys Cys  Gly Val Pro Cys Lys  Cys Ser Gly Gln Arg  Gly Asp Arg
    2030                2035                2040

Gly Pro  Ile Gly Ser Ile Gly  Pro Lys Gly Ile Pro  Gly Glu Asp
    2045                2050                2055

Gly Tyr  Arg Gly Tyr Pro Gly  Asp Glu Gly Gly Pro  Gly Glu Arg
    2060                2065                2070

Gly Pro  Pro Gly Val Asn Gly  Thr Gln Gly Phe Gln  Gly Cys Pro
    2075                2080                2085

Gly Gln  Arg Gly Val Lys Gly  Ser Arg Gly Phe Pro  Gly Glu Lys
    2090                2095                2100

Gly Glu  Val Gly Glu Ile Gly  Leu Asp Gly Leu Asp  Gly Glu Asp
    2105                2110                2115

Gly Asp  Lys Gly Leu Pro Gly  Ser Ser Gly Glu Lys  Gly Asn Pro
    2120                2125                2130

Gly Arg  Arg Gly Asp Lys Gly  Pro Arg Gly Glu Lys  Gly Glu Arg
    2135                2140                2145

Gly Asp  Val Gly Ile Arg Gly  Asp Pro Gly Asn Pro  Gly Gln Asp
    2150                2155                2160

Ser Gln  Glu Arg Gly Pro Lys  Gly Glu Thr Gly Asp  Leu Gly Pro
    2165                2170                2175

Met Gly  Val Pro Gly Arg Asp  Gly Val Pro Gly Gly  Pro Gly Glu
    2180                2185                2190

Thr Gly  Lys Asn Gly Gly Phe  Gly Arg Arg Gly Pro  Pro Gly Ala
    2195                2200                2205

Lys Gly  Asn Lys Gly Gly Pro  Gly Gln Pro Gly Phe  Glu Gly Glu
    2210                2215                2220
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Gln Gly  Thr Arg Gly Ala Gln  Gly Pro Ala Gly Pro  Ala Gly Pro
    2225                 2230                 2235

Pro Gly  Leu Ile Gly Glu Gln  Gly Ile Ser Gly Pro  Arg Gly Ser
    2240                 2245                 2250

Gly Gly  Ala Ala Gly Ala Pro  Gly Glu Arg Gly Arg  Thr Gly Pro
    2255                 2260                 2265

Leu Gly  Arg Lys Gly Glu Pro  Gly Glu Pro Gly Pro  Lys Gly Gly
    2270                 2275                 2280

Ile Gly  Asn Arg Gly Pro Arg  Gly Glu Thr Gly Asp  Asp Gly Arg
    2285                 2290                 2295

Asp Gly  Val Gly Ser Glu Gly  Arg Arg Gly Lys Lys  Gly Glu Arg
    2300                 2305                 2310

Gly Phe  Pro Gly Tyr Pro Gly  Pro Lys Gly Asn Pro  Gly Glu Pro
    2315                 2320                 2325

Gly Leu  Asn Gly Thr Thr Gly  Pro Lys Gly Ile Arg  Gly Arg Arg
    2330                 2335                 2340

Gly Asn  Ser Gly Pro Pro Gly  Ile Val Gly Gln Lys  Gly Asp Pro
    2345                 2350                 2355

Gly Tyr  Pro Gly Pro Ala Gly  Pro Lys Gly Asn Arg  Gly Asp Ser
    2360                 2365                 2370

Ile Asp  Gln Cys Ala Leu Ile  Gln Ser Ile Lys Asp  Lys Cys Pro
    2375                 2380                 2385

Cys Cys  Tyr Gly Pro Leu Glu  Cys Pro Val Phe Pro  Thr Glu Leu
    2390                 2395                 2400

Ala Phe  Ala Leu Asp Thr Ser  Glu Gly Val Asn Gln  Asp Thr Phe
    2405                 2410                 2415

Gly Arg  Met Arg Asp Val Val  Leu Ser Ile Val Asn  Asp Leu Thr
    2420                 2425                 2430

Ile Ala  Glu Ser Asn Cys Pro  Arg Gly Ala Arg Val  Ala Val Val
    2435                 2440                 2445

Thr Tyr  Asn Asn Glu Val Thr  Thr Glu Ile Arg Phe  Ala Asp Ser
    2450                 2455                 2460

Lys Arg  Lys Ser Val Leu Leu  Asp Lys Ile Lys Asn  Leu Gln Val
    2465                 2470                 2475

Ala Leu  Thr Ser Lys Gln Gln  Ser Leu Glu Thr Ala  Met Ser Phe
    2480                 2485                 2490

Val Ala  Arg Asn Thr Phe Lys  Arg Val Arg Asn Gly  Phe Leu Met
    2495                 2500                 2505

Arg Lys  Val Ala Val Phe Phe  Ser Asn Thr Pro Thr  Arg Ala Ser
    2510                 2515                 2520

Pro Gln  Leu Arg Glu Ala Val  Leu Lys Leu Ser Asp  Ala Gly Ile
    2525                 2530                 2535

Thr Pro  Leu Phe Leu Thr Arg  Gln Glu Asp Arg Gln  Leu Ile Asn
    2540                 2545                 2550

Ala Leu  Gln Ile Asn Asn Thr  Ala Val Gly His Ala  Leu Val Leu
    2555                 2560                 2565

Pro Ala  Gly Arg Asp Leu Thr  Asp Phe Leu Glu Asn  Val Leu Thr
    2570                 2575                 2580

Cys His  Val Cys Leu Asp Ile  Cys Asn Ile Asp Pro  Ser Cys Gly
    2585                 2590                 2595
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Phe Gly  Ser Trp Arg Pro Ser  Phe Arg Asp Arg Arg  Ala Ala Gly
    2600                 2605                 2610

Ser Asp  Val Asp Ile Asp Met  Ala Phe Ile Leu Asp  Ser Ala Glu
    2615                 2620                 2625

Thr Thr  Thr Leu Phe Gln Phe  Asn Glu Met Lys Lys  Tyr Ile Ala
    2630                 2635                 2640

Tyr Leu  Val Arg Gln Leu Asp  Met Ser Pro Asp Pro  Lys Ala Ser
    2645                 2650                 2655

Gln His  Phe Ala Arg Val Ala  Val Val Gln His Ala  Pro Ser Glu
    2660                 2665                 2670

Ser Val  Asp Asn Ala Ser Met  Pro Pro Val Lys Val  Glu Phe Ser
    2675                 2680                 2685

Leu Thr  Asp Tyr Gly Ser Lys  Glu Lys Leu Val Asp  Phe Leu Ser
    2690                 2695                 2700

Arg Gly  Met Thr Gln Leu Gln  Gly Thr Arg Ala Leu  Gly Ser Ala
    2705                 2710                 2715

Ile Glu  Tyr Thr Ile Glu Asn  Val Phe Glu Ser Ala  Pro Asn Pro
    2720                 2725                 2730

Arg Asp  Leu Lys Ile Val Val  Leu Met Leu Thr Gly  Glu Val Pro
    2735                 2740                 2745

Glu Gln  Gln Leu Glu Glu Ala  Gln Arg Val Ile Leu  Gln Ala Lys
    2750                 2755                 2760

Cys Lys  Gly Tyr Phe Phe Val  Val Leu Gly Ile Gly  Arg Lys Val
    2765                 2770                 2775

Asn Ile  Lys Glu Val Tyr Thr  Phe Ala Ser Glu Pro  Asn Asp Val
    2780                 2785                 2790

Phe Phe  Lys Leu Val Asp Lys  Ser Thr Glu Leu Asn  Glu Glu Pro
    2795                 2800                 2805

Leu Met  Arg Phe Gly Arg Leu  Leu Pro Ser Phe Val  Ser Ser Glu
    2810                 2815                 2820

Asn Ala  Phe Tyr Leu Ser Pro  Asp Ile Arg Lys Gln  Cys Asp Trp
    2825                 2830                 2835

Phe Gln  Gly Asp Gln Pro Thr  Lys Asn Leu Val Lys  Phe Gly His
    2840                 2845                 2850

Lys Gln  Val Asn Val Pro Asn  Asn Val Thr Ser Ser  Pro Thr Ser
    2855                 2860                 2865

Asn Pro  Val Thr Thr Thr Lys  Pro Val Thr Thr Thr  Lys Pro Val
    2870                 2875                 2880

Thr Thr  Thr Thr Lys Pro Val  Thr Thr Thr Thr Lys  Pro Val Thr
    2885                 2890                 2895

Ile Ile  Asn Gln Pro Ser Val  Lys Pro Ala Ala Ala  Lys Pro Ala
    2900                 2905                 2910

Pro Ala  Lys Pro Val Ala Ala  Lys Pro Val Ala Thr  Lys Met Ala
    2915                 2920                 2925

Thr Val  Arg Pro Pro Val Ala  Val Lys Pro Ala Thr  Ala Ala Lys
    2930                 2935                 2940

Pro Val  Ala Ala Lys Pro Ala  Ala Val Arg Pro Pro  Ala Ala Ala
    2945                 2950                 2955

Ala Ala  Lys Pro Val Ala Thr  Lys Pro Glu Val Pro  Arg Pro Gln
    2960                 2965                 2970

Ala Ala  Lys Pro Ala Ala Thr  Lys Pro Ala Thr Thr  Lys Pro Met
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    2975                 2980                 2985

Val Lys  Met Ser Arg Glu Val  Gln Val Phe Glu Ile  Thr Glu Asn
    2990                 2995                 3000

Ser Ala  Lys Leu His Trp Glu  Arg Ala Glu Pro Pro  Gly Pro Tyr
    3005                 3010                 3015

Phe Tyr  Asp Leu Thr Val Thr  Ser Ala His Asp Gln  Ser Leu Val
    3020                 3025                 3030

Leu Lys  Gln Asn Leu Thr Val  Thr Asp Arg Val Ile  Gly Gly Leu
    3035                 3040                 3045

Leu Ala  Gly Gln Thr Tyr His  Val Ala Val Val Cys  Tyr Leu Arg
    3050                 3055                 3060

Ser Gln  Val Arg Ala Thr Tyr  His Gly Ser Phe Ser  Thr Lys Lys
    3065                 3070                 3075

Ser Gln  Pro Pro Pro Pro Gln  Pro Ala Arg Ser Ala  Ser Ser Ser
    3080                 3085                 3090

Thr Ile  Asn Leu Met Val Ser  Thr Glu Pro Leu Ala  Leu Thr Glu
    3095                 3100                 3105

Thr Asp  Ile Cys Lys Leu Pro  Lys Asp Glu Gly Thr  Cys Arg Asp
    3110                 3115                 3120

Phe Ile  Leu Lys Trp Tyr Tyr  Asp Pro Asn Thr Lys  Ser Cys Ala
    3125                 3130                 3135

Arg Phe  Trp Tyr Gly Gly Cys  Gly Gly Asn Glu Asn  Lys Phe Gly
    3140                 3145                 3150

Ser Gln  Lys Glu Cys Glu Lys  Val Cys Ala Pro Val  Leu Ala Lys
    3155                 3160                 3165

Pro Gly  Val Ile Ser Val Met  Gly Thr
    3170                 3175


<210> SEQ ID NO 7
<211> LENGTH: 3063
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

Met Arg Ser Arg Leu Pro Pro Ala Leu Ala Ala Leu Gly Ala Ala Leu
1               5                   10                  15

Leu Leu Ser Ser Ile Glu Ala Glu Val Asp Pro Pro Ser Asp Leu Asn
            20                  25                  30

Phe Lys Ile Ile Asp Glu Asn Thr Val His Met Ser Trp Ala Lys Pro
        35                  40                  45

Val Asp Pro Ile Val Gly Tyr Arg Ile Thr Val Asp Pro Thr Thr Asp
    50                  55                  60

Gly Pro Thr Lys Glu Phe Thr Leu Ser Ala Ser Thr Thr Glu Thr Leu
65                  70                  75                  80

Leu Ser Glu Leu Val Pro Glu Thr Glu Tyr Val Val Thr Ile Thr Ser
                85                  90                  95

Tyr Asp Glu Val Glu Glu Ser Val Pro Val Ile Gly Gln Leu Thr Ile
            100                 105                 110

Gln Thr Gly Ser Ser Thr Lys Pro Val Glu Lys Lys Pro Gly Lys Thr
        115                 120                 125

Glu Ile Gln Lys Cys Ser Val Ser Ala Trp Thr Asp Leu Val Phe Leu
    130                 135                 140
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Val Asp Gly Ser Trp Ser Val Gly Arg Asn Asn Phe Lys Tyr Ile Leu
145                 150                 155                 160

Asp Phe Ile Ala Ala Leu Val Ser Ala Phe Asp Ile Gly Glu Glu Lys
                165                 170                 175

Thr Arg Val Gly Val Val Gln Tyr Ser Ser Asp Thr Arg Thr Glu Phe
            180                 185                 190

Asn Leu Asn Gln Tyr Tyr Gln Arg Asp Glu Leu Leu Ala Ala Ile Lys
        195                 200                 205

Lys Ile Pro Tyr Lys Gly Gly Asn Thr Met Thr Gly Asp Ala Ile Asp
    210                 215                 220

Tyr Leu Val Lys Asn Thr Phe Thr Glu Ser Ala Gly Ala Arg Val Gly
225                 230                 235                 240

Phe Pro Lys Val Ala Ile Ile Ile Thr Asp Gly Lys Ser Gln Asp Glu
                245                 250                 255

Val Glu Ile Pro Ala Arg Glu Leu Arg Asn Val Gly Val Glu Val Phe
            260                 265                 270

Ser Leu Gly Ile Lys Ala Ala Asp Ala Lys Glu Leu Lys Gln Ile Ala
        275                 280                 285

Ser Thr Pro Ser Leu Asn His Val Phe Asn Val Ala Asn Phe Asp Ala
    290                 295                 300

Ile Val Asp Ile Gln Asn Glu Ile Ile Ser Gln Val Cys Ser Gly Val
305                 310                 315                 320

Asp Glu Gln Leu Gly Glu Leu Val Ser Gly Glu Glu Val Val Glu Pro
                325                 330                 335

Pro Ser Asn Leu Ile Ala Met Glu Val Ser Ser Lys Tyr Val Lys Leu
            340                 345                 350

Asn Trp Asn Pro Ser Pro Ser Pro Val Thr Gly Tyr Lys Val Ile Leu
        355                 360                 365

Thr Pro Met Thr Ala Gly Ser Arg Gln His Ala Leu Ser Val Gly Pro
    370                 375                 380

Gln Thr Thr Thr Leu Ser Val Arg Asp Leu Ser Ala Asp Thr Glu Tyr
385                 390                 395                 400

Gln Ile Ser Val Ser Ala Met Lys Gly Met Thr Ser Ser Glu Pro Ile
                405                 410                 415

Ser Ile Met Glu Lys Thr Gln Pro Met Lys Val Gln Val Glu Cys Ser
            420                 425                 430

Arg Gly Val Asp Ile Lys Ala Asp Ile Val Phe Leu Val Asp Gly Ser
        435                 440                 445

Tyr Ser Ile Gly Ile Ala Asn Phe Val Lys Val Arg Ala Phe Leu Glu
    450                 455                 460

Val Leu Val Lys Ser Phe Glu Ile Ser Pro Asn Arg Val Gln Ile Ser
465                 470                 475                 480

Leu Val Gln Tyr Ser Arg Asp Pro His Thr Glu Phe Thr Leu Lys Lys
                485                 490                 495

Phe Thr Lys Val Glu Asp Ile Ile Glu Ala Ile Asn Thr Phe Pro Tyr
            500                 505                 510

Arg Gly Gly Ser Thr Asn Thr Gly Lys Ala Met Thr Tyr Val Arg Glu
        515                 520                 525

Lys Ile Phe Val Pro Ser Lys Gly Ser Arg Ser Asn Val Pro Lys Val
    530                 535                 540

Met Ile Leu Ile Thr Asp Gly Lys Ser Ser Asp Ala Phe Arg Asp Pro
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545                 550                 555                 560

Ala Ile Lys Leu Arg Asn Ser Asp Val Glu Ile Phe Ala Val Gly Val
                565                 570                 575

Lys Asp Ala Val Arg Ser Glu Leu Glu Ala Ile Ala Ser Pro Pro Ala
            580                 585                 590

Glu Thr His Val Phe Thr Val Glu Asp Phe Asp Ala Phe Gln Arg Ile
        595                 600                 605

Ser Phe Glu Leu Thr Gln Ser Ile Cys Leu Arg Ile Glu Gln Glu Leu
    610                 615                 620

Ala Ala Ile Lys Lys Lys Ala Tyr Val Pro Pro Lys Asp Leu Ser Phe
625                 630                 635                 640

Ser Glu Val Thr Ser Tyr Gly Phe Lys Thr Asn Trp Ser Pro Ala Gly
                645                 650                 655

Glu Asn Val Phe Ser Tyr His Ile Thr Tyr Lys Glu Ala Ala Gly Asp
            660                 665                 670

Asp Glu Val Thr Val Val Glu Pro Ala Ser Ser Thr Ser Val Val Leu
        675                 680                 685

Ser Ser Leu Lys Pro Glu Thr Leu Tyr Leu Val Asn Val Thr Ala Glu
    690                 695                 700

Tyr Glu Asp Gly Phe Ser Ile Pro Leu Ala Gly Glu Glu Thr Thr Glu
705                 710                 715                 720

Glu Val Lys Gly Ala Pro Arg Asn Leu Lys Val Thr Asp Glu Thr Thr
                725                 730                 735

Asp Ser Phe Lys Ile Thr Trp Thr Gln Ala Pro Gly Arg Val Leu Arg
            740                 745                 750

Tyr Arg Ile Ile Tyr Arg Pro Val Ala Gly Gly Glu Ser Arg Glu Val
        755                 760                 765

Thr Thr Pro Pro Asn Gln Arg Arg Arg Thr Leu Glu Asn Leu Ile Pro
    770                 775                 780

Asp Thr Lys Tyr Glu Val Ser Val Ile Pro Glu Tyr Phe Ser Gly Pro
785                 790                 795                 800

Gly Thr Pro Leu Thr Gly Asn Ala Ala Thr Glu Glu Val Arg Gly Asn
                805                 810                 815

Pro Arg Asp Leu Arg Val Ser Asp Pro Thr Thr Ser Thr Met Lys Leu
            820                 825                 830

Ser Trp Ser Gly Ala Pro Gly Lys Val Lys Gln Tyr Leu Val Thr Tyr
        835                 840                 845

Thr Pro Val Ala Gly Gly Glu Thr Gln Glu Val Thr Val Arg Gly Asp
    850                 855                 860

Thr Thr Asn Thr Val Leu Gln Gly Leu Lys Glu Gly Thr Gln Tyr Ala
865                 870                 875                 880

Leu Ser Val Thr Ala Leu Tyr Ala Ser Gly Ala Gly Asp Ala Leu Phe
                885                 890                 895

Gly Glu Gly Thr Thr Leu Glu Glu Arg Gly Ser Pro Gln Asp Leu Val
            900                 905                 910

Thr Lys Asp Ile Thr Asp Thr Ser Ile Gly Ala Tyr Trp Thr Ser Ala
        915                 920                 925

Pro Gly Met Val Arg Gly Tyr Arg Val Ser Trp Lys Ser Leu Tyr Asp
    930                 935                 940

Asp Val Asp Thr Gly Glu Lys Asn Leu Pro Glu Asp Ala Ile His Thr
945                 950                 955                 960
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Met Ile Glu Asn Leu Gln Pro Glu Thr Lys Tyr Arg Ile Ser Val Phe
                965                 970                 975

Ala Thr Tyr Ser Ser Gly Glu Gly Glu Pro Leu Thr Gly Asp Ala Thr
            980                 985                 990

Thr Glu Leu Ser Gln Asp Ser Lys  Thr Leu Lys Val Asp  Glu Glu Thr
        995                 1000                 1005

Glu Asn  Thr Met Arg Val Thr  Trp Lys Pro Ala Pro  Gly Lys Val
    1010                 1015                 1020

Val Asn  Tyr Arg Val Val Tyr  Arg Pro His Gly Arg  Gly Lys Gln
    1025                 1030                 1035

Met Val  Ala Lys Val Pro Pro  Thr Val Thr Ser Thr  Val Leu Lys
    1040                 1045                 1050

Arg Leu  Gln Pro Gln Thr Thr  Tyr Asp Ile Thr Val  Leu Pro Ile
    1055                 1060                 1065

Tyr Lys  Met Gly Glu Gly Lys  Leu Arg Gln Gly Ser  Gly Thr Thr
    1070                 1075                 1080

Ala Ser  Arg Phe Lys Ser Pro  Arg Asn Leu Lys Thr  Ser Asp Pro
    1085                 1090                 1095

Thr Met  Ser Ser Phe Arg Val  Thr Trp Glu Pro Ala  Pro Gly Glu
    1100                 1105                 1110

Val Lys  Gly Tyr Lys Val Thr  Phe His Pro Thr Gly  Asp Asp Arg
    1115                 1120                 1125

Arg Leu  Gly Glu Leu Val Val  Gly Pro Tyr Asp Asn  Thr Val Val
    1130                 1135                 1140

Leu Glu  Glu Leu Arg Ala Gly  Thr Thr Tyr Lys Val  Asn Val Phe
    1145                 1150                 1155

Gly Met  Phe Asp Gly Gly Glu  Ser Ser Pro Leu Val  Gly Gln Glu
    1160                 1165                 1170

Met Thr  Thr Leu Ser Asp Thr  Thr Val Met Pro Ile  Leu Ser Ser
    1175                 1180                 1185

Gly Met  Glu Cys Leu Thr Arg  Ala Glu Ala Asp Ile  Val Leu Leu
    1190                 1195                 1200

Val Asp  Gly Ser Trp Ser Ile  Gly Arg Ala Asn Phe  Arg Thr Val
    1205                 1210                 1215

Arg Ser  Phe Ile Ser Arg Ile  Val Glu Val Phe Asp  Ile Gly Pro
    1220                 1225                 1230

Lys Arg  Val Gln Ile Ala Leu  Ala Gln Tyr Ser Gly  Asp Pro Arg
    1235                 1240                 1245

Thr Glu  Trp Gln Leu Asn Ala  His Arg Asp Lys Lys  Ser Leu Leu
    1250                 1255                 1260

Gln Ala  Val Ala Asn Leu Pro  Tyr Lys Gly Gly Asn  Thr Leu Thr
    1265                 1270                 1275

Gly Met  Ala Leu Asn Phe Ile  Arg Gln Gln Asn Phe  Arg Thr Gln
    1280                 1285                 1290

Ala Gly  Met Arg Pro Arg Ala  Arg Lys Ile Gly Val  Leu Ile Thr
    1295                 1300                 1305

Asp Gly  Lys Ser Gln Asp Asp  Val Glu Ala Pro Ser  Lys Lys Leu
    1310                 1315                 1320

Lys Asp  Glu Gly Val Glu Leu  Phe Ala Ile Gly Ile  Lys Asn Ala
    1325                 1330                 1335
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Asp Glu  Val Glu Leu Lys Met  Ile Ala Thr Asp Pro  Asp Asp Thr
    1340                 1345                 1350

His Ala  Tyr Asn Val Ala Asp  Phe Glu Ser Leu Ser  Arg Ile Val
    1355                 1360                 1365

Asp Asp  Leu Thr Ile Asn Leu  Cys Asn Ser Val Lys  Gly Pro Gly
    1370                 1375                 1380

Asp Leu  Glu Ala Pro Ser Asn  Leu Val Ile Ser Glu  Arg Thr His
    1385                 1390                 1395

Arg Ser  Phe Arg Val Ser Trp  Thr Pro Pro Ser Asp  Ser Val Asp
    1400                 1405                 1410

Arg Tyr  Lys Val Glu Tyr Tyr  Pro Val Ser Gly Gly  Lys Arg Gln
    1415                 1420                 1425

Glu Phe  Tyr Val Ser Arg Met  Glu Thr Ser Thr Val  Leu Lys Asp
    1430                 1435                 1440

Leu Lys  Pro Glu Thr Glu Tyr  Val Val Asn Val Tyr  Ser Val Val
    1445                 1450                 1455

Glu Asp  Glu Tyr Ser Glu Pro  Leu Lys Gly Thr Glu  Lys Thr Leu
    1460                 1465                 1470

Pro Val  Pro Val Val Ser Leu  Asn Ile Tyr Asp Val  Gly Pro Thr
    1475                 1480                 1485

Thr Met  His Val Gln Trp Gln  Pro Val Gly Gly Ala  Thr Gly Tyr
    1490                 1495                 1500

Ile Leu  Ser Tyr Lys Pro Val  Lys Asp Thr Glu Pro  Thr Arg Pro
    1505                 1510                 1515

Lys Glu  Val Arg Leu Gly Pro  Thr Val Asn Asp Met  Gln Leu Thr
    1520                 1525                 1530

Asp Leu  Val Pro Asn Thr Glu  Tyr Ala Val Thr Val  Gln Ala Val
    1535                 1540                 1545

Leu His  Asp Leu Thr Ser Glu  Pro Val Thr Val Arg  Glu Val Thr
    1550                 1555                 1560

Leu Pro  Leu Pro Arg Pro Gln  Asp Leu Lys Leu Arg  Asp Val Thr
    1565                 1570                 1575

His Ser  Thr Met Asn Val Phe  Trp Glu Pro Val Pro  Gly Lys Val
    1580                 1585                 1590

Arg Lys  Tyr Ile Val Arg Tyr  Lys Thr Pro Glu Glu  Asp Val Lys
    1595                 1600                 1605

Glu Val  Glu Val Asp Arg Ser  Glu Thr Ser Thr Ser  Leu Lys Asp
    1610                 1615                 1620

Leu Phe  Ser Gln Thr Leu Tyr  Thr Val Ser Val Ser  Ala Val His
    1625                 1630                 1635

Asp Glu  Gly Glu Ser Pro Pro  Val Thr Ala Gln Glu  Thr Thr Arg
    1640                 1645                 1650

Pro Val  Pro Ala Pro Thr Asn  Leu Lys Ile Thr Glu  Val Thr Ser
    1655                 1660                 1665

Glu Gly  Phe Arg Gly Thr Trp  Asp His Gly Ala Ser  Asp Val Ser
    1670                 1675                 1680

Leu Tyr  Arg Ile Thr Trp Ala  Pro Phe Gly Ser Ser  Asp Lys Met
    1685                 1690                 1695

Glu Thr  Ile Leu Asn Gly Asp  Glu Asn Thr Leu Val  Phe Glu Asn
    1700                 1705                 1710

Leu Asn  Pro Asn Thr Ile Tyr  Glu Val Ser Ile Thr  Ala Ile Tyr
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    1715                1720                1725

Pro Asp  Glu Ser Glu Ser Asp  Asp Leu Ile Gly Ser  Glu Arg Thr
    1730                1735                1740

Leu Pro  Ile Leu Thr Thr Gln  Ala Pro Lys Ser Gly  Pro Arg Asn
    1745                1750                1755

Leu Gln  Val Tyr Asn Ala Thr  Ser Asn Ser Leu Thr  Val Lys Trp
    1760                1765                1770

Asp Pro  Ala Ser Gly Arg Val  Gln Lys Tyr Arg Ile  Thr Tyr Gln
    1775                1780                1785

Pro Ser  Thr Gly Glu Gly Asn  Glu Gln Thr Thr Thr  Ile Gly Gly
    1790                1795                1800

Arg Gln  Asn Ser Val Val Leu  Gln Lys Leu Lys Pro  Asp Thr Pro
    1805                1810                1815

Tyr Thr  Ile Thr Val Ser Ser  Leu Tyr Pro Asp Gly  Glu Gly Gly
    1820                1825                1830

Arg Met  Thr Gly Arg Gly Lys  Thr Lys Pro Leu Asn  Thr Val Arg
    1835                1840                1845

Asn Leu  Arg Val Tyr Asp Pro  Ser Thr Ser Thr Leu  Asn Val Arg
    1850                1855                1860

Trp Asp  His Ala Glu Gly Asn  Pro Arg Gln Tyr Lys  Leu Phe Tyr
    1865                1870                1875

Ala Pro  Ala Ala Gly Gly Pro  Glu Glu Leu Val Pro  Ile Pro Gly
    1880                1885                1890

Asn Thr  Asn Tyr Ala Ile Leu  Arg Asn Leu Gln Pro  Asp Thr Ser
    1895                1900                1905

Tyr Thr  Val Thr Val Val Pro  Val Tyr Thr Glu Gly  Asp Gly Gly
    1910                1915                1920

Arg Thr  Ser Asp Thr Gly Arg  Thr Leu Met Arg Gly  Leu Ala Arg
    1925                1930                1935

Asn Val  Gln Val Tyr Asn Pro  Thr Pro Asn Ser Leu  Asp Val Arg
    1940                1945                1950

Trp Asp  Pro Ala Pro Gly Pro  Val Leu Gln Tyr Arg  Val Val Tyr
    1955                1960                1965

Ser Pro  Val Asp Gly Thr Arg  Pro Ser Glu Ser Ile  Val Val Pro
    1970                1975                1980

Gly Asn  Thr Arg Met Val His  Leu Glu Arg Leu Ile  Pro Asp Thr
    1985                1990                1995

Leu Tyr  Ser Val Asn Leu Val  Ala Leu Tyr Ser Asp  Gly Glu Gly
    2000                2005                2010

Asn Pro  Ser Pro Ala Gln Gly  Arg Thr Leu Pro Arg  Ser Gly Pro
    2015                2020                2025

Arg Asn  Leu Arg Val Phe Gly  Glu Thr Thr Asn Ser  Leu Ser Val
    2030                2035                2040

Ala Trp  Asp His Ala Asp Gly  Pro Val Gln Gln Tyr  Arg Ile Ile
    2045                2050                2055

Tyr Ser  Pro Thr Val Gly Asp  Pro Ile Asp Glu Tyr  Thr Thr Val
    2060                2065                2070

Pro Gly  Arg Arg Asn Asn Val  Ile Leu Gln Pro Leu  Gln Pro Asp
    2075                2080                2085

Thr Pro  Tyr Lys Ile Thr Val  Ile Ala Val Tyr Glu  Asp Gly Asp
    2090                2095                2100
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Gly Gly  His Leu Thr Gly Asn  Gly Arg Thr Val Gly  Leu Leu Pro
    2105                 2110                 2115

Pro Gln  Asn Ile His Ile Ser  Asp Glu Trp Tyr Thr  Arg Phe Arg
    2120                 2125                 2130

Val Ser  Trp Asp Pro Ser Pro  Ser Pro Val Leu Gly  Tyr Lys Ile
    2135                 2140                 2145

Val Tyr  Lys Pro Val Gly Ser  Asn Glu Pro Met Glu  Ala Phe Val
    2150                 2155                 2160

Gly Glu  Met Thr Ser Tyr Thr  Leu His Asn Leu Asn  Pro Ser Thr
    2165                 2170                 2175

Thr Tyr  Asp Val Asn Val Tyr  Ala Gln Tyr Asp Ser  Gly Leu Ser
    2180                 2185                 2190

Val Pro  Leu Thr Asp Gln Gly  Thr Thr Leu Tyr Leu  Asn Val Thr
    2195                 2200                 2205

Asp Leu  Lys Thr Tyr Gln Ile  Gly Trp Asp Thr Phe  Cys Val Lys
    2210                 2215                 2220

Trp Ser  Pro His Arg Ala Ala  Thr Ser Tyr Arg Leu  Lys Leu Ser
    2225                 2230                 2235

Pro Ala  Asp Gly Thr Arg Gly  Gln Glu Ile Thr Val  Arg Gly Ser
    2240                 2245                 2250

Glu Thr  Ser His Cys Phe Thr  Gly Leu Ser Pro Asp  Thr Asp Tyr
    2255                 2260                 2265

Gly Val  Thr Val Phe Val Gln  Thr Pro Asn Leu Glu  Gly Pro Gly
    2270                 2275                 2280

Val Ser  Val Lys Glu His Thr  Thr Val Lys Pro Thr  Glu Ala Pro
    2285                 2290                 2295

Thr Glu  Pro Pro Thr Pro Pro  Pro Pro Pro Thr Ile  Pro Pro Ala
    2300                 2305                 2310

Arg Asp  Val Cys Lys Gly Ala  Lys Ala Asp Ile Val  Phe Leu Thr
    2315                 2320                 2325

Asp Ala  Ser Trp Ser Ile Gly  Asp Asp Asn Phe Asn  Lys Val Val
    2330                 2335                 2340

Lys Phe  Ile Phe Asn Thr Val  Gly Gly Phe Asp Glu  Ile Ser Pro
    2345                 2350                 2355

Ala Gly  Ile Gln Val Ser Phe  Val Gln Tyr Ser Asp  Glu Val Lys
    2360                 2365                 2370

Ser Glu  Phe Lys Leu Asn Thr  Tyr Asn Asp Lys Ala  Leu Ala Leu
    2375                 2380                 2385

Gly Ala  Leu Gln Asn Ile Arg  Tyr Arg Gly Gly Asn  Thr Arg Thr
    2390                 2395                 2400

Gly Lys  Ala Leu Thr Phe Ile  Lys Glu Lys Val Leu  Thr Trp Glu
    2405                 2410                 2415

Ser Gly  Met Arg Lys Asn Val  Pro Lys Val Leu Val  Val Val Thr
    2420                 2425                 2430

Asp Gly  Arg Ser Gln Asp Glu  Val Lys Lys Ala Ala  Leu Val Ile
    2435                 2440                 2445

Gln Gln  Ser Gly Phe Ser Val  Phe Val Val Gly Val  Ala Asp Val
    2450                 2455                 2460

Asp Tyr  Asn Glu Leu Ala Asn  Ile Ala Ser Lys Pro  Ser Glu Arg
    2465                 2470                 2475
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His Val  Phe Ile Val Asp Asp  Phe Glu Ser Phe Glu  Lys Ile Glu
    2480                 2485                 2490

Asp Asn  Leu Ile Thr Phe Val  Cys Glu Thr Ala Thr  Ser Ser Cys
    2495                 2500                 2505

Pro Leu  Ile Tyr Leu Asp Gly  Tyr Thr Ser Pro Gly  Phe Lys Met
    2510                 2515                 2520

Leu Glu  Ala Tyr Asn Leu Thr  Glu Lys Asn Phe Ala  Ser Val Gln
    2525                 2530                 2535

Gly Val  Ser Leu Glu Ser Gly  Ser Phe Pro Ser Tyr  Ser Ala Tyr
    2540                 2545                 2550

Arg Ile  Gln Lys Asn Ala Phe  Val Asn Gln Pro Thr  Ala Asp Leu
    2555                 2560                 2565

His Pro  Asn Gly Leu Pro Pro  Ser Tyr Thr Ile Ile  Leu Leu Phe
    2570                 2575                 2580

Arg Leu  Leu Pro Glu Thr Pro  Ser Asp Pro Phe Ala  Ile Trp Gln
    2585                 2590                 2595

Ile Thr  Asp Arg Asp Tyr Lys  Pro Gln Val Gly Val  Ile Ala Asp
    2600                 2605                 2610

Pro Ser  Ser Lys Thr Leu Ser  Phe Phe Asn Lys Asp  Thr Arg Gly
    2615                 2620                 2625

Glu Val  Gln Thr Val Thr Phe  Asp Thr Glu Glu Val  Lys Thr Leu
    2630                 2635                 2640

Phe Tyr  Gly Ser Phe His Lys  Val His Ile Val Val  Thr Ser Lys
    2645                 2650                 2655

Ser Val  Lys Ile Tyr Ile Asp  Cys Tyr Glu Ile Ile  Glu Lys Asp
    2660                 2665                 2670

Ile Lys  Glu Ala Gly Asn Ile  Thr Thr Asp Gly Tyr  Glu Ile Leu
    2675                 2680                 2685

Gly Lys  Leu Leu Lys Gly Glu  Arg Lys Ser Ala Ala  Phe Gln Ile
    2690                 2695                 2700

Gln Ser  Phe Asp Ile Val Cys  Ser Pro Val Trp Thr  Ser Arg Asp
    2705                 2710                 2715

Arg Cys  Cys Asp Ile Pro Ser  Arg Arg Asp Glu Gly  Lys Cys Pro
    2720                 2725                 2730

Ala Phe  Pro Asn Ser Cys Thr  Cys Thr Gln Asp Ser  Val Gly Pro
    2735                 2740                 2745

Pro Gly  Pro Pro Gly Pro Ala  Gly Gly Pro Gly Ala  Lys Gly Pro
    2750                 2755                 2760

Arg Gly  Glu Arg Gly Ile Ser  Gly Ala Ile Gly Pro  Pro Gly Pro
    2765                 2770                 2775

Arg Gly  Asp Ile Gly Pro Pro  Gly Pro Gln Gly Pro  Pro Gly Pro
    2780                 2785                 2790

Gln Gly  Pro Asn Gly Leu Ser  Ile Pro Gly Glu Gln  Gly Arg Gln
    2795                 2800                 2805

Gly Met  Lys Gly Asp Ala Gly  Glu Pro Gly Leu Pro  Gly Arg Thr
    2810                 2815                 2820

Gly Thr  Pro Gly Leu Pro Gly  Pro Pro Gly Pro Met  Gly Pro Pro
    2825                 2830                 2835

Gly Asp  Arg Gly Phe Thr Gly  Lys Asp Gly Ala Met  Gly Pro Arg
    2840                 2845                 2850

Gly Pro  Pro Gly Pro Pro Gly  Ser Pro Gly Ser Pro  Gly Val Thr
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    2855                2860                2865

Gly Pro  Ser Gly Lys Pro Gly  Lys Pro Gly Asp His  Gly Arg Pro
    2870                2875                2880

Gly Pro  Ser Gly Leu Lys Gly  Glu Lys Gly Asp Arg  Gly Asp Ile
    2885                2890                2895

Ala Ser  Gln Asn Met Met Arg  Ala Val Ala Arg Gln  Val Cys Glu
    2900                2905                2910

Gln Leu  Ile Ser Gly Gln Met  Asn Arg Phe Asn Gln  Met Leu Asn
    2915                2920                2925

Gln Ile  Pro Asn Asp Tyr Gln  Ser Ser Arg Asn Gln  Pro Gly Pro
    2930                2935                2940

Pro Gly  Pro Pro Gly Pro Pro  Gly Ser Ala Gly Ala  Arg Gly Glu
    2945                2950                2955

Pro Gly  Pro Gly Gly Arg Pro  Gly Phe Pro Gly Thr  Pro Gly Met
    2960                2965                2970

Gln Gly  Pro Pro Gly Glu Arg  Gly Leu Pro Gly Glu  Lys Gly Glu
    2975                2980                2985

Arg Gly  Thr Gly Ser Ser Gly  Pro Arg Gly Leu Pro  Gly Pro Pro
    2990                2995                3000

Gly Pro  Gln Gly Glu Ser Arg  Thr Gly Pro Pro Gly  Ser Thr Gly
    3005                3010                3015

Ser Arg  Gly Pro Pro Gly Pro  Pro Gly Arg Pro Gly  Asn Ser Gly
    3020                3025                3030

Ile Arg  Gly Pro Pro Gly Pro  Pro Gly Tyr Cys Asp  Ser Ser Gln
    3035                3040                3045

Cys Ala  Ser Ile Pro Tyr Asn  Gly Gln Gly Tyr Pro  Gly Ser Gly
    3050                3055                3060


<210> SEQ ID NO 8
<211> LENGTH: 1796
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

Met Lys Ile Phe Gln Arg Lys Met Arg Tyr Trp Leu Leu Pro Pro Phe
1               5                   10                  15

Leu Ala Ile Val Tyr Phe Cys Thr Ile Val Gln Gly Gln Val Ala Pro
            20                  25                  30

Pro Thr Arg Leu Arg Tyr Asn Val Ile Ser His Asp Ser Ile Gln Ile
        35                  40                  45

Ser Trp Lys Ala Pro Arg Gly Lys Phe Gly Gly Tyr Lys Leu Leu Val
    50                  55                  60

Thr Pro Thr Ser Gly Gly Lys Thr Asn Gln Leu Asn Leu Gln Asn Thr
65                  70                  75                  80

Ala Thr Lys Ala Ile Ile Gln Gly Leu Met Pro Asp Gln Asn Tyr Thr
                85                  90                  95

Val Gln Ile Ile Ala Tyr Asn Lys Asp Lys Glu Ser Lys Pro Ala Gln
            100                 105                 110

Gly Gln Phe Arg Ile Lys Asp Leu Glu Lys Arg Lys Asp Pro Lys Pro
        115                 120                 125

Arg Val Lys Val Val Asp Arg Gly Asn Gly Ser Arg Pro Ser Ser Pro
    130                 135                 140
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Glu Glu Val Lys Phe Val Cys Gln Thr Pro Ala Ile Ala Asp Ile Val
145                 150                 155                 160

Ile Leu Val Asp Gly Ser Trp Ser Ile Gly Arg Phe Asn Phe Arg Leu
                165                 170                 175

Val Arg His Phe Leu Glu Asn Leu Val Thr Ala Phe Asp Val Gly Ser
            180                 185                 190

Glu Lys Thr Arg Ile Gly Leu Ala Gln Tyr Ser Gly Asp Pro Arg Ile
        195                 200                 205

Glu Trp His Leu Asn Ala Phe Ser Thr Lys Asp Glu Val Ile Glu Ala
    210                 215                 220

Val Arg Asn Leu Pro Tyr Lys Gly Gly Asn Thr Leu Thr Gly Leu Ala
225                 230                 235                 240

Leu Asn Tyr Ile Phe Glu Asn Ser Phe Lys Pro Glu Ala Gly Ser Arg
                245                 250                 255

Thr Gly Val Ser Lys Ile Gly Ile Leu Ile Thr Asp Gly Lys Ser Gln
            260                 265                 270

Asp Asp Ile Ile Pro Pro Ser Arg Asn Leu Arg Glu Ser Gly Val Glu
        275                 280                 285

Leu Phe Ala Ile Gly Val Lys Asn Ala Asp Val Asn Glu Leu Gln Glu
    290                 295                 300

Ile Ala Ser Glu Pro Asp Ser Thr His Val Tyr Asn Val Ala Glu Phe
305                 310                 315                 320

Asp Leu Met His Thr Val Val Glu Ser Leu Thr Arg Thr Leu Cys Ser
                325                 330                 335

Arg Val Glu Glu Gln Asp Arg Glu Ile Lys Ala Ser Ala His Ala Ile
            340                 345                 350

Thr Gly Pro Pro Thr Glu Leu Ile Thr Ser Glu Val Thr Ala Arg Ser
        355                 360                 365

Phe Met Val Asn Trp Thr His Ala Pro Gly Asn Val Glu Lys Tyr Arg
    370                 375                 380

Val Val Tyr Tyr Pro Thr Arg Gly Gly Lys Pro Asp Glu Val Val Val
385                 390                 395                 400

Asp Gly Thr Val Ser Ser Thr Val Leu Lys Asn Leu Met Ser Leu Thr
                405                 410                 415

Glu Tyr Gln Ile Ala Val Phe Ala Ile Tyr Ala His Thr Ala Ser Glu
            420                 425                 430

Gly Leu Arg Gly Thr Glu Thr Thr Leu Ala Leu Pro Met Ala Ser Asp
        435                 440                 445

Leu Leu Leu Tyr Asp Val Thr Glu Asn Ser Met Arg Val Lys Trp Asp
    450                 455                 460

Ala Val Pro Gly Ala Ser Gly Tyr Leu Ile Leu Tyr Ala Pro Leu Thr
465                 470                 475                 480

Glu Gly Leu Ala Gly Asp Glu Lys Glu Met Lys Ile Gly Glu Thr His
                485                 490                 495

Thr Asp Ile Glu Leu Ser Gly Leu Leu Pro Asn Thr Glu Tyr Thr Val
            500                 505                 510

Thr Val Tyr Ala Met Phe Gly Glu Glu Ala Ser Asp Pro Val Thr Gly
        515                 520                 525

Gln Glu Thr Thr Leu Ala Leu Ser Pro Pro Arg Asn Leu Arg Ile Ser
    530                 535                 540

Asn Val Gly Ser Asn Ser Ala Arg Leu Thr Trp Asp Pro Thr Ser Arg
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545                 550                 555                 560

Gln Ile Asn Gly Tyr Arg Ile Val Tyr Asn Asn Ala Asp Gly Thr Glu
                565                 570                 575

Ile Asn Glu Val Glu Val Asp Pro Ile Thr Thr Phe Pro Leu Lys Gly
            580                 585                 590

Leu Thr Pro Leu Thr Glu Tyr Thr Ile Ala Ile Phe Ser Ile Tyr Asp
        595                 600                 605

Glu Gly Gln Ser Glu Pro Leu Thr Gly Val Phe Thr Thr Glu Glu Val
    610                 615                 620

Pro Ala Gln Gln Tyr Leu Glu Ile Asp Glu Val Thr Thr Asp Ser Phe
625                 630                 635                 640

Arg Val Thr Trp His Pro Leu Ser Ala Asp Glu Gly Leu His Lys Leu
                645                 650                 655

Met Trp Ile Pro Val Tyr Gly Gly Lys Thr Glu Glu Val Val Leu Lys
            660                 665                 670

Glu Glu Gln Asp Ser His Val Ile Glu Gly Leu Glu Pro Gly Thr Glu
        675                 680                 685

Tyr Glu Val Ser Leu Leu Ala Val Leu Asp Asp Gly Ser Glu Ser Glu
    690                 695                 700

Val Val Thr Ala Val Gly Thr Thr Leu Asp Ser Phe Trp Thr Glu Pro
705                 710                 715                 720

Ala Thr Thr Ile Val Pro Thr Thr Ser Val Thr Ser Val Phe Gln Thr
                725                 730                 735

Gly Ile Arg Asn Leu Val Val Gly Asp Glu Thr Thr Ser Ser Leu Arg
            740                 745                 750

Val Lys Trp Asp Ile Ser Asp Ser Asp Val Gln Gln Phe Arg Val Thr
        755                 760                 765

Tyr Met Thr Ala Gln Gly Asp Pro Glu Glu Glu Val Ile Gly Thr Val
    770                 775                 780

Met Val Pro Gly Ser Gln Asn Asn Leu Leu Leu Lys Pro Leu Leu Pro
785                 790                 795                 800

Asp Thr Glu Tyr Lys Val Thr Val Thr Pro Ile Tyr Thr Asp Gly Glu
                805                 810                 815

Gly Val Ser Val Ser Ala Pro Gly Lys Thr Leu Pro Ser Ser Gly Pro
            820                 825                 830

Gln Asn Leu Arg Val Ser Glu Glu Trp Tyr Asn Arg Leu Arg Ile Thr
        835                 840                 845

Trp Asp Pro Pro Ser Ser Pro Val Lys Gly Tyr Arg Ile Val Tyr Lys
    850                 855                 860

Pro Val Ser Val Pro Gly Pro Thr Leu Glu Thr Phe Val Gly Ala Asp
865                 870                 875                 880

Ile Asn Thr Ile Leu Ile Thr Asn Leu Leu Ser Gly Met Asp Tyr Asn
                885                 890                 895

Val Lys Ile Phe Ala Ser Gln Ala Ser Gly Phe Ser Asp Ala Leu Thr
            900                 905                 910

Gly Met Val Lys Thr Leu Phe Leu Gly Val Thr Asn Leu Gln Ala Lys
        915                 920                 925

His Val Glu Met Thr Ser Leu Cys Ala His Trp Gln Val His Arg His
    930                 935                 940

Ala Thr Ala Tyr Arg Val Val Ile Glu Ser Leu Gln Asp Arg Gln Lys
945                 950                 955                 960
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Gln Glu Ser Thr Val Gly Gly Gly Thr Thr Arg His Cys Phe Tyr Gly
                965                 970                 975

Leu Gln Pro Asp Ser Glu Tyr Lys Ile Ser Val Tyr Thr Lys Leu Gln
            980                 985                 990

Glu Ile Glu Gly Pro Ser Val Ser  Ile Met Glu Lys Thr  Gln Ser Leu
        995                 1000                 1005

Pro Thr  Arg Pro Pro Thr Phe  Pro Pro Thr Ile Pro  Pro Ala Lys
    1010                 1015                 1020

Glu Val  Cys Lys Ala Ala Lys  Ala Asp Leu Val Phe  Met Val Asp
    1025                 1030                 1035

Gly Ser  Trp Ser Ile Gly Asp  Glu Asn Phe Asn Lys  Ile Ile Ser
    1040                 1045                 1050

Phe Leu  Tyr Ser Thr Val Gly  Ala Leu Asn Lys Ile  Gly Thr Asp
    1055                 1060                 1065

Gly Thr  Gln Val Ala Met Val  Gln Phe Thr Asp Asp  Pro Arg Thr
    1070                 1075                 1080

Glu Phe  Lys Leu Asn Ala Tyr  Lys Thr Lys Glu Thr  Leu Leu Asp
    1085                 1090                 1095

Ala Ile  Lys His Ile Ser Tyr  Lys Gly Gly Asn Thr  Lys Thr Gly
    1100                 1105                 1110

Lys Ala  Ile Lys Tyr Val Arg  Asp Thr Leu Phe Thr  Ala Glu Ser
    1115                 1120                 1125

Gly Thr  Arg Arg Gly Ile Pro  Lys Val Ile Val Val  Ile Thr Asp
    1130                 1135                 1140

Gly Arg  Ser Gln Asp Asp Val  Asn Lys Ile Ser Arg  Glu Met Gln
    1145                 1150                 1155

Leu Asp  Gly Tyr Ser Ile Phe  Ala Ile Gly Val Ala  Asp Ala Asp
    1160                 1165                 1170

Tyr Ser  Glu Leu Val Ser Ile  Gly Ser Lys Pro Ser  Ala Arg His
    1175                 1180                 1185

Val Phe  Phe Val Asp Asp Phe  Asp Ala Phe Lys Lys  Ile Glu Asp
    1190                 1195                 1200

Glu Leu  Ile Thr Phe Val Cys  Glu Thr Ala Ser Ala  Thr Cys Pro
    1205                 1210                 1215

Val Val  His Lys Asp Gly Ile  Asp Leu Ala Gly Phe  Lys Met Met
    1220                 1225                 1230

Glu Met  Phe Gly Leu Val Glu  Lys Asp Phe Ser Ser  Val Glu Gly
    1235                 1240                 1245

Val Ser  Met Glu Pro Gly Thr  Phe Asn Val Phe Pro  Cys Tyr Gln
    1250                 1255                 1260

Leu His  Lys Asp Ala Leu Val  Ser Gln Pro Thr Arg  Tyr Leu His
    1265                 1270                 1275

Pro Glu  Gly Leu Pro Ser Asp  Tyr Thr Ile Ser Phe  Leu Phe Arg
    1280                 1285                 1290

Ile Leu  Pro Asp Thr Pro Gln  Glu Pro Phe Ala Leu  Trp Glu Ile
    1295                 1300                 1305

Leu Asn  Lys Asn Ser Asp Pro  Leu Val Gly Val Ile  Leu Asp Asn
    1310                 1315                 1320

Gly Gly  Lys Thr Leu Thr Tyr  Phe Asn Tyr Asp Gln  Ser Gly Asp
    1325                 1330                 1335
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Phe Gln Thr Val Thr Phe Glu Gly Pro Glu Ile Arg Lys Ile Phe
1340 1345 1350

Tyr Gly Ser Phe His Lys Leu His Ile Val Val Ser Glu Thr Leu
1355 1360 1365

Val Lys Val Val Ile Asp Cys Lys Gln Val Gly Glu Lys Ala Met
1370 1375 1380

Asn Ala Ser Ala Asn Ile Thr Ser Asp Gly Val Glu Val Leu Gly
1385 1390 1395

Lys Met Val Arg Ser Arg Gly Pro Gly Gly Asn Ser Ala Pro Phe
1400 1405 1410

Gln Leu Gln Met Phe Asp Ile Val Cys Ser Thr Ser Trp Ala Asn
1415 1420 1425

Thr Asp Lys Cys Cys Glu Leu Pro Gly Leu Arg Asp Asp Glu Ser
1430 1435 1440

Cys Pro Asp Leu Pro His Ser Cys Ser Cys Ser Glu Thr Asn Glu
1445 1450 1455

Val Ala Leu Gly Pro Ala Gly Pro Pro Gly Gly Pro Gly Leu Arg
1460 1465 1470

Gly Pro Lys Gly Gln Gln Gly Glu Pro Gly Pro Lys Gly Pro Asp
1475 1480 1485

Gly Pro Arg Gly Glu Ile Gly Leu Pro Gly Pro Gln Gly Pro Pro
1490 1495 1500

Gly Pro Gln Gly Pro Ser Gly Leu Ser Ile Gln Gly Met Pro Gly
1505 1510 1515

Met Pro Gly Glu Lys Gly Glu Lys Gly Asp Thr Gly Leu Pro Gly
1520 1525 1530

Pro Gln Gly Ile Pro Gly Gly Val Gly Ser Pro Gly Arg Asp Gly
1535 1540 1545

Ser Pro Gly Gln Arg Gly Leu Pro Gly Lys Asp Gly Ser Ser Gly
1550 1555 1560

Pro Pro Gly Pro Pro Gly Pro Ile Gly Ile Pro Gly Thr Pro Gly
1565 1570 1575

Val Pro Gly Ile Thr Gly Ser Met Gly Pro Gln Gly Ala Leu Gly
1580 1585 1590

Pro Pro Gly Val Pro Gly Ala Lys Gly Glu Arg Gly Glu Arg Gly
1595 1600 1605

Asp Leu Gln Ser Gln Ala Met Val Arg Ser Val Ala Arg Gln Val
1610 1615 1620

Cys Glu Gln Leu Ile Gln Ser His Met Ala Arg Tyr Thr Ala Ile
1625 1630 1635

Leu Asn Gln Ile Pro Ser His Ser Ser Ser Ile Arg Thr Val Gln
1640 1645 1650

Gly Pro Pro Gly Glu Pro Gly Arg Pro Gly Ser Pro Gly Ala Pro
1655 1660 1665

Gly Glu Gln Gly Pro Pro Gly Thr Pro Gly Phe Pro Gly Asn Ala
1670 1675 1680

Gly Val Pro Gly Thr Pro Gly Glu Arg Gly Leu Thr Gly Ile Lys
1685 1690 1695

Gly Glu Lys Gly Asn Pro Gly Val Gly Thr Gln Gly Pro Arg Gly
1700 1705 1710

Pro Pro Gly Pro Ala Gly Pro Ser Gly Glu Ser Arg Pro Gly Ser

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1715 1720 1725

Pro Gly Pro Pro Gly Ser Pro Gly Pro Arg Gly Pro Pro Gly His
1730 1735 1740

Leu Gly Val Pro Gly Pro Gln Gly Pro Ser Gly Gln Pro Gly Tyr
1745 1750 1755

Cys Asp Pro Ser Ser Cys Ser Ala Tyr Gly Val Arg Ala Pro His
1760 1765 1770

Pro Asp Gln Pro Glu Phe Thr Pro Val Gln Asp Glu Leu Glu Ala
1775 1780 1785

Met Glu Leu Trp Gly Pro Gly Val
1790 1795

<210> SEQ ID NO 9
<211> LENGTH: 1388
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

Met Ala Pro Arg Arg Asn Asn Gly Gln Cys Trp Cys Leu Leu Met Leu
1 5 10 15

Leu Ser Val Ser Thr Pro Leu Pro Ala Val Thr Gln Thr Arg Gly Ala
20 25 30

Thr Glu Thr Ala Ser Gln Gly His Leu Asp Leu Thr Gln Leu Ile Gly
35 40 45

Val Pro Leu Pro Ser Ser Val Ser Phe Val Thr Gly Tyr Gly Gly Phe
50 55 60

Pro Ala Tyr Ser Phe Gly Pro Gly Ala Asn Val Gly Arg Pro Ala Arg
65 70 75 80

Thr Leu Ile Pro Ser Thr Phe Phe Arg Asp Phe Ala Ile Ser Val Val
85 90 95

Val Lys Pro Ser Ser Thr Arg Gly Gly Val Leu Phe Ala Ile Thr Asp
100 105 110

Ala Phe Gln Lys Val Ile Tyr Leu Gly Leu Arg Leu Ser Gly Val Glu
115 120 125

Asp Gly His Gln Arg Ile Ile Leu Tyr Tyr Thr Glu Pro Gly Ser His
130 135 140

Val Ser Gln Glu Ala Ala Ala Phe Ser Val Pro Val Met Thr His Arg
145 150 155 160

Trp Asn Arg Phe Ala Met Ile Val Gln Gly Glu Glu Val Thr Leu Leu
165 170 175

Val Asn Cys Glu Glu His Ser Arg Ile Pro Phe Gln Arg Ser Ser Gln
180 185 190

Ala Leu Ala Phe Glu Ser Ser Ala Gly Ile Phe Met Gly Asn Ala Gly
195 200 205

Ala Thr Gly Leu Glu Arg Phe Thr Gly Ser Leu Gln Gln Leu Thr Val
210 215 220

His Pro Asp Pro Arg Thr Pro Glu Glu Leu Cys Asp Pro Glu Glu Ser
225 230 235 240

Ser Ala Ser Gly Glu Thr Ser Gly Leu Gln Glu Ala Asp Gly Val Ala
245 250 255

Glu Ile Leu Glu Ala Val Thr Tyr Thr Gln Ala Ser Pro Lys Glu Ala
260 265 270

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Lys Val Glu Pro Ile Asn Thr Pro Pro Thr Pro Ser Ser Pro Phe Glu
        275                 280                 285

Asp Met Glu Leu Ser Gly Glu Pro Val Pro Glu Gly Thr Leu Glu Thr
    290                 295                 300

Thr Asn Met Ser Ile Ile Gln His Ser Ser Pro Lys Gln Gly Ser Gly
305                 310                 315                 320

Glu Ile Leu Asn Asp Thr Leu Glu Gly Val His Ser Val Asp Gly Asp
                325                 330                 335

Pro Ile Thr Asp Ser Gly Ser Gly Ala Gly Ala Phe Leu Asp Ile Ala
            340                 345                 350

Glu Glu Lys Asn Leu Ala Ala Thr Ala Ala Gly Leu Ala Glu Val Pro
        355                 360                 365

Ile Ser Thr Ala Gly Glu Ala Glu Ala Ser Ser Val Pro Thr Gly Gly
    370                 375                 380

Pro Thr Leu Ser Met Ser Thr Glu Asn Pro Glu Glu Gly Val Thr Pro
385                 390                 395                 400

Gly Pro Asp Asn Glu Glu Arg Leu Ala Ala Thr Ala Ala Gly Glu Ala
                405                 410                 415

Glu Ala Leu Ala Ser Met Pro Gly Glu Val Glu Ala Ser Gly Val Ala
            420                 425                 430

Pro Gly Glu Leu Asp Leu Ser Met Ser Ala Gln Ser Leu Gly Glu Glu
        435                 440                 445

Ala Thr Val Gly Pro Ser Ser Glu Asp Ser Leu Thr Thr Ala Ala Ala
    450                 455                 460

Ala Thr Glu Val Ser Leu Ser Thr Phe Glu Asp Glu Glu Ala Ser Gly
465                 470                 475                 480

Val Pro Thr Asp Gly Leu Ala Pro Leu Thr Ala Thr Met Ala Pro Glu
                485                 490                 495

Arg Ala Val Thr Ser Gly Pro Gly Asp Glu Glu Asp Leu Ala Ala Ala
            500                 505                 510

Thr Thr Glu Glu Pro Leu Ile Thr Ala Gly Gly Glu Glu Ser Gly Ser
        515                 520                 525

Pro Pro Pro Asp Gly Pro Pro Leu Pro Leu Pro Thr Val Ala Pro Glu
    530                 535                 540

Arg Trp Ile Thr Pro Ala Gln Arg Glu His Val Gly Met Lys Gly Gln
545                 550                 555                 560

Ala Gly Pro Lys Gly Glu Lys Gly Asp Ala Gly Glu Glu Leu Pro Gly
                565                 570                 575

Pro Pro Glu Pro Ser Gly Pro Val Gly Pro Thr Ala Gly Ala Glu Ala
            580                 585                 590

Glu Gly Ser Gly Leu Gly Trp Gly Ser Asp Val Gly Ser Gly Ser Gly
        595                 600                 605

Asp Leu Val Gly Ser Glu Gln Leu Leu Arg Gly Pro Pro Gly Pro Pro
    610                 615                 620

Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Lys Pro Gly Thr Asp Val
625                 630                 635                 640

Phe Met Gly Pro Pro Gly Ser Pro Gly Glu Asp Gly Pro Ala Gly Glu
                645                 650                 655

Pro Gly Pro Pro Gly Pro Glu Gly Gln Pro Gly Val Asp Gly Ala Thr
            660                 665                 670

Gly Leu Pro Gly Met Lys Gly Glu Lys Gly Ala Arg Gly Pro Asn Gly
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        675                 680                 685

Ser Val Gly Glu Lys Gly Asp Pro Gly Asn Arg Gly Leu Pro Gly Pro
    690                 695                 700

Pro Gly Lys Lys Gly Gln Ala Gly Pro Pro Gly Val Met Gly Pro Pro
705                 710                 715                 720

Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Gly Cys Thr Met Gly
                725                 730                 735

Leu Gly Phe Glu Asp Thr Glu Gly Ser Gly Ser Thr Gln Leu Leu Asn
            740                 745                 750

Glu Pro Lys Leu Ser Arg Pro Thr Ala Ala Ile Gly Leu Lys Gly Glu
        755                 760                 765

Lys Gly Asp Arg Gly Pro Lys Gly Glu Arg Gly Met Asp Gly Ala Ser
    770                 775                 780

Ile Val Gly Pro Pro Gly Pro Arg Gly Pro Pro Gly His Ile Lys Val
785                 790                 795                 800

Leu Ser Asn Ser Leu Ile Asn Ile Thr His Gly Phe Met Asn Phe Ser
                805                 810                 815

Asp Ile Pro Glu Leu Val Gly Pro Pro Gly Pro Asp Gly Leu Pro Gly
            820                 825                 830

Leu Pro Gly Phe Pro Gly Pro Arg Gly Pro Lys Gly Asp Thr Gly Leu
        835                 840                 845

Pro Gly Phe Pro Gly Leu Lys Gly Glu Gln Gly Glu Lys Gly Glu Pro
    850                 855                 860

Gly Ala Ile Leu Thr Glu Asp Ile Pro Leu Glu Arg Leu Met Gly Lys
865                 870                 875                 880

Lys Gly Glu Pro Gly Met His Gly Ala Pro Gly Pro Met Gly Pro Lys
                885                 890                 895

Gly Pro Pro Gly His Lys Gly Glu Phe Gly Leu Pro Gly Arg Pro Gly
            900                 905                 910

Arg Pro Gly Leu Asn Gly Leu Lys Gly Thr Lys Gly Asp Pro Gly Val
        915                 920                 925

Ile Met Gln Gly Pro Pro Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly
    930                 935                 940

Pro Pro Gly Ala Val Ile Asn Ile Lys Gly Ala Ile Phe Pro Ile Pro
945                 950                 955                 960

Val Arg Pro His Cys Lys Met Pro Val Asp Thr Ala His Pro Gly Ser
                965                 970                 975

Pro Glu Leu Ile Thr Phe His Gly Val Lys Gly Glu Lys Gly Ser Trp
            980                 985                 990

Gly Leu Pro Gly Ser Lys Gly Glu  Lys Gly Asp Gln Gly  Ala Gln Gly
        995                 1000                 1005

Pro Pro  Gly Pro Pro Leu Asp  Leu Ala Tyr Leu Arg  His Phe Leu
    1010                 1015                 1020

Asn Asn  Leu Lys Gly Glu Asn  Gly Asp Lys Gly Phe  Lys Gly Glu
    1025                 1030                 1035

Lys Gly  Glu Lys Gly Asp Ile  Asn Gly Ser Phe Leu  Met Ser Gly
    1040                 1045                 1050

Pro Pro  Gly Leu Pro Gly Asn  Pro Gly Pro Ala Gly  Gln Lys Gly
    1055                 1060                 1065

Glu Thr  Val Val Gly Pro Gln  Gly Pro Pro Gly Ala  Pro Gly Leu
    1070                 1075                 1080
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Pro Gly Pro Pro Gly Phe Gly Arg Pro Gly Asp Pro Gly Pro Pro
1085 1090 1095

Gly Pro Pro Gly Pro Pro Gly Pro Pro Ala Ile Leu Gly Ala Ala
1100 1105 1110

Val Ala Leu Pro Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly Leu
1115 1120 1125

Pro Gly Ser Arg Asn Leu Val Thr Ala Phe Ser Asn Met Asp Asp
1130 1135 1140

Met Leu Gln Lys Ala His Leu Val Ile Glu Gly Thr Phe Ile Tyr
1145 1150 1155

Leu Arg Asp Ser Thr Glu Phe Phe Ile Arg Val Arg Asp Gly Trp
1160 1165 1170

Lys Lys Leu Gln Leu Gly Glu Leu Ile Pro Ile Pro Ala Asp Ser
1175 1180 1185

Pro Pro Pro Pro Ala Leu Ser Ser Asn Pro His Gln Leu Leu Pro
1190 1195 1200

Pro Pro Asn Pro Ile Ser Ser Ala Asn Tyr Glu Lys Pro Ala Leu
1205 1210 1215

His Leu Ala Ala Leu Asn Met Pro Phe Ser Gly Asp Ile Arg Ala
1220 1225 1230

Asp Phe Gln Cys Phe Lys Gln Ala Arg Ala Ala Gly Leu Leu Ser
1235 1240 1245

Thr Tyr Arg Ala Phe Leu Ser Ser His Leu Gln Asp Leu Ser Thr
1250 1255 1260

Ile Val Arg Lys Ala Glu Arg Tyr Ser Leu Pro Ile Val Asn Leu
1265 1270 1275

Lys Gly Gln Val Leu Phe Asn Asn Trp Asp Ser Ile Phe Ser Gly
1280 1285 1290

His Gly Gly Gln Phe Asn Met His Ile Pro Ile Tyr Ser Phe Asp
1295 1300 1305

Gly Arg Asp Ile Met Thr Asp Pro Ser Trp Pro Gln Lys Val Ile
1310 1315 1320

Trp His Gly Ser Ser Pro His Gly Val Arg Leu Val Asp Asn Tyr
1325 1330 1335

Cys Glu Ala Trp Arg Thr Ala Asp Thr Ala Val Thr Gly Leu Ala
1340 1345 1350

Ser Pro Leu Ser Thr Gly Lys Ile Leu Asp Gln Lys Ala Tyr Ser
1355 1360 1365

Cys Ala Asn Arg Leu Ile Val Leu Cys Ile Glu Asn Ser Phe Met
1370 1375 1380

Thr Asp Ala Arg Lys
1385

<210> SEQ ID NO 10
<211> LENGTH: 1751
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

Met Ala Pro Tyr Pro Cys Gly Cys His Ile Leu Leu Leu Leu Phe Cys
1 5 10 15

Cys Leu Ala Ala Ala Arg Ala Asn Leu Leu Asn Leu Asn Trp Leu Trp

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            20                  25                  30

Phe Asn Asn Glu Asp Thr Ser His Ala Ala Thr Thr Ile Pro Glu Pro
        35                  40                  45

Gln Gly Pro Leu Pro Val Gln Pro Thr Ala Asp Thr Thr Thr His Val
    50                  55                  60

Thr Pro Arg Asn Gly Ser Thr Glu Pro Ala Thr Ala Pro Gly Ser Pro
65                  70                  75                  80

Glu Pro Pro Ser Glu Leu Leu Glu Asp Gly Gln Asp Thr Pro Thr Ser
                85                  90                  95

Ala Glu Ser Pro Asp Ala Pro Glu Glu Asn Ile Ala Gly Val Gly Ala
            100                 105                 110

Glu Ile Leu Asn Val Ala Lys Gly Ile Arg Ser Phe Val Gln Leu Trp
        115                 120                 125

Asn Asp Thr Val Pro Thr Glu Ser Leu Ala Arg Ala Glu Thr Leu Val
    130                 135                 140

Leu Glu Thr Pro Val Gly Pro Leu Ala Leu Ala Gly Pro Ser Ser Thr
145                 150                 155                 160

Pro Gln Glu Asn Gly Thr Thr Leu Trp Pro Ser Arg Gly Ile Pro Ser
                165                 170                 175

Ser Pro Gly Ala His Thr Thr Glu Ala Gly Thr Leu Pro Ala Pro Thr
            180                 185                 190

Pro Ser Pro Pro Ser Leu Gly Arg Pro Trp Ala Pro Leu Thr Gly Pro
        195                 200                 205

Ser Val Pro Pro Pro Ser Ser Gly Arg Ala Ser Leu Ser Ser Leu Leu
    210                 215                 220

Gly Gly Ala Pro Pro Trp Gly Ser Leu Gln Asp Pro Asp Ser Gln Gly
225                 230                 235                 240

Leu Ser Pro Ala Ala Ala Ala Pro Ser Gln Gln Leu Gln Arg Pro Asp
                245                 250                 255

Val Arg Leu Arg Thr Pro Leu Leu His Pro Leu Val Met Gly Ser Leu
            260                 265                 270

Gly Lys His Ala Ala Pro Ser Ala Phe Ser Ser Gly Leu Pro Gly Ala
        275                 280                 285

Leu Ser Gln Val Ala Val Thr Thr Leu Thr Arg Asp Ser Gly Ala Trp
    290                 295                 300

Val Ser His Val Ala Asn Ser Val Gly Pro Gly Leu Ala Asn Asn Ser
305                 310                 315                 320

Ala Leu Leu Gly Ala Asp Pro Glu Ala Pro Ala Gly Arg Cys Leu Pro
                325                 330                 335

Leu Pro Pro Ser Leu Pro Val Cys Gly His Leu Gly Ile Ser Arg Phe
            340                 345                 350

Trp Leu Pro Asn His Leu His His Glu Ser Gly Glu Gln Val Arg Ala
        355                 360                 365

Gly Ala Arg Ala Trp Gly Gly Leu Leu Gln Thr His Cys His Pro Phe
    370                 375                 380

Leu Ala Trp Phe Phe Cys Leu Leu Leu Val Pro Pro Cys Gly Ser Val
385                 390                 395                 400

Pro Pro Pro Ala Pro Pro Pro Cys Cys Gln Phe Cys Glu Ala Leu Gln
                405                 410                 415

Asp Ala Cys Trp Ser Arg Leu Gly Gly Gly Arg Leu Pro Val Ala Cys
            420                 425                 430
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Ala Ser Leu Pro Thr Gln Glu Asp Gly Tyr Cys Val Leu Ile Gly Pro
        435                 440                 445

Ala Ala Glu Arg Ile Ser Glu Glu Val Gly Leu Leu Gln Leu Leu Gly
    450                 455                 460

Asp Pro Pro Pro Gln Gln Val Thr Gln Thr Asp Asp Pro Asp Val Gly
465                 470                 475                 480

Leu Ala Tyr Val Phe Gly Pro Asp Ala Asn Ser Gly Gln Val Ala Arg
                485                 490                 495

Tyr His Phe Pro Ser Leu Phe Phe Arg Asp Phe Ser Leu Leu Phe His
            500                 505                 510

Ile Arg Pro Ala Thr Glu Gly Pro Gly Val Leu Phe Ala Ile Thr Asp
        515                 520                 525

Ser Ala Gln Ala Met Val Leu Leu Gly Val Lys Leu Ser Gly Val Gln
    530                 535                 540

Asp Gly His Gln Asp Ile Ser Leu Leu Tyr Thr Glu Pro Gly Ala Gly
545                 550                 555                 560

Gln Thr His Thr Ala Ala Ser Phe Arg Leu Pro Ala Phe Val Gly Gln
                565                 570                 575

Trp Thr His Leu Ala Leu Ser Val Ala Gly Gly Phe Val Ala Leu Tyr
            580                 585                 590

Val Asp Cys Glu Glu Phe Gln Arg Met Pro Leu Ala Arg Ser Ser Arg
        595                 600                 605

Gly Leu Glu Leu Glu Pro Gly Ala Gly Leu Phe Val Ala Gln Ala Gly
    610                 615                 620

Gly Ala Asp Pro Asp Lys Phe Gln Gly Val Ile Ala Glu Leu Lys Val
625                 630                 635                 640

Arg Arg Asp Pro Gln Val Ser Pro Met His Cys Leu Asp Glu Glu Gly
                645                 650                 655

Asp Asp Ser Asp Gly Ala Ser Gly Asp Ser Gly Ser Gly Leu Gly Asp
            660                 665                 670

Ala Arg Glu Leu Leu Arg Glu Glu Thr Gly Ala Ala Leu Lys Pro Arg
        675                 680                 685

Leu Pro Ala Pro Pro Pro Val Thr Thr Pro Pro Leu Ala Gly Gly Ser
    690                 695                 700

Ser Thr Glu Asp Ser Arg Ser Glu Glu Val Glu Glu Gln Thr Thr Val
705                 710                 715                 720

Ala Ser Leu Gly Ala Gln Thr Leu Pro Gly Ser Asp Ser Val Ser Thr
                725                 730                 735

Trp Asp Gly Ser Val Arg Thr Pro Gly Gly Arg Val Lys Glu Gly Gly
            740                 745                 750

Leu Lys Gly Gln Lys Gly Glu Pro Gly Val Pro Gly Pro Pro Gly Arg
        755                 760                 765

Ala Gly Pro Pro Gly Ser Pro Cys Leu Pro Gly Pro Pro Gly Leu Pro
    770                 775                 780

Cys Pro Val Ser Pro Leu Gly Pro Ala Gly Pro Ala Leu Gln Thr Val
785                 790                 795                 800

Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Arg Asp Gly Thr Pro
                805                 810                 815

Gly Arg Asp Gly Glu Pro Gly Asp Pro Gly Glu Asp Gly Lys Pro Gly
            820                 825                 830
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Asp Thr Gly Pro Gln Gly Phe Pro Gly Thr Pro Gly Asp Val Gly Pro
        835                 840                 845

Lys Gly Asp Lys Gly Asp Pro Gly Val Gly Glu Arg Gly Pro Pro Gly
    850                 855                 860

Pro Gln Gly Pro Pro Gly Pro Pro Gly Pro Ser Phe Arg His Asp Lys
865                 870                 875                 880

Leu Thr Phe Ile Asp Met Glu Gly Ser Gly Phe Gly Gly Asp Leu Glu
                885                 890                 895

Ala Leu Arg Gly Pro Arg Gly Phe Pro Gly Pro Pro Gly Pro Pro Gly
            900                 905                 910

Val Pro Gly Leu Pro Gly Glu Pro Gly Arg Phe Gly Val Asn Ser Ser
        915                 920                 925

Asp Val Pro Gly Pro Ala Gly Leu Pro Gly Val Pro Gly Arg Glu Gly
    930                 935                 940

Pro Pro Gly Phe Pro Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Arg
945                 950                 955                 960

Glu Gly Pro Pro Gly Arg Thr Gly Gln Lys Gly Ser Leu Gly Glu Ala
                965                 970                 975

Gly Ala Pro Gly His Lys Gly Ser Lys Gly Ala Pro Gly Pro Ala Gly
            980                 985                 990

Ala Arg Gly Glu Ser Gly Leu Ala  Gly Ala Pro Gly Pro  Ala Gly Pro
        995                 1000                 1005

Pro Gly  Pro Pro Gly Pro Pro  Gly Pro Pro Gly Pro  Gly Leu Pro
    1010                 1015                 1020

Ala Gly  Phe Asp Asp Met Glu  Gly Ser Gly Gly Pro  Phe Trp Ser
    1025                 1030                 1035

Thr Ala  Arg Ser Ala Asp Gly  Pro Gln Gly Pro Pro  Gly Leu Pro
    1040                 1045                 1050

Gly Leu  Lys Gly Asp Pro Gly  Val Pro Gly Leu Pro  Gly Ala Lys
    1055                 1060                 1065

Gly Glu  Val Gly Ala Asp Gly  Val Pro Gly Phe Pro  Gly Leu Pro
    1070                 1075                 1080

Gly Arg  Glu Gly Ile Ala Gly  Pro Gln Gly Pro Lys  Gly Asp Arg
    1085                 1090                 1095

Gly Ser  Arg Gly Glu Lys Gly  Asp Pro Gly Lys Asp  Gly Val Gly
    1100                 1105                 1110

Gln Pro  Gly Leu Pro Gly Pro  Pro Gly Pro Pro Gly  Pro Val Val
    1115                 1120                 1125

Tyr Val  Ser Glu Gln Asp Gly  Ser Val Leu Ser Val  Pro Gly Pro
    1130                 1135                 1140

Glu Gly  Arg Pro Gly Phe Ala  Gly Phe Pro Gly Pro  Ala Gly Pro
    1145                 1150                 1155

Lys Gly  Asn Leu Gly Ser Lys  Gly Glu Arg Gly Ser  Pro Gly Pro
    1160                 1165                 1170

Lys Gly  Glu Lys Gly Glu Pro  Gly Ser Ile Phe Ser  Pro Asp Gly
    1175                 1180                 1185

Gly Ala  Leu Gly Pro Ala Gln  Lys Gly Ala Lys Gly  Glu Pro Gly
    1190                 1195                 1200

Phe Arg  Gly Pro Pro Gly Pro  Tyr Gly Arg Pro Gly  Tyr Lys Gly
    1205                 1210                 1215

Glu Ile  Gly Phe Pro Gly Arg  Pro Gly Arg Pro Gly  Met Asn Gly
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    1220                1225                1230

Leu Lys  Gly Glu Lys Gly Glu  Pro Gly Asp Ala Ser  Leu Gly Phe
    1235                1240                1245

Gly Met  Arg Gly Met Pro Gly  Pro Pro Gly Pro Pro  Gly Pro Pro
    1250                1255                1260

Gly Pro  Pro Gly Thr Pro Val  Tyr Asp Ser Asn Val  Phe Ala Glu
    1265                1270                1275

Ser Ser  Arg Pro Gly Pro Pro  Gly Leu Pro Gly Asn  Gln Gly Pro
    1280                1285                1290

Pro Gly  Pro Lys Gly Ala Lys  Gly Glu Val Gly Pro  Pro Gly Pro
    1295                1300                1305

Pro Gly  Gln Phe Pro Phe Asp  Phe Leu Gln Leu Glu  Ala Glu Met
    1310                1315                1320

Lys Gly  Glu Lys Gly Asp Arg  Gly Asp Ala Gly Gln  Lys Gly Glu
    1325                1330                1335

Arg Gly  Glu Pro Gly Gly Gly  Gly Phe Phe Gly Ser  Ser Leu Pro
    1340                1345                1350

Gly Pro  Pro Gly Pro Pro Gly  Pro Arg Gly Tyr Pro  Gly Ile Pro
    1355                1360                1365

Gly Pro  Lys Gly Glu Ser Ile  Arg Gly Gln Pro Gly  Pro Pro Gly
    1370                1375                1380

Pro Gln  Gly Pro Pro Gly Ile  Gly Tyr Glu Gly Arg  Gln Gly Pro
    1385                1390                1395

Pro Gly  Pro Pro Gly Pro Pro  Gly Pro Pro Ser Phe  Pro Gly Pro
    1400                1405                1410

His Arg  Gln Thr Ile Ser Val  Pro Gly Pro Pro Gly  Pro Pro Gly
    1415                1420                1425

Pro Pro  Gly Pro Pro Gly Thr  Met Gly Ala Ser Ser  Gly Val Arg
    1430                1435                1440

Leu Trp  Ala Thr Arg Gln Ala  Met Leu Gly Gln Val  His Glu Val
    1445                1450                1455

Pro Glu  Gly Trp Leu Ile Phe  Val Ala Glu Gln Glu  Glu Leu Tyr
    1460                1465                1470

Val Arg  Val Gln Asn Gly Phe  Arg Lys Val Gln Leu  Glu Ala Arg
    1475                1480                1485

Thr Pro  Leu Pro Arg Gly Thr  Asp Asn Glu Val Ala  Ala Leu Gln
    1490                1495                1500

Pro Pro  Val Val Gln Leu His  Asp Ser Asn Pro Tyr  Pro Arg Arg
    1505                1510                1515

Glu His  Pro His Pro Thr Ala  Arg Pro Trp Arg Ala  Asp Asp Ile
    1520                1525                1530

Leu Ala  Ser Pro Pro Arg Leu  Pro Glu Pro Gln Pro  Tyr Pro Gly
    1535                1540                1545

Ala Pro  His His Ser Ser Tyr  Val His Leu Arg Pro  Ala Arg Pro
    1550                1555                1560

Thr Ser  Pro Pro Ala His Ser  His Arg Asp Phe Gln  Pro Val Leu
    1565                1570                1575

His Leu  Val Ala Leu Asn Ser  Pro Leu Ser Gly Gly  Met Arg Gly
    1580                1585                1590

Ile Arg  Gly Ala Asp Phe Gln  Cys Phe Gln Gln Ala  Arg Ala Val
    1595                1600                1605
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Gly Leu Ala Gly Thr Phe Arg Ala Phe Leu Ser Ser Arg Leu Gln
1610 1615 1620

Asp Leu Tyr Ser Ile Val Arg Arg Ala Asp Arg Ala Ala Val Pro
1625 1630 1635

Ile Val Asn Leu Lys Asp Glu Leu Leu Phe Pro Ser Trp Glu Ala
1640 1645 1650

Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro Gly Ala Arg Ile
1655 1660 1665

Phe Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro Thr Trp Pro
1670 1675 1680

Gln Lys Ser Val Trp His Gly Ser Asp Pro Asn Gly Arg Arg Leu
1685 1690 1695

Thr Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Ala Pro Ser Ala
1700 1705 1710

Thr Gly Gln Ala Ser Ser Leu Leu Gly Gly Arg Leu Leu Gly Gln
1715 1720 1725

Ser Ala Ala Ser Cys His His Ala Tyr Ile Val Leu Cys Ile Glu
1730 1735 1740

Asn Ser Phe Met Thr Ala Ser Lys
1745 1750

<210> SEQ ID NO 11
<211> LENGTH: 1142
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

Met Arg Leu Thr Gly Pro Trp Lys Leu Trp Leu Trp Met Ser Ile Phe
1 5 10 15

Leu Leu Pro Ala Ser Thr Ser Val Thr Val Arg Asp Lys Thr Glu Glu
20 25 30

Ser Cys Pro Ile Leu Arg Ile Glu Gly His Gln Leu Thr Tyr Asp Asn
35 40 45

Ile Asn Lys Leu Glu Val Ser Gly Phe Asp Leu Gly Asp Ser Phe Ser
50 55 60

Leu Arg Arg Ala Phe Cys Glu Ser Asp Lys Thr Cys Phe Lys Leu Gly
65 70 75 80

Ser Ala Leu Leu Ile Arg Asp Thr Ile Lys Ile Phe Pro Lys Gly Leu
85 90 95

Pro Glu Glu Tyr Ser Val Ala Ala Met Phe Arg Val Arg Arg Asn Ala
100 105 110

Lys Lys Glu Arg Trp Phe Leu Trp Gln Val Leu Asn Gln Gln Asn Ile
115 120 125

Pro Gln Ile Ser Ile Val Val Asp Gly Gly Lys Lys Val Val Glu Phe
130 135 140

Met Phe Gln Ala Thr Glu Gly Asp Val Leu Asn Tyr Ile Phe Arg Asn
145 150 155 160

Arg Glu Leu Arg Pro Leu Phe Asp Arg Gln Trp His Lys Leu Gly Ile
165 170 175

Ser Ile Gln Ser Gln Val Ile Ser Leu Tyr Met Asp Cys Asn Leu Ile
180 185 190

Ala Arg Arg Gln Thr Asp Glu Lys Asp Thr Val Asp Phe His Gly Arg

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        195                 200                 205

Thr Val Ile Ala Thr Arg Ala Ser Asp Gly Lys Pro Val Asp Ile Glu
    210                 215                 220

Leu His Gln Leu Lys Ile Tyr Cys Ser Ala Asn Leu Ile Ala Gln Glu
225                 230                 235                 240

Thr Cys Cys Glu Ile Ser Asp Thr Lys Cys Pro Glu Gln Asp Gly Phe
                245                 250                 255

Gly Asn Ile Ala Ser Ser Trp Val Thr Ala His Ala Ser Lys Met Ser
            260                 265                 270

Ser Tyr Leu Pro Ala Lys Gln Glu Leu Lys Asp Gln Cys Gln Cys Ile
        275                 280                 285

Pro Asn Lys Gly Glu Ala Gly Leu Pro Gly Ala Pro Gly Ser Pro Gly
    290                 295                 300

Gln Lys Gly His Lys Gly Glu Pro Gly Glu Asn Gly Leu His Gly Ala
305                 310                 315                 320

Pro Gly Phe Pro Gly Gln Lys Gly Glu Gln Gly Phe Glu Gly Ser Lys
                325                 330                 335

Gly Glu Thr Gly Glu Lys Gly Glu Gln Gly Glu Lys Gly Asp Pro Ala
            340                 345                 350

Leu Ala Gly Leu Asn Gly Glu Asn Gly Leu Lys Gly Asp Leu Gly Pro
        355                 360                 365

His Gly Pro Pro Gly Pro Lys Gly Glu Lys Gly Asp Thr Gly Pro Pro
    370                 375                 380

Gly Pro Pro Ala Leu Pro Gly Ser Leu Gly Ile Gln Gly Pro Gln Gly
385                 390                 395                 400

Pro Pro Gly Lys Glu Gly Gln Arg Gly Arg Arg Gly Lys Thr Gly Pro
                405                 410                 415

Pro Gly Lys Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ile Gln
            420                 425                 430

Gly Ile His Gln Thr Leu Gly Gly Tyr Tyr Asn Lys Asp Asn Lys Gly
        435                 440                 445

Asn Asp Glu His Glu Ala Gly Gly Leu Lys Gly Asp Lys Gly Glu Thr
    450                 455                 460

Gly Leu Pro Gly Phe Pro Gly Ser Val Gly Pro Lys Gly Gln Lys Gly
465                 470                 475                 480

Glu Pro Gly Glu Pro Phe Thr Lys Gly Glu Lys Gly Asp Arg Gly Glu
                485                 490                 495

Pro Gly Val Ile Gly Ser Gln Gly Val Lys Gly Glu Pro Gly Asp Pro
            500                 505                 510

Gly Pro Pro Gly Leu Ile Gly Ser Pro Gly Leu Lys Gly Gln Gln Gly
        515                 520                 525

Ser Ala Gly Ser Met Gly Pro Arg Gly Pro Pro Gly Asp Val Gly Leu
    530                 535                 540

Pro Gly Glu His Gly Ile Pro Gly Lys Gln Gly Ile Lys Gly Glu Lys
545                 550                 555                 560

Gly Asp Pro Gly Gly Ile Ile Gly Pro Pro Gly Leu Pro Gly Pro Lys
                565                 570                 575

Gly Glu Ala Gly Pro Pro Gly Lys Ser Leu Pro Gly Glu Pro Gly Leu
            580                 585                 590

Asp Gly Asn Pro Gly Ala Pro Gly Pro Arg Gly Pro Lys Gly Glu Arg
        595                 600                 605
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Gly Leu Pro Gly Val His Gly Ser Pro Gly Asp Ile Gly Pro Gln Gly
    610                 615                 620

Ile Gly Ile Pro Gly Arg Thr Gly Ala Gln Gly Pro Ala Gly Glu Pro
625                 630                 635                 640

Gly Ile Gln Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Thr Pro Gly
                645                 650                 655

Thr Pro Gly Asn Asp Gly Val Pro Gly Arg Asp Gly Lys Pro Gly Leu
            660                 665                 670

Pro Gly Pro Pro Gly Asp Pro Ile Ala Leu Pro Leu Leu Gly Asp Ile
        675                 680                 685

Gly Ala Leu Leu Lys Asn Phe Cys Gly Asn Cys Gln Ala Ser Val Pro
    690                 695                 700

Gly Leu Lys Ser Asn Lys Gly Glu Glu Gly Gly Ala Gly Glu Pro Gly
705                 710                 715                 720

Lys Tyr Asp Ser Met Ala Arg Lys Gly Asp Ile Gly Pro Arg Gly Pro
                725                 730                 735

Pro Gly Ile Pro Gly Arg Glu Gly Pro Lys Gly Ser Lys Gly Glu Arg
            740                 745                 750

Gly Tyr Pro Gly Ile Pro Gly Glu Lys Gly Asp Glu Gly Leu Gln Gly
        755                 760                 765

Ile Pro Gly Ile Pro Gly Ala Pro Gly Pro Thr Gly Pro Pro Gly Leu
    770                 775                 780

Met Gly Arg Thr Gly His Pro Gly Pro Thr Gly Ala Lys Gly Glu Lys
785                 790                 795                 800

Gly Ser Asp Gly Pro Pro Gly Lys Pro Gly Pro Pro Gly Pro Pro Gly
                805                 810                 815

Ile Pro Phe Asn Glu Arg Asn Gly Met Ser Ser Leu Tyr Lys Ile Lys
            820                 825                 830

Gly Gly Val Asn Val Pro Ser Tyr Pro Gly Pro Pro Gly Pro Pro Gly
        835                 840                 845

Pro Lys Gly Asp Pro Gly Pro Val Gly Glu Pro Gly Ala Met Gly Leu
    850                 855                 860

Pro Gly Leu Glu Gly Phe Pro Gly Val Lys Gly Asp Arg Gly Pro Ala
865                 870                 875                 880

Gly Pro Pro Gly Ile Ala Gly Met Ser Gly Lys Pro Gly Ala Pro Gly
                885                 890                 895

Pro Pro Gly Val Pro Gly Glu Pro Gly Glu Arg Gly Pro Val Gly Asp
            900                 905                 910

Ile Gly Phe Pro Gly Pro Glu Gly Pro Ser Gly Lys Pro Gly Ile Asn
        915                 920                 925

Gly Lys Asp Gly Ile Pro Gly Ala Gln Gly Ile Met Gly Lys Pro Gly
    930                 935                 940

Asp Arg Gly Pro Lys Gly Glu Arg Gly Asp Gln Gly Ile Pro Gly Asp
945                 950                 955                 960

Arg Gly Ser Gln Gly Glu Arg Gly Lys Pro Gly Leu Thr Gly Met Lys
                965                 970                 975

Gly Ala Ile Gly Pro Met Gly Pro Pro Gly Asn Lys Gly Ser Met Gly
            980                 985                 990

Ser Pro Gly His Gln Gly Pro Pro  Gly Ser Pro Gly Ile  Pro Gly Ile
        995                 1000                 1005
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Pro Ala  Asp Ala Val Ser Phe  Glu Glu Ile Lys Lys  Tyr Ile Asn
    1010                 1015                 1020

Gln Glu  Val Leu Arg Ile Phe  Glu Glu Arg Met Ala  Val Phe Leu
    1025                 1030                 1035

Ser Gln  Leu Lys Leu Pro Ala  Ala Met Leu Ala Ala  Gln Ala Tyr
    1040                 1045                 1050

Gly Arg  Pro Gly Pro Pro Gly  Lys Asp Gly Leu Pro  Gly Pro Pro
    1055                 1060                 1065

Gly Asp  Pro Gly Pro Gln Gly  Tyr Arg Gly Gln Lys  Gly Glu Arg
    1070                 1075                 1080

Gly Glu  Pro Gly Ile Gly Leu  Pro Gly Ser Pro Gly  Leu Pro Gly
    1085                 1090                 1095

Thr Ser  Ala Leu Gly Leu Pro  Gly Ser Pro Gly Ala  Pro Gly Pro
    1100                 1105                 1110

Gln Gly  Pro Pro Gly Pro Ser  Gly Arg Cys Asn Pro  Glu Asp Cys
    1115                 1120                 1125

Leu Tyr  Pro Val Ser His Ala  His Gln Arg Thr Gly  Gly Asn
    1130                 1135                 1140


<210> SEQ ID NO 12
<211> LENGTH: 1366
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

Met Leu Ser Phe Val Asp Thr Arg Thr Leu Leu Leu Leu Ala Val Thr
1               5                   10                  15

Leu Cys Leu Ala Thr Cys Gln Ser Leu Gln Glu Glu Thr Val Arg Lys
            20                  25                  30

Gly Pro Ala Gly Asp Arg Gly Pro Arg Gly Glu Arg Gly Pro Pro Gly
        35                  40                  45

Pro Pro Gly Arg Asp Gly Glu Asp Gly Pro Thr Gly Pro Pro Gly Pro
    50                  55                  60

Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala Ala Gln
65                  70                  75                  80

Tyr Asp Gly Lys Gly Val Gly Leu Gly Pro Gly Pro Met Gly Leu Met
                85                  90                  95

Gly Pro Arg Gly Pro Pro Gly Ala Ala Gly Ala Pro Gly Pro Gln Gly
            100                 105                 110

Phe Gln Gly Pro Ala Gly Glu Pro Gly Glu Pro Gly Gln Thr Gly Pro
        115                 120                 125

Ala Gly Ala Arg Gly Pro Ala Gly Pro Pro Gly Lys Ala Gly Glu Asp
    130                 135                 140

Gly His Pro Gly Lys Pro Gly Arg Pro Gly Glu Arg Gly Val Val Gly
145                 150                 155                 160

Pro Gln Gly Ala Arg Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Phe
                165                 170                 175

Lys Gly Ile Arg Gly His Asn Gly Leu Asp Gly Leu Lys Gly Gln Pro
            180                 185                 190

Gly Ala Pro Gly Val Lys Gly Glu Pro Gly Ala Pro Gly Glu Asn Gly
        195                 200                 205

Thr Pro Gly Gln Thr Gly Ala Arg Gly Leu Pro Gly Glu Arg Gly Arg
    210                 215                 220
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Val Gly Ala Pro Gly Pro Ala Gly Ala Arg Gly Ser Asp Gly Ser Val
225                 230                 235                 240

Gly Pro Val Gly Pro Ala Gly Pro Ile Gly Ser Ala Gly Pro Pro Gly
                245                 250                 255

Phe Pro Gly Ala Pro Gly Pro Lys Gly Glu Ile Gly Ala Val Gly Asn
            260                 265                 270

Ala Gly Pro Ala Gly Pro Ala Gly Pro Arg Gly Glu Val Gly Leu Pro
        275                 280                 285

Gly Leu Ser Gly Pro Val Gly Pro Pro Gly Asn Pro Gly Ala Asn Gly
    290                 295                 300

Leu Thr Gly Ala Lys Gly Ala Ala Gly Leu Pro Gly Val Ala Gly Ala
305                 310                 315                 320

Pro Gly Leu Pro Gly Pro Arg Gly Ile Pro Gly Pro Val Gly Ala Ala
                325                 330                 335

Gly Ala Thr Gly Ala Arg Gly Leu Val Gly Glu Pro Gly Pro Ala Gly
            340                 345                 350

Ser Lys Gly Glu Ser Gly Asn Lys Gly Glu Pro Gly Ser Ala Gly Pro
        355                 360                 365

Gln Gly Pro Pro Gly Pro Ser Gly Glu Glu Gly Lys Arg Gly Pro Asn
    370                 375                 380

Gly Glu Ala Gly Ser Ala Gly Pro Pro Gly Pro Pro Gly Leu Arg Gly
385                 390                 395                 400

Ser Pro Gly Ser Arg Gly Leu Pro Gly Ala Asp Gly Arg Ala Gly Val
                405                 410                 415

Met Gly Pro Pro Gly Ser Arg Gly Ala Ser Gly Pro Ala Gly Val Arg
            420                 425                 430

Gly Pro Asn Gly Asp Ala Gly Arg Pro Gly Glu Pro Gly Leu Met Gly
        435                 440                 445

Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly Lys
    450                 455                 460

Glu Gly Pro Val Gly Leu Pro Gly Ile Asp Gly Arg Pro Gly Pro Ile
465                 470                 475                 480

Gly Pro Ala Gly Ala Arg Gly Glu Pro Gly Asn Ile Gly Phe Pro Gly
                485                 490                 495

Pro Lys Gly Pro Thr Gly Asp Pro Gly Lys Asn Gly Asp Lys Gly His
            500                 505                 510

Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn
        515                 520                 525

Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Gly Lys Gly
    530                 535                 540

Glu Gln Gly Pro Pro Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro
545                 550                 555                 560

Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His
                565                 570                 575

Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly
            580                 585                 590

Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly Pro Ile Gly Ser
        595                 600                 605

Arg Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro
    610                 615                 620
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Gly Val Val Gly Ala Val Gly Thr Ala Gly Pro Ser Gly Pro Ser Gly
625                 630                 635                 640

Leu Pro Gly Glu Arg Gly Ala Ala Gly Ile Pro Gly Gly Lys Gly Glu
                645                 650                 655

Lys Gly Glu Pro Gly Leu Arg Gly Glu Ile Gly Asn Pro Gly Arg Asp
            660                 665                 670

Gly Ala Arg Gly Ala Pro Gly Ala Val Gly Ala Pro Gly Pro Ala Gly
        675                 680                 685

Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro
    690                 695                 700

Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Val Gly Pro Ala
705                 710                 715                 720

Gly Pro Asn Gly Phe Ala Gly Pro Ala Gly Ala Ala Gly Gln Pro Gly
                725                 730                 735

Ala Lys Gly Glu Arg Gly Ala Lys Gly Pro Lys Gly Glu Asn Gly Val
            740                 745                 750

Val Gly Pro Thr Gly Pro Val Gly Ala Ala Gly Pro Ala Gly Pro Asn
        755                 760                 765

Gly Pro Pro Gly Pro Ala Gly Ser Arg Gly Asp Gly Gly Pro Pro Gly
    770                 775                 780

Met Thr Gly Phe Pro Gly Ala Ala Gly Arg Thr Gly Pro Pro Gly Pro
785                 790                 795                 800

Ser Gly Ile Ser Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Lys Glu
                805                 810                 815

Gly Leu Arg Gly Pro Arg Gly Asp Gln Gly Pro Val Gly Arg Thr Gly
            820                 825                 830

Glu Val Gly Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro
        835                 840                 845

Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln
    850                 855                 860

Gly Leu Leu Gly Ala Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg Gly
865                 870                 875                 880

Glu Arg Gly Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro
                885                 890                 895

Leu Gly Ile Ala Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Ala Val
            900                 905                 910

Gly Ser Pro Gly Val Asn Gly Ala Pro Gly Glu Ala Gly Arg Asp Gly
        915                 920                 925

Asn Pro Gly Asn Asp Gly Pro Pro Gly Arg Asp Gly Gln Pro Gly His
    930                 935                 940

Lys Gly Glu Arg Gly Tyr Pro Gly Asn Ile Gly Pro Val Gly Ala Ala
945                 950                 955                 960

Gly Ala Pro Gly Pro His Gly Pro Val Gly Pro Ala Gly Lys His Gly
                965                 970                 975

Asn Arg Gly Glu Thr Gly Pro Ser Gly Pro Val Gly Pro Ala Gly Ala
            980                 985                 990

Val Gly Pro Arg Gly Pro Ser Gly  Pro Gln Gly Ile Arg  Gly Asp Lys
        995                 1000                 1005

Gly Glu  Pro Gly Glu Lys Gly  Pro Arg Gly Leu Pro  Gly Leu Lys
    1010                 1015                 1020

Gly His  Asn Gly Leu Gln Gly  Leu Pro Gly Ile Ala  Gly His His
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    1025                1030                1035

Gly Asp  Gln Gly Ala Pro Gly  Ser Val Gly Pro Ala  Gly Pro Arg
    1040                1045                1050

Gly Pro  Ala Gly Pro Ser Gly  Pro Ala Gly Lys Asp  Gly Arg Thr
    1055                1060                1065

Gly His  Pro Gly Thr Val Gly  Pro Ala Gly Ile Arg  Gly Pro Gln
    1070                1075                1080

Gly His  Gln Gly Pro Ala Gly  Pro Pro Gly Pro Pro  Gly Pro Pro
    1085                1090                1095

Gly Pro  Pro Gly Val Ser Gly  Gly Gly Tyr Asp Phe  Gly Tyr Asp
    1100                1105                1110

Gly Asp  Phe Tyr Arg Ala Asp  Gln Pro Arg Ser Ala  Pro Ser Leu
    1115                1120                1125

Arg Pro  Lys Asp Tyr Glu Val  Asp Ala Thr Leu Lys  Ser Leu Asn
    1130                1135                1140

Asn Gln  Ile Glu Thr Leu Leu  Thr Pro Glu Gly Ser  Arg Lys Asn
    1145                1150                1155

Pro Ala  Arg Thr Cys Arg Asp  Leu Arg Leu Ser His  Pro Glu Trp
    1160                1165                1170

Ser Ser  Gly Tyr Tyr Trp Ile  Asp Pro Asn Gln Gly  Cys Thr Met
    1175                1180                1185

Asp Ala  Ile Lys Val Tyr Cys  Asp Phe Ser Thr Gly  Glu Thr Cys
    1190                1195                1200

Ile Arg  Ala Gln Pro Glu Asn  Ile Pro Ala Lys Asn  Trp Tyr Arg
    1205                1210                1215

Ser Ser  Lys Asp Lys Lys His  Val Trp Leu Gly Glu  Thr Ile Asn
    1220                1225                1230

Ala Gly  Ser Gln Phe Glu Tyr  Asn Val Glu Gly Val  Thr Ser Lys
    1235                1240                1245

Glu Met  Ala Thr Gln Leu Ala  Phe Met Arg Leu Leu  Ala Asn Tyr
    1250                1255                1260

Ala Ser  Gln Asn Ile Thr Tyr  His Cys Lys Asn Ser  Ile Ala Tyr
    1265                1270                1275

Met Asp  Glu Glu Thr Gly Asn  Leu Lys Lys Ala Val  Ile Leu Gln
    1280                1285                1290

Gly Ser  Asn Asp Val Glu Leu  Val Ala Glu Gly Asn  Ser Arg Phe
    1295                1300                1305

Thr Tyr  Thr Val Leu Val Asp  Gly Cys Ser Lys Lys  Thr Asn Glu
    1310                1315                1320

Trp Gly  Lys Thr Ile Ile Glu  Tyr Lys Thr Asn Lys  Pro Ser Arg
    1325                1330                1335

Leu Pro  Phe Leu Asp Ile Ala  Pro Leu Asp Ile Gly  Gly Ala Asp
    1340                1345                1350

Gln Glu  Phe Phe Val Asp Ile  Gly Pro Val Cys Phe  Lys
    1355                1360                1365


<210> SEQ ID NO 13
<211> LENGTH: 2386
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13
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Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys
1               5                   10                  15

Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln
            20                  25                  30

Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser
        35                  40                  45

Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln
    50                  55                  60

Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly
65                  70                  75                  80

Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr
                85                  90                  95

Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr
            100                 105                 110

Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala
        115                 120                 125

Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly
    130                 135                 140

Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr
145                 150                 155                 160

Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu
                165                 170                 175

Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly
            180                 185                 190

Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp
        195                 200                 205

Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr
    210                 215                 220

Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr
225                 230                 235                 240

Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu
                245                 250                 255

Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg
            260                 265                 270

His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp
        275                 280                 285

Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro
    290                 295                 300

Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met
305                 310                 315                 320

Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu
                325                 330                 335

Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly
            340                 345                 350

Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly
        355                 360                 365

Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln Asp Gly His Leu
    370                 375                 380

Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser Phe
385                 390                 395                 400

Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser Asn
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                405                 410                 415

Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr Thr
            420                 425                 430

Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly Thr
        435                 440                 445

Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met Ala
    450                 455                 460

Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg Ile
465                 470                 475                 480

Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg Cys
                485                 490                 495

Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr Ser
            500                 505                 510

Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val Asn
        515                 520                 525

Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys Thr
    530                 535                 540

Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp Gln
545                 550                 555                 560

Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser Trp
                565                 570                 575

Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly Arg
            580                 585                 590

Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser Ser
        595                 600                 605

Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro Asn
    610                 615                 620

Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser Lys
625                 630                 635                 640

Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg Trp Lys Glu
                645                 650                 655

Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu Lys
            660                 665                 670

Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr Gly
        675                 680                 685

His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser Thr
    690                 695                 700

Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr Pro Phe Ser Pro
705                 710                 715                 720

Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr Ala Ser Ser Phe
                725                 730                 735

Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg Val
            740                 745                 750

Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp Leu
        755                 760                 765

Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly Arg
    770                 775                 780

Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp Gly Glu Gln Ser
785                 790                 795                 800

Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp Ala Pro Pro Asp
                805                 810                 815
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Thr Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val Val Arg Trp Ser
            820                 825                 830

Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val Tyr Ser Pro Ser
        835                 840                 845

Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu Thr Ala Asn Ser
    850                 855                 860

Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr Asn Ile Thr Ile
865                 870                 875                 880

Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val Val Ile Gln Gln
                885                 890                 895

Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro Ser Pro Arg Asp
            900                 905                 910

Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr Ile Met Trp Thr
        915                 920                 925

Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp Val Ile Pro Val
    930                 935                 940

Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile Ser Arg Asn Thr
945                 950                 955                 960

Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr Tyr Tyr Phe Lys
                965                 970                 975

Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro Leu Thr Ala Gln
            980                 985                 990

Gln Thr Thr Lys Leu Asp Ala Pro  Thr Asn Leu Gln Phe  Val Asn Glu
        995                 1000                 1005

Thr Asp  Ser Thr Val Leu Val  Arg Trp Thr Pro Pro  Arg Ala Gln
    1010                 1015                 1020

Ile Thr  Gly Tyr Arg Leu Thr  Val Gly Leu Thr Arg  Arg Gly Gln
    1025                 1030                 1035

Pro Arg  Gln Tyr Asn Val Gly  Pro Ser Val Ser Lys  Tyr Pro Leu
    1040                 1045                 1050

Arg Asn  Leu Gln Pro Ala Ser  Glu Tyr Thr Val Ser  Leu Val Ala
    1055                 1060                 1065

Ile Lys  Gly Asn Gln Glu Ser  Pro Lys Ala Thr Gly  Val Phe Thr
    1070                 1075                 1080

Thr Leu  Gln Pro Gly Ser Ser  Ile Pro Pro Tyr Asn  Thr Glu Val
    1085                 1090                 1095

Thr Glu  Thr Thr Ile Val Ile  Thr Trp Thr Pro Ala  Pro Arg Ile
    1100                 1105                 1110

Gly Phe  Lys Leu Gly Val Arg  Pro Ser Gln Gly Gly  Glu Ala Pro
    1115                 1120                 1125

Arg Glu  Val Thr Ser Asp Ser  Gly Ser Ile Val Val  Ser Gly Leu
    1130                 1135                 1140

Thr Pro  Gly Val Glu Tyr Val  Tyr Thr Ile Gln Val  Leu Arg Asp
    1145                 1150                 1155

Gly Gln  Glu Arg Asp Ala Pro  Ile Val Asn Lys Val  Val Thr Pro
    1160                 1165                 1170

Leu Ser  Pro Pro Thr Asn Leu  His Leu Glu Ala Asn  Pro Asp Thr
    1175                 1180                 1185

Gly Val  Leu Thr Val Ser Trp  Glu Arg Ser Thr Thr  Pro Asp Ile
    1190                 1195                 1200
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Thr Gly  Tyr Arg Ile Thr Thr  Thr Pro Thr Asn Gly  Gln Gln Gly
    1205                 1210                 1215

Asn Ser  Leu Glu Glu Val Val  His Ala Asp Gln Ser  Ser Cys Thr
    1220                 1225                 1230

Phe Asp  Asn Leu Ser Pro Gly  Leu Glu Tyr Asn Val  Ser Val Tyr
    1235                 1240                 1245

Thr Val  Lys Asp Asp Lys Glu  Ser Val Pro Ile Ser  Asp Thr Ile
    1250                 1255                 1260

Ile Pro  Ala Val Pro Pro Pro  Thr Asp Leu Arg Phe  Thr Asn Ile
    1265                 1270                 1275

Gly Pro  Asp Thr Met Arg Val  Thr Trp Ala Pro Pro  Pro Ser Ile
    1280                 1285                 1290

Asp Leu  Thr Asn Phe Leu Val  Arg Tyr Ser Pro Val  Lys Asn Glu
    1295                 1300                 1305

Glu Asp  Val Ala Glu Leu Ser  Ile Ser Pro Ser Asp  Asn Ala Val
    1310                 1315                 1320

Val Leu  Thr Asn Leu Leu Pro  Gly Thr Glu Tyr Val  Val Ser Val
    1325                 1330                 1335

Ser Ser  Val Tyr Glu Gln His  Glu Ser Thr Pro Leu  Arg Gly Arg
    1340                 1345                 1350

Gln Lys  Thr Gly Leu Asp Ser  Pro Thr Gly Ile Asp  Phe Ser Asp
    1355                 1360                 1365

Ile Thr  Ala Asn Ser Phe Thr  Val His Trp Ile Ala  Pro Arg Ala
    1370                 1375                 1380

Thr Ile  Thr Gly Tyr Arg Ile  Arg His His Pro Glu  His Phe Ser
    1385                 1390                 1395

Gly Arg  Pro Arg Glu Asp Arg  Val Pro His Ser Arg  Asn Ser Ile
    1400                 1405                 1410

Thr Leu  Thr Asn Leu Thr Pro  Gly Thr Glu Tyr Val  Val Ser Ile
    1415                 1420                 1425

Val Ala  Leu Asn Gly Arg Glu  Glu Ser Pro Leu Leu  Ile Gly Gln
    1430                 1435                 1440

Gln Ser  Thr Val Ser Asp Val  Pro Arg Asp Leu Glu  Val Val Ala
    1445                 1450                 1455

Ala Thr  Pro Thr Ser Leu Leu  Ile Ser Trp Asp Ala  Pro Ala Val
    1460                 1465                 1470

Thr Val  Arg Tyr Tyr Arg Ile  Thr Tyr Gly Glu Thr  Gly Gly Asn
    1475                 1480                 1485

Ser Pro  Val Gln Glu Phe Thr  Val Pro Gly Ser Lys  Ser Thr Ala
    1490                 1495                 1500

Thr Ile  Ser Gly Leu Lys Pro  Gly Val Asp Tyr Thr  Ile Thr Val
    1505                 1510                 1515

Tyr Ala  Val Thr Gly Arg Gly  Asp Ser Pro Ala Ser  Ser Lys Pro
    1520                 1525                 1530

Ile Ser  Ile Asn Tyr Arg Thr  Glu Ile Asp Lys Pro  Ser Gln Met
    1535                 1540                 1545

Gln Val  Thr Asp Val Gln Asp  Asn Ser Ile Ser Val  Lys Trp Leu
    1550                 1555                 1560

Pro Ser  Ser Ser Pro Val Thr  Gly Tyr Arg Val Thr  Thr Thr Pro
    1565                 1570                 1575

Lys Asn  Gly Pro Gly Pro Thr  Lys Thr Lys Thr Ala  Gly Pro Asp
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    1580                1585                1590

Gln Thr  Glu Met Thr Ile Glu  Gly Leu Gln Pro Thr  Val Glu Tyr
    1595                1600                1605

Val Val  Ser Val Tyr Ala Gln  Asn Pro Ser Gly Glu  Ser Gln Pro
    1610                1615                1620

Leu Val  Gln Thr Ala Val Thr  Asn Ile Asp Arg Pro  Lys Gly Leu
    1625                1630                1635

Ala Phe  Thr Asp Val Asp Val  Asp Ser Ile Lys Ile  Ala Trp Glu
    1640                1645                1650

Ser Pro  Gln Gly Gln Val Ser  Arg Tyr Arg Val Thr  Tyr Ser Ser
    1655                1660                1665

Pro Glu  Asp Gly Ile His Glu  Leu Phe Pro Ala Pro  Asp Gly Glu
    1670                1675                1680

Glu Asp  Thr Ala Glu Leu Gln  Gly Leu Arg Pro Gly  Ser Glu Tyr
    1685                1690                1695

Thr Val  Ser Val Val Ala Leu  His Asp Asp Met Glu  Ser Gln Pro
    1700                1705                1710

Leu Ile  Gly Thr Gln Ser Thr  Ala Ile Pro Ala Pro  Thr Asp Leu
    1715                1720                1725

Lys Phe  Thr Gln Val Thr Pro  Thr Ser Leu Ser Ala  Gln Trp Thr
    1730                1735                1740

Pro Pro  Asn Val Gln Leu Thr  Gly Tyr Arg Val Arg  Val Thr Pro
    1745                1750                1755

Lys Glu  Lys Thr Gly Pro Met  Lys Glu Ile Asn Leu  Ala Pro Asp
    1760                1765                1770

Ser Ser  Ser Val Val Val Ser  Gly Leu Met Val Ala  Thr Lys Tyr
    1775                1780                1785

Glu Val  Ser Val Tyr Ala Leu  Lys Asp Thr Leu Thr  Ser Arg Pro
    1790                1795                1800

Ala Gln  Gly Val Val Thr Thr  Leu Glu Asn Val Ser  Pro Pro Arg
    1805                1810                1815

Arg Ala  Arg Val Thr Asp Ala  Thr Glu Thr Thr Ile  Thr Ile Ser
    1820                1825                1830

Trp Arg  Thr Lys Thr Glu Thr  Ile Thr Gly Phe Gln  Val Asp Ala
    1835                1840                1845

Val Pro  Ala Asn Gly Gln Thr  Pro Ile Gln Arg Thr  Ile Lys Pro
    1850                1855                1860

Asp Val  Arg Ser Tyr Thr Ile  Thr Gly Leu Gln Pro  Gly Thr Asp
    1865                1870                1875

Tyr Lys  Ile Tyr Leu Tyr Thr  Leu Asn Asp Asn Ala  Arg Ser Ser
    1880                1885                1890

Pro Val  Val Ile Asp Ala Ser  Thr Ala Ile Asp Ala  Pro Ser Asn
    1895                1900                1905

Leu Arg  Phe Leu Ala Thr Thr  Pro Asn Ser Leu Leu  Val Ser Trp
    1910                1915                1920

Gln Pro  Pro Arg Ala Arg Ile  Thr Gly Tyr Ile Ile  Lys Tyr Glu
    1925                1930                1935

Lys Pro  Gly Ser Pro Pro Arg  Glu Val Val Pro Arg  Pro Arg Pro
    1940                1945                1950

Gly Val  Thr Glu Ala Thr Ile  Thr Gly Leu Glu Pro  Gly Thr Glu
    1955                1960                1965
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Tyr Thr  Ile Tyr Val Ile Ala  Leu Lys Asn Asn Gln  Lys Ser Glu
    1970                 1975                 1980

Pro Leu  Ile Gly Arg Lys Lys  Thr Asp Glu Leu Pro  Gln Leu Val
    1985                 1990                 1995

Thr Leu  Pro His Pro Asn Leu  His Gly Pro Glu Ile  Leu Asp Val
    2000                 2005                 2010

Pro Ser  Thr Val Gln Lys Thr  Pro Phe Val Thr His  Pro Gly Tyr
    2015                 2020                 2025

Asp Thr  Gly Asn Gly Ile Gln  Leu Pro Gly Thr Ser  Gly Gln Gln
    2030                 2035                 2040

Pro Ser  Val Gly Gln Gln Met  Ile Phe Glu Glu His  Gly Phe Arg
    2045                 2050                 2055

Arg Thr  Thr Pro Pro Thr Thr  Ala Thr Pro Ile Arg  His Arg Pro
    2060                 2065                 2070

Arg Pro  Tyr Pro Pro Asn Val  Gly Glu Glu Ile Gln  Ile Gly His
    2075                 2080                 2085

Ile Pro  Arg Glu Asp Val Asp  Tyr His Leu Tyr Pro  His Gly Pro
    2090                 2095                 2100

Gly Leu  Asn Pro Asn Ala Ser  Thr Gly Gln Glu Ala  Leu Ser Gln
    2105                 2110                 2115

Thr Thr  Ile Ser Trp Ala Pro  Phe Gln Asp Thr Ser  Glu Tyr Ile
    2120                 2125                 2130

Ile Ser  Cys His Pro Val Gly  Thr Asp Glu Glu Pro  Leu Gln Phe
    2135                 2140                 2145

Arg Val  Pro Gly Thr Ser Thr  Ser Ala Thr Leu Thr  Gly Leu Thr
    2150                 2155                 2160

Arg Gly  Ala Thr Tyr Asn Val  Ile Val Glu Ala Leu  Lys Asp Gln
    2165                 2170                 2175

Gln Arg  His Lys Val Arg Glu  Glu Val Val Thr Val  Gly Asn Ser
    2180                 2185                 2190

Val Asn  Glu Gly Leu Asn Gln  Pro Thr Asp Asp Ser  Cys Phe Asp
    2195                 2200                 2205

Pro Tyr  Thr Val Ser His Tyr  Ala Val Gly Asp Glu  Trp Glu Arg
    2210                 2215                 2220

Met Ser  Glu Ser Gly Phe Lys  Leu Leu Cys Gln Cys  Leu Gly Phe
    2225                 2230                 2235

Gly Ser  Gly His Phe Arg Cys  Asp Ser Ser Arg Trp  Cys His Asp
    2240                 2245                 2250

Asn Gly  Val Asn Tyr Lys Ile  Gly Glu Lys Trp Asp  Arg Gln Gly
    2255                 2260                 2265

Glu Asn  Gly Gln Met Met Ser  Cys Thr Cys Leu Gly  Asn Gly Lys
    2270                 2275                 2280

Gly Glu  Phe Lys Cys Asp Pro  His Glu Ala Thr Cys  Tyr Asp Asp
    2285                 2290                 2295

Gly Lys  Thr Tyr His Val Gly  Glu Gln Trp Gln Lys  Glu Tyr Leu
    2300                 2305                 2310

Gly Ala  Ile Cys Ser Cys Thr  Cys Phe Gly Gly Gln  Arg Gly Trp
    2315                 2320                 2325

Arg Cys  Asp Asn Cys Arg Arg  Pro Gly Gly Glu Pro  Ser Pro Glu
    2330                 2335                 2340
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Gly Thr  Thr Gly Gln Ser Tyr  Asn Gln Tyr Ser Gln  Arg Tyr His
    2345                 2350                 2355

Gln Arg  Thr Asn Thr Asn Val  Asn Cys Pro Ile Glu  Cys Phe Met
    2360                 2365                 2370

Pro Leu  Asp Val Gln Ala Asp  Arg Glu Asp Ser Arg  Glu
    2375                 2380                 2385


<210> SEQ ID NO 14
<211> LENGTH: 2871
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

Met Arg Arg Gly Arg Leu Leu Glu Ile Ala Leu Gly Phe Thr Val Leu
1               5                   10                  15

Leu Ala Ser Tyr Thr Ser His Gly Ala Asp Ala Asn Leu Glu Ala Gly
            20                  25                  30

Asn Val Lys Glu Thr Arg Ala Ser Arg Ala Lys Arg Arg Gly Gly Gly
        35                  40                  45

Gly His Asp Ala Leu Lys Gly Pro Asn Val Cys Gly Ser Arg Tyr Asn
    50                  55                  60

Ala Tyr Cys Cys Pro Gly Trp Lys Thr Leu Pro Gly Gly Asn Gln Cys
65                  70                  75                  80

Ile Val Pro Ile Cys Arg His Ser Cys Gly Asp Gly Phe Cys Ser Arg
                85                  90                  95

Pro Asn Met Cys Thr Cys Pro Ser Gly Gln Ile Ala Pro Ser Cys Gly
            100                 105                 110

Ser Arg Ser Ile Gln His Cys Asn Ile Arg Cys Met Asn Gly Gly Ser
        115                 120                 125

Cys Ser Asp Asp His Cys Leu Cys Gln Lys Gly Tyr Ile Gly Thr His
    130                 135                 140

Cys Gly Gln Pro Val Cys Glu Ser Gly Cys Leu Asn Gly Gly Arg Cys
145                 150                 155                 160

Val Ala Pro Asn Arg Cys Ala Cys Thr Tyr Gly Phe Thr Gly Pro Gln
                165                 170                 175

Cys Glu Arg Asp Tyr Arg Thr Gly Pro Cys Phe Thr Val Ile Ser Asn
            180                 185                 190

Gln Met Cys Gln Gly Gln Leu Ser Gly Ile Val Cys Thr Lys Thr Leu
        195                 200                 205

Cys Cys Ala Thr Val Gly Arg Ala Trp Gly His Pro Cys Glu Met Cys
    210                 215                 220

Pro Ala Gln Pro His Pro Cys Arg Arg Gly Phe Ile Pro Asn Ile Arg
225                 230                 235                 240

Thr Gly Ala Cys Gln Asp Val Asp Glu Cys Gln Ala Ile Pro Gly Leu
                245                 250                 255

Cys Gln Gly Gly Asn Cys Ile Asn Thr Val Gly Ser Phe Glu Cys Lys
            260                 265                 270

Cys Pro Ala Gly His Lys Leu Asn Glu Val Ser Gln Lys Cys Glu Asp
        275                 280                 285

Ile Asp Glu Cys Ser Thr Ile Pro Gly Ile Cys Glu Gly Gly Glu Cys
    290                 295                 300

Thr Asn Thr Val Ser Ser Tyr Phe Cys Lys Cys Pro Pro Gly Phe Tyr
305                 310                 315                 320
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Thr Ser Pro Asp Gly Thr Arg Cys Ile Asp Val Arg Pro Gly Tyr Cys
                325                 330                 335

Tyr Thr Ala Leu Thr Asn Gly Arg Cys Ser Asn Gln Leu Pro Gln Ser
            340                 345                 350

Ile Thr Lys Met Gln Cys Cys Cys Asp Ala Gly Arg Cys Trp Ser Pro
        355                 360                 365

Gly Val Thr Val Ala Pro Glu Met Cys Pro Ile Arg Ala Thr Glu Asp
    370                 375                 380

Phe Asn Lys Leu Cys Ser Val Pro Met Val Ile Pro Gly Arg Pro Glu
385                 390                 395                 400

Tyr Pro Pro Pro Pro Leu Gly Pro Ile Pro Pro Val Leu Pro Val Pro
                405                 410                 415

Pro Gly Phe Pro Pro Gly Pro Gln Ile Pro Val Pro Arg Pro Pro Val
            420                 425                 430

Glu Tyr Leu Tyr Pro Ser Arg Glu Pro Pro Arg Val Leu Pro Val Asn
        435                 440                 445

Val Thr Asp Tyr Cys Gln Leu Val Arg Tyr Leu Cys Gln Asn Gly Arg
    450                 455                 460

Cys Ile Pro Thr Pro Gly Ser Tyr Arg Cys Glu Cys Asn Lys Gly Phe
465                 470                 475                 480

Gln Leu Asp Leu Arg Gly Glu Cys Ile Asp Val Asp Glu Cys Glu Lys
                485                 490                 495

Asn Pro Cys Ala Gly Gly Glu Cys Ile Asn Asn Gln Gly Ser Tyr Thr
            500                 505                 510

Cys Gln Cys Arg Ala Gly Tyr Gln Ser Thr Leu Thr Arg Thr Glu Cys
        515                 520                 525

Arg Asp Ile Asp Glu Cys Leu Gln Asn Gly Arg Ile Cys Asn Asn Gly
    530                 535                 540

Arg Cys Ile Asn Thr Asp Gly Ser Phe His Cys Val Cys Asn Ala Gly
545                 550                 555                 560

Phe His Val Thr Arg Asp Gly Lys Asn Cys Glu Asp Met Asp Glu Cys
                565                 570                 575

Ser Ile Arg Asn Met Cys Leu Asn Gly Met Cys Ile Asn Glu Asp Gly
            580                 585                 590

Ser Phe Lys Cys Ile Cys Lys Pro Gly Phe Gln Leu Ala Ser Asp Gly
        595                 600                 605

Arg Tyr Cys Lys Asp Ile Asn Glu Cys Glu Thr Pro Gly Ile Cys Met
    610                 615                 620

Asn Gly Arg Cys Val Asn Thr Asp Gly Ser Tyr Arg Cys Glu Cys Phe
625                 630                 635                 640

Pro Gly Leu Ala Val Gly Leu Asp Gly Arg Val Cys Val Asp Thr His
                645                 650                 655

Met Arg Ser Thr Cys Tyr Gly Gly Tyr Lys Arg Gly Gln Cys Ile Lys
            660                 665                 670

Pro Leu Phe Gly Ala Val Thr Lys Ser Glu Cys Cys Cys Ala Ser Thr
        675                 680                 685

Glu Tyr Ala Phe Gly Glu Pro Cys Gln Pro Cys Pro Ala Gln Asn Ser
    690                 695                 700

Ala Glu Tyr Gln Ala Leu Cys Ser Ser Gly Pro Gly Met Thr Ser Ala
705                 710                 715                 720
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Gly Ser Asp Ile Asn Glu Cys Ala Leu Asp Pro Asp Ile Cys Pro Asn
                725                 730                 735

Gly Ile Cys Glu Asn Leu Arg Gly Thr Tyr Lys Cys Ile Cys Asn Ser
            740                 745                 750

Gly Tyr Glu Val Asp Ser Thr Gly Lys Asn Cys Val Asp Ile Asn Glu
        755                 760                 765

Cys Val Leu Asn Ser Leu Leu Cys Asp Asn Gly Gln Cys Arg Asn Thr
    770                 775                 780

Pro Gly Ser Phe Val Cys Thr Cys Pro Lys Gly Phe Ile Tyr Lys Pro
785                 790                 795                 800

Asp Leu Lys Thr Cys Glu Asp Ile Asp Glu Cys Glu Ser Ser Pro Cys
                805                 810                 815

Ile Asn Gly Val Cys Lys Asn Ser Pro Gly Ser Phe Ile Cys Glu Cys
            820                 825                 830

Ser Ser Glu Ser Thr Leu Asp Pro Thr Lys Thr Ile Cys Ile Glu Thr
        835                 840                 845

Ile Lys Gly Thr Cys Trp Gln Thr Val Ile Asp Gly Arg Cys Glu Ile
    850                 855                 860

Asn Ile Asn Gly Ala Thr Leu Lys Ser Gln Cys Cys Ser Ser Leu Gly
865                 870                 875                 880

Ala Ala Trp Gly Ser Pro Cys Thr Leu Cys Gln Val Asp Pro Ile Cys
                885                 890                 895

Gly Lys Gly Tyr Ser Arg Ile Lys Gly Thr Gln Cys Glu Asp Ile Asp
            900                 905                 910

Glu Cys Glu Val Phe Pro Gly Val Cys Lys Asn Gly Leu Cys Val Asn
        915                 920                 925

Thr Arg Gly Ser Phe Lys Cys Gln Cys Pro Ser Gly Met Thr Leu Asp
    930                 935                 940

Ala Thr Gly Arg Ile Cys Leu Asp Ile Arg Leu Glu Thr Cys Phe Leu
945                 950                 955                 960

Arg Tyr Glu Asp Glu Glu Cys Thr Leu Pro Ile Ala Gly Arg His Arg
                965                 970                 975

Met Asp Ala Cys Cys Cys Ser Val Gly Ala Ala Trp Gly Thr Glu Glu
            980                 985                 990

Cys Glu Glu Cys Pro Met Arg Asn  Thr Pro Glu Tyr Glu  Glu Leu Cys
        995                 1000                 1005

Pro Arg  Gly Pro Gly Phe Ala  Thr Lys Glu Ile Thr  Asn Gly Lys
    1010                 1015                 1020

Pro Phe  Phe Lys Asp Ile Asn  Glu Cys Lys Met Ile  Pro Ser Leu
    1025                 1030                 1035

Cys Thr  His Gly Lys Cys Arg  Asn Thr Ile Gly Ser  Phe Lys Cys
    1040                 1045                 1050

Arg Cys  Asp Ser Gly Phe Ala  Leu Asp Ser Glu Glu  Arg Asn Cys
    1055                 1060                 1065

Thr Asp  Ile Asp Glu Cys Arg  Ile Ser Pro Asp Leu  Cys Gly Arg
    1070                 1075                 1080

Gly Gln  Cys Val Asn Thr Pro  Gly Asp Phe Glu Cys  Lys Cys Asp
    1085                 1090                 1095

Glu Gly  Tyr Glu Ser Gly Phe  Met Met Met Lys Asn  Cys Met Asp
    1100                 1105                 1110

Ile Asp  Glu Cys Gln Arg Asp  Pro Leu Leu Cys Arg  Gly Gly Val
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    1115                1120                1125

Cys His  Asn Thr Glu Gly Ser  Tyr Arg Cys Glu Cys  Pro Pro Gly
    1130                1135                1140

His Gln  Leu Ser Pro Asn Ile  Ser Ala Cys Ile Asp  Ile Asn Glu
    1145                1150                1155

Cys Glu  Leu Ser Ala His Leu  Cys Pro Asn Gly Arg  Cys Val Asn
    1160                1165                1170

Leu Ile  Gly Lys Tyr Gln Cys  Ala Cys Asn Pro Gly  Tyr His Ser
    1175                1180                1185

Thr Pro  Asp Arg Leu Phe Cys  Val Asp Ile Asp Glu  Cys Ser Ile
    1190                1195                1200

Met Asn  Gly Gly Cys Glu Thr  Phe Cys Thr Asn Ser  Glu Gly Ser
    1205                1210                1215

Tyr Glu  Cys Ser Cys Gln Pro  Gly Phe Ala Leu Met  Pro Asp Gln
    1220                1225                1230

Arg Ser  Cys Thr Asp Ile Asp  Glu Cys Glu Asp Asn  Pro Asn Ile
    1235                1240                1245

Cys Asp  Gly Gly Gln Cys Thr  Asn Ile Pro Gly Glu  Tyr Arg Cys
    1250                1255                1260

Leu Cys  Tyr Asp Gly Phe Met  Ala Ser Glu Asp Met  Lys Thr Cys
    1265                1270                1275

Val Asp  Val Asn Glu Cys Asp  Leu Asn Pro Asn Ile  Cys Leu Ser
    1280                1285                1290

Gly Thr  Cys Glu Asn Thr Lys  Gly Ser Phe Ile Cys  His Cys Asp
    1295                1300                1305

Met Gly  Tyr Ser Gly Lys Lys  Gly Lys Thr Gly Cys  Thr Asp Ile
    1310                1315                1320

Asn Glu  Cys Glu Ile Gly Ala  His Asn Cys Gly Lys  His Ala Val
    1325                1330                1335

Cys Thr  Asn Thr Ala Gly Ser  Phe Lys Cys Ser Cys  Ser Pro Gly
    1340                1345                1350

Trp Ile  Gly Asp Gly Ile Lys  Cys Thr Asp Leu Asp  Glu Cys Ser
    1355                1360                1365

Asn Gly  Thr His Met Cys Ser  Gln His Ala Asp Cys  Lys Asn Thr
    1370                1375                1380

Met Gly  Ser Tyr Arg Cys Leu  Cys Lys Glu Gly Tyr  Thr Gly Asp
    1385                1390                1395

Gly Phe  Thr Cys Thr Asp Leu  Asp Glu Cys Ser Glu  Asn Leu Asn
    1400                1405                1410

Leu Cys  Gly Asn Gly Gln Cys  Leu Asn Ala Pro Gly  Gly Tyr Arg
    1415                1420                1425

Cys Glu  Cys Asp Met Gly Phe  Val Pro Ser Ala Asp  Gly Lys Ala
    1430                1435                1440

Cys Glu  Asp Ile Asp Glu Cys  Ser Leu Pro Asn Ile  Cys Val Phe
    1445                1450                1455

Gly Thr  Cys His Asn Leu Pro  Gly Leu Phe Arg Cys  Glu Cys Glu
    1460                1465                1470

Ile Gly  Tyr Glu Leu Asp Arg  Ser Gly Gly Asn Cys  Thr Asp Val
    1475                1480                1485

Asn Glu  Cys Leu Asp Pro Thr  Thr Cys Ile Ser Gly  Asn Cys Val
    1490                1495                1500
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Asn Thr  Pro Gly Ser Tyr Ile  Cys Asp Cys Pro Pro  Asp Phe Glu
    1505                 1510                 1515

Leu Asn  Pro Thr Arg Val Gly  Cys Val Asp Thr Arg  Ser Gly Asn
    1520                 1525                 1530

Cys Tyr  Leu Asp Ile Arg Pro  Arg Gly Asp Asn Gly  Asp Thr Ala
    1535                 1540                 1545

Cys Ser  Asn Glu Ile Gly Val  Gly Val Ser Lys Ala  Ser Cys Cys
    1550                 1555                 1560

Cys Ser  Leu Gly Lys Ala Trp  Gly Thr Pro Cys Glu  Met Cys Pro
    1565                 1570                 1575

Ala Val  Asn Thr Ser Glu Tyr  Lys Ile Leu Cys Pro  Gly Gly Glu
    1580                 1585                 1590

Gly Phe  Arg Pro Asn Pro Ile  Thr Val Ile Leu Glu  Asp Ile Asp
    1595                 1600                 1605

Glu Cys  Gln Glu Leu Pro Gly  Leu Cys Gln Gly Gly  Lys Cys Ile
    1610                 1615                 1620

Asn Thr  Phe Gly Ser Phe Gln  Cys Arg Cys Pro Thr  Gly Tyr Tyr
    1625                 1630                 1635

Leu Asn  Glu Asp Thr Arg Val  Cys Asp Asp Val Asn  Glu Cys Glu
    1640                 1645                 1650

Thr Pro  Gly Ile Cys Gly Pro  Gly Thr Cys Tyr Asn  Thr Val Gly
    1655                 1660                 1665

Asn Tyr  Thr Cys Ile Cys Pro  Pro Asp Tyr Met Gln  Val Asn Gly
    1670                 1675                 1680

Gly Asn  Asn Cys Met Asp Met  Arg Arg Ser Leu Cys  Tyr Arg Asn
    1685                 1690                 1695

Tyr Tyr  Ala Asp Asn Gln Thr  Cys Asp Gly Glu Leu  Leu Phe Asn
    1700                 1705                 1710

Met Thr  Lys Lys Met Cys Cys  Cys Ser Tyr Asn Ile  Gly Arg Ala
    1715                 1720                 1725

Trp Asn  Lys Pro Cys Glu Gln  Cys Pro Ile Pro Ser  Thr Asp Glu
    1730                 1735                 1740

Phe Ala  Thr Leu Cys Gly Ser  Gln Arg Pro Gly Phe  Val Ile Asp
    1745                 1750                 1755

Ile Tyr  Thr Gly Leu Pro Val  Asp Ile Asp Glu Cys  Arg Glu Ile
    1760                 1765                 1770

Pro Gly  Val Cys Glu Asn Gly  Val Cys Ile Asn Met  Val Gly Ser
    1775                 1780                 1785

Phe Arg  Cys Glu Cys Pro Val  Gly Phe Phe Tyr Asn  Asp Lys Leu
    1790                 1795                 1800

Leu Val  Cys Glu Asp Ile Asp  Glu Cys Gln Asn Gly  Pro Val Cys
    1805                 1810                 1815

Gln Arg  Asn Ala Glu Cys Ile  Asn Thr Ala Gly Ser  Tyr Arg Cys
    1820                 1825                 1830

Asp Cys  Lys Pro Gly Tyr Arg  Phe Thr Ser Thr Gly  Gln Cys Asn
    1835                 1840                 1845

Asp Arg  Asn Glu Cys Gln Glu  Ile Pro Asn Ile Cys  Ser His Gly
    1850                 1855                 1860

Gln Cys  Ile Asp Thr Val Gly  Ser Phe Tyr Cys Leu  Cys His Thr
    1865                 1870                 1875
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Gly Phe  Lys Thr Asn Asp Asp  Gln Thr Met Cys Leu  Asp Ile Asn
    1880                1885                1890

Glu Cys  Glu Arg Asp Ala Cys  Gly Asn Gly Thr Cys  Arg Asn Thr
    1895                1900                1905

Ile Gly  Ser Phe Asn Cys Arg  Cys Asn His Gly Phe  Ile Leu Ser
    1910                1915                1920

His Asn  Asn Asp Cys Ile Asp  Val Asp Glu Cys Ala  Ser Gly Asn
    1925                1930                1935

Gly Asn  Leu Cys Arg Asn Gly  Gln Cys Ile Asn Thr  Val Gly Ser
    1940                1945                1950

Phe Gln  Cys Gln Cys Asn Glu  Gly Tyr Glu Val Ala  Pro Asp Gly
    1955                1960                1965

Arg Thr  Cys Val Asp Ile Asn  Glu Cys Leu Leu Glu  Pro Arg Lys
    1970                1975                1980

Cys Ala  Pro Gly Thr Cys Gln  Asn Leu Asp Gly Ser  Tyr Arg Cys
    1985                1990                1995

Ile Cys  Pro Pro Gly Tyr Ser  Leu Gln Asn Glu Lys  Cys Glu Asp
    2000                2005                2010

Ile Asp  Glu Cys Val Glu Glu  Pro Glu Ile Cys Ala  Leu Gly Thr
    2015                2020                2025

Cys Ser  Asn Thr Glu Gly Ser  Phe Lys Cys Leu Cys  Pro Glu Gly
    2030                2035                2040

Phe Ser  Leu Ser Ser Ser Gly  Arg Arg Cys Gln Asp  Leu Arg Met
    2045                2050                2055

Ser Tyr  Cys Tyr Ala Lys Phe  Glu Gly Gly Lys Cys  Ser Ser Pro
    2060                2065                2070

Lys Ser  Arg Asn His Ser Lys  Gln Glu Cys Cys Cys  Ala Leu Lys
    2075                2080                2085

Gly Glu  Gly Trp Gly Asp Pro  Cys Glu Leu Cys Pro  Thr Glu Pro
    2090                2095                2100

Asp Glu  Ala Phe Arg Gln Ile  Cys Pro Tyr Gly Ser  Gly Ile Ile
    2105                2110                2115

Val Gly  Pro Asp Asp Ser Ala  Val Asp Met Asp Glu  Cys Lys Glu
    2120                2125                2130

Pro Asp  Val Cys Lys His Gly  Gln Cys Ile Asn Thr  Asp Gly Ser
    2135                2140                2145

Tyr Arg  Cys Glu Cys Pro Phe  Gly Tyr Ile Leu Ala  Gly Asn Glu
    2150                2155                2160

Cys Val  Asp Thr Asp Glu Cys  Ser Val Gly Asn Pro  Cys Gly Asn
    2165                2170                2175

Gly Thr  Cys Lys Asn Val Ile  Gly Gly Phe Glu Cys  Thr Cys Glu
    2180                2185                2190

Glu Gly  Phe Glu Pro Gly Pro  Met Met Thr Cys Glu  Asp Ile Asn
    2195                2200                2205

Glu Cys  Ala Gln Asn Pro Leu  Leu Cys Ala Phe Arg  Cys Val Asn
    2210                2215                2220

Thr Tyr  Gly Ser Tyr Glu Cys  Lys Cys Pro Val Gly  Tyr Val Leu
    2225                2230                2235

Arg Glu  Asp Arg Arg Met Cys  Lys Asp Glu Asp Glu  Cys Glu Glu
    2240                2245                2250

Gly Lys  His Asp Cys Thr Glu  Lys Gln Met Glu Cys  Lys Asn Leu
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    2255                2260                2265

Ile Gly  Thr Tyr Met Cys Ile  Cys Gly Pro Gly Tyr  Gln Arg Arg
    2270                2275                2280

Pro Asp  Gly Glu Gly Cys Val  Asp Glu Asn Glu Cys  Gln Thr Lys
    2285                2290                2295

Pro Gly  Ile Cys Glu Asn Gly  Arg Cys Leu Asn Thr  Arg Gly Ser
    2300                2305                2310

Tyr Thr  Cys Glu Cys Asn Asp  Gly Phe Thr Ala Ser  Pro Asn Gln
    2315                2320                2325

Asp Glu  Cys Leu Asp Asn Arg  Glu Gly Tyr Cys Phe  Thr Glu Val
    2330                2335                2340

Leu Gln  Asn Met Cys Gln Ile  Gly Ser Ser Asn Arg  Asn Pro Val
    2345                2350                2355

Thr Lys  Ser Glu Cys Cys Cys  Asp Gly Gly Arg Gly  Trp Gly Pro
    2360                2365                2370

His Cys  Glu Ile Cys Pro Phe  Gln Gly Thr Val Ala  Phe Lys Lys
    2375                2380                2385

Leu Cys  Pro His Gly Arg Gly  Phe Met Thr Asn Gly  Ala Asp Ile
    2390                2395                2400

Asp Glu  Cys Lys Val Ile His  Asp Val Cys Arg Asn  Gly Glu Cys
    2405                2410                2415

Val Asn  Asp Arg Gly Ser Tyr  His Cys Ile Cys Lys  Thr Gly Tyr
    2420                2425                2430

Thr Pro  Asp Ile Thr Gly Thr  Ser Cys Val Asp Leu  Asn Glu Cys
    2435                2440                2445

Asn Gln  Ala Pro Lys Pro Cys  Asn Phe Ile Cys Lys  Asn Thr Glu
    2450                2455                2460

Gly Ser  Tyr Gln Cys Ser Cys  Pro Lys Gly Tyr Ile  Leu Gln Glu
    2465                2470                2475

Asp Gly  Arg Ser Cys Lys Asp  Leu Asp Glu Cys Ala  Thr Lys Gln
    2480                2485                2490

His Asn  Cys Gln Phe Leu Cys  Val Asn Thr Ile Gly  Gly Phe Thr
    2495                2500                2505

Cys Lys  Cys Pro Pro Gly Phe  Thr Gln His His Thr  Ser Cys Ile
    2510                2515                2520

Asp Asn  Asn Glu Cys Thr Ser  Asp Ile Asn Leu Cys  Gly Ser Lys
    2525                2530                2535

Gly Ile  Cys Gln Asn Thr Pro  Gly Ser Phe Thr Cys  Glu Cys Gln
    2540                2545                2550

Arg Gly  Phe Ser Leu Asp Gln  Thr Gly Ser Ser Cys  Glu Asp Val
    2555                2560                2565

Asp Glu  Cys Glu Gly Asn His  Arg Cys Gln His Gly  Cys Gln Asn
    2570                2575                2580

Ile Ile  Gly Gly Tyr Arg Cys  Ser Cys Pro Gln Gly  Tyr Leu Gln
    2585                2590                2595

His Tyr  Gln Trp Asn Gln Cys  Val Asp Glu Asn Glu  Cys Leu Ser
    2600                2605                2610

Ala His  Ile Cys Gly Gly Ala  Ser Cys His Asn Thr  Leu Gly Ser
    2615                2620                2625

Tyr Lys  Cys Met Cys Pro Ala  Gly Phe Gln Tyr Glu  Gln Phe Ser
    2630                2635                2640
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Gly Gly Cys Gln Asp Ile Asn Glu Cys Gly Ser Ala Gln Ala Pro
2645 2650 2655

Cys Ser Tyr Gly Cys Ser Asn Thr Glu Gly Gly Tyr Leu Cys Gly
2660 2665 2670

Cys Pro Pro Gly Tyr Phe Arg Ile Gly Gln Gly His Cys Val Ser
2675 2680 2685

Gly Met Gly Met Gly Arg Gly Asn Pro Glu Pro Pro Val Ser Gly
2690 2695 2700

Glu Met Asp Asp Asn Ser Leu Ser Pro Glu Ala Cys Tyr Glu Cys
2705 2710 2715

Lys Ile Asn Gly Tyr Pro Lys Arg Gly Arg Lys Arg Arg Ser Thr
2720 2725 2730

Asn Glu Thr Asp Ala Ser Asn Ile Glu Asp Gln Ser Glu Thr Glu
2735 2740 2745

Ala Asn Val Ser Leu Ala Ser Trp Asp Val Glu Lys Thr Ala Ile
2750 2755 2760

Phe Ala Phe Asn Ile Ser His Val Ser Asn Lys Val Arg Ile Leu
2765 2770 2775

Glu Leu Leu Pro Ala Leu Thr Thr Leu Thr Asn His Asn Arg Tyr
2780 2785 2790

Leu Ile Glu Ser Gly Asn Glu Asp Gly Phe Phe Lys Ile Asn Gln
2795 2800 2805

Lys Glu Gly Ile Ser Tyr Leu His Phe Thr Lys Lys Lys Pro Val
2810 2815 2820

Ala Gly Thr Tyr Ser Leu Gln Ile Ser Ser Thr Pro Leu Tyr Lys
2825 2830 2835

Lys Lys Glu Leu Asn Gln Leu Glu Asp Lys Tyr Asp Lys Asp Tyr
2840 2845 2850

Leu Ser Gly Glu Leu Gly Asp Asn Leu Lys Met Lys Ile Gln Val
2855 2860 2865

Leu Leu His
2870

<210> SEQ ID NO 15
<211> LENGTH: 201
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

Met Asp Leu Ser Leu Leu Trp Val Leu Met Pro Leu Val Thr Met Ala
1 5 10 15

Trp Gly Gln Tyr Gly Asp Tyr Gly Tyr Pro Tyr Gln Gln Tyr His Asp
20 25 30

Tyr Ser Asp Asp Gly Trp Val Asn Leu Asn Arg Gln Gly Phe Ser Tyr
35 40 45

Gln Cys Pro Gln Gly Gln Val Ile Val Ala Val Arg Ser Ile Phe Ser
50 55 60

Lys Lys Glu Gly Ser Asp Arg Gln Trp Asn Tyr Ala Cys Met Pro Thr
65 70 75 80

Pro Gln Ser Leu Gly Glu Pro Thr Glu Cys Trp Trp Glu Glu Ile Asn
85 90 95

Arg Ala Gly Met Glu Trp Tyr Gln Thr Cys Ser Asn Asn Gly Leu Val

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            100                 105                 110

Ala Gly Phe Gln Ser Arg Tyr Phe Glu Ser Val Leu Asp Arg Glu Trp
        115                 120                 125

Gln Phe Tyr Cys Cys Arg Tyr Ser Lys Arg Cys Pro Tyr Ser Cys Trp
    130                 135                 140

Leu Thr Thr Glu Tyr Pro Gly His Tyr Gly Glu Glu Met Asp Met Ile
145                 150                 155                 160

Ser Tyr Asn Tyr Asp Tyr Tyr Ile Arg Gly Ala Thr Thr Thr Phe Ser
                165                 170                 175

Ala Val Glu Arg Asp Arg Gln Trp Lys Phe Ile Met Cys Arg Met Thr
            180                 185                 190

Glu Tyr Asp Cys Glu Phe Ala Asn Val
        195                 200


<210> SEQ ID NO 16
<211> LENGTH: 207
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
1               5                   10                  15

Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
            20                  25                  30

Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
        35                  40                  45

Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
    50                  55                  60

Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
65                  70                  75                  80

Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
                85                  90                  95

His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
            100                 105                 110

Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
        115                 120                 125

Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
    130                 135                 140

Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Ile Pro Cys
145                 150                 155                 160

Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
                165                 170                 175

Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
            180                 185                 190

Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
        195                 200                 205


<210> SEQ ID NO 17
<211> LENGTH: 135
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu
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1               5                   10                  15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val
            20                  25                  30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro
        35                  40                  45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys
    50                  55                  60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe
65                  70                  75                  80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn
                85                  90                  95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg
            100                 105                 110

Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys
        115                 120                 125

Ile Lys Cys Val Ala Phe Asp
    130                 135


<210> SEQ ID NO 18
<211> LENGTH: 338
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
1               5                   10                  15

Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Pro Ser Ile Tyr Gly Gln
            20                  25                  30

Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro
        35                  40                  45

Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val
    50                  55                  60

Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His
65                  70                  75                  80

Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile
                85                  90                  95

Leu Asp His Asn Val Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe
            100                 105                 110

Ser Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu
        115                 120                 125

Thr Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu
    130                 135                 140

Thr His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn
145                 150                 155                 160

Leu Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val
                165                 170                 175

Ser Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser
            180                 185                 190

Phe Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu
        195                 200                 205

Thr Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr
    210                 215                 220
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Phe Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu
225 230 235 240

Leu Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu
245 250 255

Val Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val
260 265 270

Asn Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys
275 280 285

Phe Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser
290 295 300

Lys Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Glu Thr Ser
305 310 315 320

Leu Pro Pro Asp Met Tyr Glu Cys Leu Arg Val Ala Asn Glu Val Thr
325 330 335

Leu Asn

<210> SEQ ID NO 19
<211> LENGTH: 382
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

Met Arg Ser Pro Leu Cys Trp Leu Leu Pro Leu Leu Ile Leu Ala Ser
1 5 10 15

Val Ala Gln Gly Gln Pro Thr Arg Arg Pro Arg Pro Gly Thr Gly Pro
20 25 30

Gly Arg Arg Pro Arg Pro Arg Pro Arg Pro Thr Pro Ser Phe Pro Gln
35 40 45

Pro Asp Glu Pro Ala Glu Pro Thr Asp Leu Pro Pro Pro Leu Pro Pro
50 55 60

Gly Pro Pro Ser Ile Phe Pro Asp Cys Pro Arg Glu Cys Tyr Cys Pro
65 70 75 80

Pro Asp Phe Pro Ser Ala Leu Tyr Cys Asp Ser Arg Asn Leu Arg Lys
85 90 95

Val Pro Val Ile Pro Pro Arg Ile His Tyr Leu Tyr Leu Gln Asn Asn
100 105 110

Phe Ile Thr Glu Leu Pro Val Glu Ser Phe Gln Asn Ala Thr Gly Leu
115 120 125

Arg Trp Ile Asn Leu Asp Asn Asn Arg Ile Arg Lys Ile Asp Gln Arg
130 135 140

Val Leu Glu Lys Leu Pro Gly Leu Val Phe Leu Tyr Met Glu Lys Asn
145 150 155 160

Gln Leu Glu Glu Val Pro Ser Ala Leu Pro Arg Asn Leu Glu Gln Leu
165 170 175

Arg Leu Ser Gln Asn His Ile Ser Arg Ile Pro Pro Gly Val Phe Ser
180 185 190

Lys Leu Glu Asn Leu Leu Leu Leu Asp Leu Gln His Asn Arg Leu Ser
195 200 205

Asp Gly Val Phe Lys Pro Asp Thr Phe His Gly Leu Lys Asn Leu Met
210 215 220

Gln Leu Asn Leu Ala His Asn Ile Leu Arg Lys Met Pro Pro Arg Val
225 230 235 240

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Pro Thr Ala Ile His Gln Leu Tyr Leu Asp Ser Asn Lys Ile Glu Thr
245 250 255

Ile Pro Asn Gly Tyr Phe Lys Ser Phe Pro Asn Leu Ala Phe Ile Arg
260 265 270

Leu Asn Tyr Asn Lys Leu Thr Asp Arg Gly Leu Pro Lys Asn Ser Phe
275 280 285

Asn Ile Ser Asn Leu Leu Val Leu His Leu Ser His Asn Arg Ile Ser
290 295 300

Ser Val Pro Ala Ile Asn Asn Arg Leu Glu His Leu Tyr Leu Asn Asn
305 310 315 320

Asn Ser Ile Glu Lys Ile Asn Gly Thr Gln Ile Cys Pro Asn Asp Leu
325 330 335

Val Ala Phe His Asp Phe Ser Ser Asp Leu Glu Asn Val Pro His Leu
340 345 350

Arg Tyr Leu Arg Leu Asp Gly Asn Tyr Leu Lys Pro Pro Ile Pro Leu
355 360 365

Asp Leu Met Met Cys Phe Arg Leu Leu Gln Ser Val Val Ile
370 375 380

<210> SEQ ID NO 20
<211> LENGTH: 2201
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

Met Gly Ala Met Thr Gln Leu Leu Ala Gly Val Phe Leu Ala Phe Leu
1 5 10 15

Ala Leu Ala Thr Glu Gly Gly Val Leu Lys Lys Val Ile Arg His Lys
20 25 30

Arg Gln Ser Gly Val Asn Ala Thr Leu Pro Glu Glu Asn Gln Pro Val
35 40 45

Val Phe Asn His Val Tyr Asn Ile Lys Leu Pro Val Gly Ser Gln Cys
50 55 60

Ser Val Asp Leu Glu Ser Ala Ser Gly Glu Lys Asp Leu Ala Pro Pro
65 70 75 80

Ser Glu Pro Ser Glu Ser Phe Gln Glu His Thr Val Asp Gly Glu Asn
85 90 95

Gln Ile Val Phe Thr His Arg Ile Asn Ile Pro Arg Arg Ala Cys Gly
100 105 110

Cys Ala Ala Ala Pro Asp Val Lys Glu Leu Leu Ser Arg Leu Glu Glu
115 120 125

Leu Glu Asn Leu Val Ser Ser Leu Arg Glu Gln Cys Thr Ala Gly Ala
130 135 140

Gly Cys Cys Leu Gln Pro Ala Thr Gly Arg Leu Asp Thr Arg Pro Phe
145 150 155 160

Cys Ser Gly Arg Gly Asn Phe Ser Thr Glu Gly Cys Gly Cys Val Cys
165 170 175

Glu Pro Gly Trp Lys Gly Pro Asn Cys Ser Glu Pro Glu Cys Pro Gly
180 185 190

Asn Cys His Leu Arg Gly Arg Cys Ile Asp Gly Gln Cys Ile Cys Asp
195 200 205

Asp Gly Phe Thr Gly Glu Asp Cys Ser Gln Leu Ala Cys Pro Ser Asp
210 215 220

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Cys Asn Asp Gln Gly Lys Cys Val Asn Gly Val Cys Ile Cys Phe Glu
225                 230                 235                 240

Gly Tyr Ala Gly Ala Asp Cys Ser Arg Glu Ile Cys Pro Val Pro Cys
                245                 250                 255

Ser Glu Glu His Gly Thr Cys Val Asp Gly Leu Cys Val Cys His Asp
            260                 265                 270

Gly Phe Ala Gly Asp Asp Cys Asn Lys Pro Leu Cys Leu Asn Asn Cys
        275                 280                 285

Tyr Asn Arg Gly Arg Cys Val Glu Asn Glu Cys Val Cys Asp Glu Gly
    290                 295                 300

Phe Thr Gly Glu Asp Cys Ser Glu Leu Ile Cys Pro Asn Asp Cys Phe
305                 310                 315                 320

Asp Arg Gly Arg Cys Ile Asn Gly Thr Cys Tyr Cys Glu Glu Gly Phe
                325                 330                 335

Thr Gly Glu Asp Cys Gly Lys Pro Thr Cys Pro His Ala Cys His Thr
            340                 345                 350

Gln Gly Arg Cys Glu Glu Gly Gln Cys Val Cys Asp Glu Gly Phe Ala
        355                 360                 365

Gly Val Asp Cys Ser Glu Lys Arg Cys Pro Ala Asp Cys His Asn Arg
    370                 375                 380

Gly Arg Cys Val Asp Gly Arg Cys Glu Cys Asp Asp Gly Phe Thr Gly
385                 390                 395                 400

Ala Asp Cys Gly Glu Leu Lys Cys Pro Asn Gly Cys Ser Gly His Gly
                405                 410                 415

Arg Cys Val Asn Gly Gln Cys Val Cys Asp Glu Gly Tyr Thr Gly Glu
            420                 425                 430

Asp Cys Ser Gln Leu Arg Cys Pro Asn Asp Cys His Ser Arg Gly Arg
        435                 440                 445

Cys Val Glu Gly Lys Cys Val Cys Glu Gln Gly Phe Lys Gly Tyr Asp
    450                 455                 460

Cys Ser Asp Met Ser Cys Pro Asn Asp Cys His Gln His Gly Arg Cys
465                 470                 475                 480

Val Asn Gly Met Cys Val Cys Asp Asp Gly Tyr Thr Gly Glu Asp Cys
                485                 490                 495

Arg Asp Arg Gln Cys Pro Arg Asp Cys Ser Asn Arg Gly Leu Cys Val
            500                 505                 510

Asp Gly Gln Cys Val Cys Glu Asp Gly Phe Thr Gly Pro Asp Cys Ala
        515                 520                 525

Glu Leu Ser Cys Pro Asn Asp Cys His Gly Gln Gly Arg Cys Val Asn
    530                 535                 540

Gly Gln Cys Val Cys His Glu Gly Phe Met Gly Lys Asp Cys Lys Glu
545                 550                 555                 560

Gln Arg Cys Pro Ser Asp Cys His Gly Gln Gly Arg Cys Val Asp Gly
                565                 570                 575

Gln Cys Ile Cys His Glu Gly Phe Thr Gly Leu Asp Cys Gly Gln His
            580                 585                 590

Ser Cys Pro Ser Asp Cys Asn Asn Leu Gly Gln Cys Val Ser Gly Arg
        595                 600                 605

Cys Ile Cys Asn Glu Gly Tyr Ser Gly Glu Asp Cys Ser Glu Val Ser
    610                 615                 620
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Pro Pro Lys Asp Leu Val Val Thr Glu Val Thr Glu Glu Thr Val Asn
625                 630                 635                 640

Leu Ala Trp Asp Asn Glu Met Arg Val Thr Glu Tyr Leu Val Val Tyr
                645                 650                 655

Thr Pro Thr His Glu Gly Gly Leu Glu Met Gln Phe Arg Val Pro Gly
            660                 665                 670

Asp Gln Thr Ser Thr Ile Ile Gln Glu Leu Glu Pro Gly Val Glu Tyr
        675                 680                 685

Phe Ile Arg Val Phe Ala Ile Leu Glu Asn Lys Lys Ser Ile Pro Val
    690                 695                 700

Ser Ala Arg Val Ala Thr Tyr Leu Pro Ala Pro Glu Gly Leu Lys Phe
705                 710                 715                 720

Lys Ser Ile Lys Glu Thr Ser Val Glu Val Glu Trp Asp Pro Leu Asp
                725                 730                 735

Ile Ala Phe Glu Thr Trp Glu Ile Ile Phe Arg Asn Met Asn Lys Glu
            740                 745                 750

Asp Glu Gly Glu Ile Thr Lys Ser Leu Arg Arg Pro Glu Thr Ser Tyr
        755                 760                 765

Arg Gln Thr Gly Leu Ala Pro Gly Gln Glu Tyr Glu Ile Ser Leu His
    770                 775                 780

Ile Val Lys Asn Asn Thr Arg Gly Pro Gly Leu Lys Arg Val Thr Thr
785                 790                 795                 800

Thr Arg Leu Asp Ala Pro Ser Gln Ile Glu Val Lys Asp Val Thr Asp
                805                 810                 815

Thr Thr Ala Leu Ile Thr Trp Phe Lys Pro Leu Ala Glu Ile Asp Gly
            820                 825                 830

Ile Glu Leu Thr Tyr Gly Ile Lys Asp Val Pro Gly Asp Arg Thr Thr
        835                 840                 845

Ile Asp Leu Thr Glu Asp Glu Asn Gln Tyr Ser Ile Gly Asn Leu Lys
    850                 855                 860

Pro Asp Thr Glu Tyr Glu Val Ser Leu Ile Ser Arg Arg Gly Asp Met
865                 870                 875                 880

Ser Ser Asn Pro Ala Lys Glu Thr Phe Thr Thr Gly Leu Asp Ala Pro
                885                 890                 895

Arg Asn Leu Arg Arg Val Ser Gln Thr Asp Asn Ser Ile Thr Leu Glu
            900                 905                 910

Trp Arg Asn Gly Lys Ala Ala Ile Asp Ser Tyr Arg Ile Lys Tyr Ala
        915                 920                 925

Pro Ile Ser Gly Gly Asp His Ala Glu Val Asp Val Pro Lys Ser Gln
    930                 935                 940

Gln Ala Thr Thr Lys Thr Thr Leu Thr Gly Leu Arg Pro Gly Thr Glu
945                 950                 955                 960

Tyr Gly Ile Gly Val Ser Ala Val Lys Glu Asp Lys Glu Ser Asn Pro
                965                 970                 975

Ala Thr Ile Asn Ala Ala Thr Glu Leu Asp Thr Pro Lys Asp Leu Gln
            980                 985                 990

Val Ser Glu Thr Ala Glu Thr Ser  Leu Thr Leu Leu Trp  Lys Thr Pro
        995                 1000                 1005

Leu Ala  Lys Phe Asp Arg Tyr  Arg Leu Asn Tyr Ser  Leu Pro Thr
    1010                 1015                 1020

Gly Gln  Trp Val Gly Val Gln  Leu Pro Arg Asn Thr  Thr Ser Tyr
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    1025                 1030                 1035

Val Leu  Arg Gly Leu Glu Pro  Gly Gln Glu Tyr Asn  Val Leu Leu
    1040                 1045                 1050

Thr Ala  Glu Lys Gly Arg His  Lys Ser Lys Pro Ala  Arg Val Lys
    1055                 1060                 1065

Ala Ser  Thr Glu Gln Ala Pro  Glu Leu Glu Asn Leu  Thr Val Thr
    1070                 1075                 1080

Glu Val  Gly Trp Asp Gly Leu  Arg Leu Asn Trp Thr  Ala Ala Asp
    1085                 1090                 1095

Gln Ala  Tyr Glu His Phe Ile  Ile Gln Val Gln Glu  Ala Asn Lys
    1100                 1105                 1110

Val Glu  Ala Ala Arg Asn Leu  Thr Val Pro Gly Ser  Leu Arg Ala
    1115                 1120                 1125

Val Asp  Ile Pro Gly Leu Lys  Ala Ala Thr Pro Tyr  Thr Val Ser
    1130                 1135                 1140

Ile Tyr  Gly Val Ile Gln Gly  Tyr Arg Thr Pro Val  Leu Ser Ala
    1145                 1150                 1155

Glu Ala  Ser Thr Gly Glu Thr  Pro Asn Leu Gly Glu  Val Val Val
    1160                 1165                 1170

Ala Glu  Val Gly Trp Asp Ala  Leu Lys Leu Asn Trp  Thr Ala Pro
    1175                 1180                 1185

Glu Gly  Ala Tyr Glu Tyr Phe  Phe Ile Gln Val Gln  Glu Ala Asp
    1190                 1195                 1200

Thr Val  Glu Ala Ala Gln Asn  Leu Thr Val Pro Gly  Gly Leu Arg
    1205                 1210                 1215

Ser Thr  Asp Leu Pro Gly Leu  Lys Ala Ala Thr His  Tyr Thr Ile
    1220                 1225                 1230

Thr Ile  Arg Gly Val Thr Gln  Asp Phe Ser Thr Thr  Pro Leu Ser
    1235                 1240                 1245

Val Glu  Val Leu Thr Glu Glu  Val Pro Asp Met Gly  Asn Leu Thr
    1250                 1255                 1260

Val Thr  Glu Val Ser Trp Asp  Ala Leu Arg Leu Asn  Trp Thr Thr
    1265                 1270                 1275

Pro Asp  Gly Thr Tyr Asp Gln  Phe Thr Ile Gln Val  Gln Glu Ala
    1280                 1285                 1290

Asp Gln  Val Glu Glu Ala His  Asn Leu Thr Val Pro  Gly Ser Leu
    1295                 1300                 1305

Arg Ser  Met Glu Ile Pro Gly  Leu Arg Ala Gly Thr  Pro Tyr Thr
    1310                 1315                 1320

Val Thr  Leu His Gly Glu Val  Arg Gly His Ser Thr  Arg Pro Leu
    1325                 1330                 1335

Ala Val  Glu Val Val Thr Glu  Asp Leu Pro Gln Leu  Gly Asp Leu
    1340                 1345                 1350

Ala Val  Ser Glu Val Gly Trp  Asp Gly Leu Arg Leu  Asn Trp Thr
    1355                 1360                 1365

Ala Ala  Asp Asn Ala Tyr Glu  His Phe Val Ile Gln  Val Gln Glu
    1370                 1375                 1380

Val Asn  Lys Val Glu Ala Ala  Gln Asn Leu Thr Leu  Pro Gly Ser
    1385                 1390                 1395

Leu Arg  Ala Val Asp Ile Pro  Gly Leu Glu Ala Ala  Thr Pro Tyr
    1400                 1405                 1410
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Arg Val  Ser Ile Tyr Gly Val  Ile Arg Gly Tyr Arg  Thr Pro Val
    1415                 1420                 1425

Leu Ser  Ala Glu Ala Ser Thr  Ala Lys Glu Pro Glu  Ile Gly Asn
    1430                 1435                 1440

Leu Asn  Val Ser Asp Ile Thr  Pro Glu Ser Phe Asn  Leu Ser Trp
    1445                 1450                 1455

Met Ala  Thr Asp Gly Ile Phe  Glu Thr Phe Thr Ile  Glu Ile Ile
    1460                 1465                 1470

Asp Ser  Asn Arg Leu Leu Glu  Thr Val Glu Tyr Asn  Ile Ser Gly
    1475                 1480                 1485

Ala Glu  Arg Thr Ala His Ile  Ser Gly Leu Pro Pro  Ser Thr Asp
    1490                 1495                 1500

Phe Ile  Val Tyr Leu Ser Gly  Leu Ala Pro Ser Ile  Arg Thr Lys
    1505                 1510                 1515

Thr Ile  Ser Ala Thr Ala Thr  Thr Glu Ala Leu Pro  Leu Leu Glu
    1520                 1525                 1530

Asn Leu  Thr Ile Ser Asp Ile  Asn Pro Tyr Gly Phe  Thr Val Ser
    1535                 1540                 1545

Trp Met  Ala Ser Glu Asn Ala  Phe Asp Ser Phe Leu  Val Thr Val
    1550                 1555                 1560

Val Asp  Ser Gly Lys Leu Leu  Asp Pro Gln Glu Phe  Thr Leu Ser
    1565                 1570                 1575

Gly Thr  Gln Arg Lys Leu Glu  Leu Arg Gly Leu Ile  Thr Gly Ile
    1580                 1585                 1590

Gly Tyr  Glu Val Met Val Ser  Gly Phe Thr Gln Gly  His Gln Thr
    1595                 1600                 1605

Lys Pro  Leu Arg Ala Glu Ile  Val Thr Glu Ala Glu  Pro Glu Val
    1610                 1615                 1620

Asp Asn  Leu Leu Val Ser Asp  Ala Thr Pro Asp Gly  Phe Arg Leu
    1625                 1630                 1635

Ser Trp  Thr Ala Asp Glu Gly  Val Phe Asp Asn Phe  Val Leu Lys
    1640                 1645                 1650

Ile Arg  Asp Thr Lys Lys Gln  Ser Glu Pro Leu Glu  Ile Thr Leu
    1655                 1660                 1665

Leu Ala  Pro Glu Arg Thr Arg  Asp Ile Thr Gly Leu  Arg Glu Ala
    1670                 1675                 1680

Thr Glu  Tyr Glu Ile Glu Leu  Tyr Gly Ile Ser Lys  Gly Arg Arg
    1685                 1690                 1695

Ser Gln  Thr Val Ser Ala Ile  Ala Thr Thr Ala Met  Gly Ser Pro
    1700                 1705                 1710

Lys Glu  Val Ile Phe Ser Asp  Ile Thr Glu Asn Ser  Ala Thr Val
    1715                 1720                 1725

Ser Trp  Arg Ala Pro Thr Ala  Gln Val Glu Ser Phe  Arg Ile Thr
    1730                 1735                 1740

Tyr Val  Pro Ile Thr Gly Gly  Thr Pro Ser Met Val  Thr Val Asp
    1745                 1750                 1755

Gly Thr  Lys Thr Gln Thr Arg  Leu Val Lys Leu Ile  Pro Gly Val
    1760                 1765                 1770

Glu Tyr  Leu Val Ser Ile Ile  Ala Met Lys Gly Phe  Glu Glu Ser
    1775                 1780                 1785
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Glu Pro  Val Ser Gly Ser Phe  Thr Thr Ala Leu Asp  Gly Pro Ser
    1790                 1795                 1800

Gly Leu  Val Thr Ala Asn Ile  Thr Asp Ser Glu Ala  Leu Ala Arg
    1805                 1810                 1815

Trp Gln  Pro Ala Ile Ala Thr  Val Asp Ser Tyr Val  Ile Ser Tyr
    1820                 1825                 1830

Thr Gly  Glu Lys Val Pro Glu  Ile Thr Arg Thr Val  Ser Gly Asn
    1835                 1840                 1845

Thr Val  Glu Tyr Ala Leu Thr  Asp Leu Glu Pro Ala  Thr Glu Tyr
    1850                 1855                 1860

Thr Leu  Arg Ile Phe Ala Glu  Lys Gly Pro Gln Lys  Ser Ser Thr
    1865                 1870                 1875

Ile Thr  Ala Lys Phe Thr Thr  Asp Leu Asp Ser Pro  Arg Asp Leu
    1880                 1885                 1890

Thr Ala  Thr Glu Val Gln Ser  Glu Thr Ala Leu Leu  Thr Trp Arg
    1895                 1900                 1905

Pro Pro  Arg Ala Ser Val Thr  Gly Tyr Leu Leu Val  Tyr Glu Ser
    1910                 1915                 1920

Val Asp  Gly Thr Val Lys Glu  Val Ile Val Gly Pro  Asp Thr Thr
    1925                 1930                 1935

Ser Tyr  Ser Leu Ala Asp Leu  Ser Pro Ser Thr His  Tyr Thr Ala
    1940                 1945                 1950

Lys Ile  Gln Ala Leu Asn Gly  Pro Leu Arg Ser Asn  Met Ile Gln
    1955                 1960                 1965

Thr Ile  Phe Thr Thr Ile Gly  Leu Leu Tyr Pro Phe  Pro Lys Asp
    1970                 1975                 1980

Cys Ser  Gln Ala Met Leu Asn  Gly Asp Thr Thr Ser  Gly Leu Tyr
    1985                 1990                 1995

Thr Ile  Tyr Leu Asn Gly Asp  Lys Ala Glu Ala Leu  Glu Val Phe
    2000                 2005                 2010

Cys Asp  Met Thr Ser Asp Gly  Gly Gly Trp Ile Val  Phe Leu Arg
    2015                 2020                 2025

Arg Lys  Asn Gly Arg Glu Asn  Phe Tyr Gln Asn Trp  Lys Ala Tyr
    2030                 2035                 2040

Ala Ala  Gly Phe Gly Asp Arg  Arg Glu Glu Phe Trp  Leu Gly Leu
    2045                 2050                 2055

Asp Asn  Leu Asn Lys Ile Thr  Ala Gln Gly Gln Tyr  Glu Leu Arg
    2060                 2065                 2070

Val Asp  Leu Arg Asp His Gly  Glu Thr Ala Phe Ala  Val Tyr Asp
    2075                 2080                 2085

Lys Phe  Ser Val Gly Asp Ala  Lys Thr Arg Tyr Lys  Leu Lys Val
    2090                 2095                 2100

Glu Gly  Tyr Ser Gly Thr Ala  Gly Asp Ser Met Ala  Tyr His Asn
    2105                 2110                 2115

Gly Arg  Ser Phe Ser Thr Phe  Asp Lys Asp Thr Asp  Ser Ala Ile
    2120                 2125                 2130

Thr Asn  Cys Ala Leu Ser Tyr  Lys Gly Ala Phe Trp  Tyr Arg Asn
    2135                 2140                 2145

Cys His  Arg Val Asn Leu Met  Gly Arg Tyr Gly Asp  Asn Asn His
    2150                 2155                 2160

Ser Gln  Gly Val Asn Trp Phe  His Trp Lys Gly His  Glu His Ser
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    2165                 2170                 2175

Ile Gln  Phe Ala Glu Met Lys  Leu Arg Pro Ser Asn  Phe Arg Asn
    2180                 2185                 2190

Leu Glu  Gly Arg Arg Lys Arg  Ala
    2195                 2200


<210> SEQ ID NO 21
<211> LENGTH: 478
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

Met Ala Pro Leu Arg Pro Leu Leu Ile Leu Ala Leu Leu Ala Trp Val
1               5                   10                  15

Ala Leu Ala Asp Gln Glu Ser Cys Lys Gly Arg Cys Thr Glu Gly Phe
            20                  25                  30

Asn Val Asp Lys Lys Cys Gln Cys Asp Glu Leu Cys Ser Tyr Tyr Gln
        35                  40                  45

Ser Cys Cys Thr Asp Tyr Thr Ala Glu Cys Lys Pro Gln Val Thr Arg
    50                  55                  60

Gly Asp Val Phe Thr Met Pro Glu Asp Glu Tyr Thr Val Tyr Asp Asp
65                  70                  75                  80

Gly Glu Glu Lys Asn Asn Ala Thr Val His Glu Gln Val Gly Gly Pro
                85                  90                  95

Ser Leu Thr Ser Asp Leu Gln Ala Gln Ser Lys Gly Asn Pro Glu Gln
            100                 105                 110

Thr Pro Val Leu Lys Pro Glu Glu Glu Ala Pro Ala Pro Glu Val Gly
        115                 120                 125

Ala Ser Lys Pro Glu Gly Ile Asp Ser Arg Pro Glu Thr Leu His Pro
    130                 135                 140

Gly Arg Pro Gln Pro Pro Ala Glu Glu Glu Leu Cys Ser Gly Lys Pro
145                 150                 155                 160

Phe Asp Ala Phe Thr Asp Leu Lys Asn Gly Ser Leu Phe Ala Phe Arg
                165                 170                 175

Gly Gln Tyr Cys Tyr Glu Leu Asp Glu Lys Ala Val Arg Pro Gly Tyr
            180                 185                 190

Pro Lys Leu Ile Arg Asp Val Trp Gly Ile Glu Gly Pro Ile Asp Ala
        195                 200                 205

Ala Phe Thr Arg Ile Asn Cys Gln Gly Lys Thr Tyr Leu Phe Lys Gly
    210                 215                 220

Ser Gln Tyr Trp Arg Phe Glu Asp Gly Val Leu Asp Pro Asp Tyr Pro
225                 230                 235                 240

Arg Asn Ile Ser Asp Gly Phe Asp Gly Ile Pro Asp Asn Val Asp Ala
                245                 250                 255

Ala Leu Ala Leu Pro Ala His Ser Tyr Ser Gly Arg Glu Arg Val Tyr
            260                 265                 270

Phe Phe Lys Gly Lys Gln Tyr Trp Glu Tyr Gln Phe Gln His Gln Pro
        275                 280                 285

Ser Gln Glu Glu Cys Glu Gly Ser Ser Leu Ser Ala Val Phe Glu His
    290                 295                 300

Phe Ala Met Met Gln Arg Asp Ser Trp Glu Asp Ile Phe Glu Leu Leu
305                 310                 315                 320
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Phe Trp Gly Arg Thr Ser Ala Gly Thr Arg Gln Pro Gln Phe Ile Ser
325 330 335

Arg Asp Trp His Gly Val Pro Gly Gln Val Asp Ala Ala Met Ala Gly
340 345 350

Arg Ile Tyr Ile Ser Gly Met Ala Pro Arg Pro Ser Leu Ala Lys Lys
355 360 365

Gln Arg Phe Arg His Arg Asn Arg Lys Gly Tyr Arg Ser Gln Arg Gly
370 375 380

His Ser Arg Gly Arg Asn Gln Asn Ser Arg Arg Pro Ser Arg Ala Thr
385 390 395 400

Trp Leu Ser Leu Phe Ser Ser Glu Glu Ser Asn Leu Gly Ala Asn Asn
405 410 415

Tyr Asp Asp Tyr Arg Met Asp Trp Leu Val Pro Ala Thr Cys Glu Pro
420 425 430

Ile Gln Ser Val Phe Phe Phe Ser Gly Asp Lys Tyr Tyr Arg Val Asn
435 440 445

Leu Arg Thr Arg Arg Val Asp Thr Val Asp Pro Pro Tyr Pro Arg Ser
450 455 460

Ile Ala Gln Tyr Trp Leu Gly Cys Pro Ala Pro Gly His Leu
465 470 475

<210> SEQ ID NO 22
<211> LENGTH: 4289
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

Met Met Pro Ala Gln Tyr Ala Leu Thr Ser Ser Leu Val Leu Leu Val
1 5 10 15

Leu Leu Ser Thr Ala Arg Ala Gly Pro Phe Ser Ser Arg Ser Asn Val
20 25 30

Thr Leu Pro Ala Pro Arg Pro Pro Pro Gln Pro Gly Gly His Thr Val
35 40 45

Gly Ala Gly Val Gly Ser Pro Ser Ser Gln Leu Tyr Glu His Thr Val
50 55 60

Glu Gly Gly Glu Lys Gln Val Val Phe Thr His Arg Ile Asn Leu Pro
65 70 75 80

Pro Ser Thr Gly Cys Gly Cys Pro Pro Gly Thr Glu Pro Pro Val Leu
85 90 95

Ala Ser Glu Val Gln Ala Leu Arg Val Arg Leu Glu Ile Leu Glu Glu
100 105 110

Leu Val Lys Gly Leu Lys Glu Gln Cys Thr Gly Gly Cys Cys Pro Ala
115 120 125

Ser Ala Gln Ala Gly Thr Gly Gln Thr Asp Val Arg Thr Leu Cys Ser
130 135 140

Leu His Gly Val Phe Asp Leu Ser Arg Cys Thr Cys Ser Cys Glu Pro
145 150 155 160

Gly Trp Gly Gly Pro Thr Cys Ser Asp Pro Thr Asp Ala Glu Ile Pro
165 170 175

Pro Ser Ser Pro Pro Ser Ala Ser Gly Ser Cys Pro Asp Asp Cys Asn
180 185 190

Asp Gln Gly Arg Cys Val Arg Gly Arg Cys Val Cys Phe Pro Gly Tyr
195 200 205

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Thr Gly Pro Ser Cys Gly Trp Pro Ser Cys Pro Gly Asp Cys Gln Gly
    210                 215                 220

Arg Gly Arg Cys Val Gln Gly Val Cys Val Cys Arg Ala Gly Phe Ser
225                 230                 235                 240

Gly Pro Asp Cys Ser Gln Arg Ser Cys Pro Arg Gly Cys Ser Gln Arg
                245                 250                 255

Gly Arg Cys Glu Gly Gly Arg Cys Val Cys Asp Pro Gly Tyr Thr Gly
            260                 265                 270

Asp Asp Cys Gly Met Arg Ser Cys Pro Arg Gly Cys Ser Gln Arg Gly
        275                 280                 285

Arg Cys Glu Asn Gly Arg Cys Val Cys Asn Pro Gly Tyr Thr Gly Glu
    290                 295                 300

Asp Cys Gly Val Arg Ser Cys Pro Arg Gly Cys Ser Gln Arg Gly Arg
305                 310                 315                 320

Cys Lys Asp Gly Arg Cys Val Cys Asp Pro Gly Tyr Thr Gly Glu Asp
                325                 330                 335

Cys Gly Thr Arg Ser Cys Pro Trp Asp Cys Gly Glu Gly Gly Arg Cys
            340                 345                 350

Val Asp Gly Arg Cys Val Cys Trp Pro Gly Tyr Thr Gly Glu Asp Cys
        355                 360                 365

Ser Thr Arg Thr Cys Pro Arg Asp Cys Arg Gly Arg Gly Arg Cys Glu
    370                 375                 380

Asp Gly Glu Cys Ile Cys Asp Thr Gly Tyr Ser Gly Asp Asp Cys Gly
385                 390                 395                 400

Val Arg Ser Cys Pro Gly Asp Cys Asn Gln Arg Gly Arg Cys Glu Asp
                405                 410                 415

Gly Arg Cys Val Cys Trp Pro Gly Tyr Thr Gly Thr Asp Cys Gly Ser
            420                 425                 430

Arg Ala Cys Pro Arg Asp Cys Arg Gly Arg Gly Arg Cys Glu Asn Gly
        435                 440                 445

Val Cys Val Cys Asn Ala Gly Tyr Ser Gly Glu Asp Cys Gly Val Arg
    450                 455                 460

Ser Cys Pro Gly Asp Cys Arg Gly Arg Gly Arg Cys Glu Ser Gly Arg
465                 470                 475                 480

Cys Met Cys Trp Pro Gly Tyr Thr Gly Arg Asp Cys Gly Thr Arg Ala
                485                 490                 495

Cys Pro Gly Asp Cys Arg Gly Arg Gly Arg Cys Val Asp Gly Arg Cys
            500                 505                 510

Val Cys Asn Pro Gly Phe Thr Gly Glu Asp Cys Gly Ser Arg Arg Cys
        515                 520                 525

Pro Gly Asp Cys Arg Gly His Gly Leu Cys Glu Asp Gly Val Cys Val
    530                 535                 540

Cys Asp Ala Gly Tyr Ser Gly Glu Asp Cys Ser Thr Arg Ser Cys Pro
545                 550                 555                 560

Gly Gly Cys Arg Gly Arg Gly Gln Cys Leu Asp Gly Arg Cys Val Cys
                565                 570                 575

Glu Asp Gly Tyr Ser Gly Glu Asp Cys Gly Val Arg Gln Cys Pro Asn
            580                 585                 590

Asp Cys Ser Gln His Gly Val Cys Gln Asp Gly Val Cys Ile Cys Trp
        595                 600                 605
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Glu Gly Tyr Val Ser Glu Asp Cys Ser Ile Arg Thr Cys Pro Ser Asn
    610                 615                 620

Cys His Gly Arg Gly Arg Cys Glu Glu Gly Arg Cys Leu Cys Asp Pro
625                 630                 635                 640

Gly Tyr Thr Gly Pro Thr Cys Ala Thr Arg Met Cys Pro Ala Asp Cys
                645                 650                 655

Arg Gly Arg Gly Arg Cys Val Gln Gly Val Cys Leu Cys His Val Gly
            660                 665                 670

Tyr Gly Gly Glu Asp Cys Gly Gln Glu Glu Pro Pro Ala Ser Ala Cys
        675                 680                 685

Pro Gly Gly Cys Gly Pro Arg Glu Leu Cys Arg Ala Gly Gln Cys Val
    690                 695                 700

Cys Val Glu Gly Phe Arg Gly Pro Asp Cys Ala Ile Gln Thr Cys Pro
705                 710                 715                 720

Gly Asp Cys Arg Gly Arg Gly Glu Cys His Asp Gly Ser Cys Val Cys
                725                 730                 735

Lys Asp Gly Tyr Ala Gly Glu Asp Cys Gly Glu Ala Arg Val Pro Ser
            740                 745                 750

Ser Ala Ser Ala Tyr Asp Gln Arg Gly Leu Ala Pro Gly Gln Glu Tyr
        755                 760                 765

Gln Val Thr Val Arg Ala Leu Arg Gly Thr Ser Trp Gly Leu Pro Ala
    770                 775                 780

Ser Lys Thr Ile Thr Thr Met Ile Asp Gly Pro Gln Asp Leu Arg Val
785                 790                 795                 800

Val Ala Val Thr Pro Thr Thr Leu Glu Leu Gly Trp Leu Arg Pro Gln
                805                 810                 815

Ala Glu Val Asp Arg Phe Val Val Ser Tyr Val Ser Ala Gly Asn Gln
            820                 825                 830

Arg Val Arg Leu Glu Val Pro Pro Glu Ala Asp Gly Thr Leu Leu Thr
        835                 840                 845

Asp Leu Met Pro Gly Val Glu Tyr Val Val Thr Val Thr Ala Glu Arg
    850                 855                 860

Gly Arg Ala Val Ser Tyr Pro Ala Ser Val Arg Ala Asn Thr Glu Glu
865                 870                 875                 880

Arg Glu Glu Glu Ser Pro Pro Arg Pro Ser Leu Ser Gln Pro Pro Arg
                885                 890                 895

Arg Pro Trp Gly Asn Leu Thr Ala Glu Leu Ser Arg Phe Arg Gly Thr
            900                 905                 910

Val Gln Asp Leu Glu Arg His Leu Arg Ala His Gly Tyr Pro Leu Arg
        915                 920                 925

Ala Asn Gln Thr Tyr Thr Ser Val Ala Arg His Ile His Glu Tyr Leu
    930                 935                 940

Gln Arg Gln Val Leu Gly Ser Ser Ala Asp Gly Ala Leu Leu Val Ser
945                 950                 955                 960

Leu Asp Gly Leu Arg Gly Gln Phe Glu Arg Val Val Leu Arg Trp Arg
                965                 970                 975

Pro Gln Pro Pro Ala Glu Gly Pro Gly Gly Glu Leu Thr Val Pro Gly
            980                 985                 990

Thr Thr Arg Thr Val Ser Leu Pro  Asp Leu Arg Pro Gly  Thr Thr Tyr
        995                      1000                 1005

His Val  Glu Val His Gly Val  Arg Ala Gly Gln Thr  Ser Lys Ser
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1010 1015 1020

Tyr Ala Phe Ile Thr Thr Thr Gly Pro Ser Thr Thr Gln Gly Ala
1025 1030 1035

Gln Ala Pro Leu Leu Gln Gln Arg Pro Gln Glu Leu Gly Glu Leu
1040 1045 1050

Arg Val Leu Gly Arg Asp Glu Thr Gly Arg Leu Arg Val Val Trp
1055 1060 1065

Thr Ala Gln Pro Asp Thr Phe Ala Tyr Phe Gln Leu Arg Met Arg
1070 1075 1080

Val Pro Glu Gly Pro Gly Ala His Glu Glu Val Leu Pro Gly Asp
1085 1090 1095

Val Arg Gln Ala Leu Val Pro Pro Pro Pro Pro Gly Thr Pro Tyr
1100 1105 1110

Glu Leu Ser Leu His Gly Val Pro Pro Gly Gly Lys Pro Ser Asp
1115 1120 1125

Pro Ile Ile Tyr Gln Gly Ile Met Asp Lys Asp Glu Glu Lys Pro
1130 1135 1140

Gly Lys Ser Ser Gly Pro Pro Arg Leu Gly Glu Leu Thr Val Thr
1145 1150 1155

Asp Arg Thr Ser Asp Ser Leu Leu Leu Arg Trp Thr Val Pro Glu
1160 1165 1170

Gly Glu Phe Asp Ser Phe Val Ile Gln Tyr Lys Asp Arg Asp Gly
1175 1180 1185

Gln Pro Gln Val Val Pro Val Glu Gly Pro Gln Arg Ser Ala Val
1190 1195 1200

Ile Thr Ser Leu Asp Pro Gly Arg Lys Tyr Lys Phe Val Leu Tyr
1205 1210 1215

Gly Phe Val Gly Lys Lys Arg His Gly Pro Leu Val Ala Glu Ala
1220 1225 1230

Lys Ile Leu Pro Gln Ser Asp Pro Ser Pro Gly Thr Pro Pro His
1235 1240 1245

Leu Gly Asn Leu Trp Val Thr Asp Pro Thr Pro Asp Ser Leu His
1250 1255 1260

Leu Ser Trp Thr Val Pro Glu Gly Gln Phe Asp Thr Phe Met Val
1265 1270 1275

Gln Tyr Arg Asp Arg Asp Gly Arg Pro Gln Val Val Pro Val Glu
1280 1285 1290

Gly Pro Glu Arg Ser Phe Val Val Ser Ser Leu Asp Pro Asp His
1295 1300 1305

Lys Tyr Arg Phe Thr Leu Phe Gly Ile Ala Asn Lys Lys Arg Tyr
1310 1315 1320

Gly Pro Leu Thr Ala Asp Gly Thr Thr Ala Pro Glu Arg Lys Glu
1325 1330 1335

Glu Pro Pro Arg Pro Glu Phe Leu Glu Gln Pro Leu Leu Gly Glu
1340 1345 1350

Leu Thr Val Thr Gly Val Thr Pro Asp Ser Leu Arg Leu Ser Trp
1355 1360 1365

Thr Val Ala Gln Gly Pro Phe Asp Ser Phe Met Val Gln Tyr Lys
1370 1375 1380

Asp Ala Gln Gly Gln Pro Gln Ala Val Pro Val Ala Gly Asp Glu
1385 1390 1395

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Asn Glu  Val Thr Val Pro Gly  Leu Asp Pro Asp Arg  Lys Tyr Lys
    1400                 1405                 1410

Met Asn  Leu Tyr Gly Leu Arg  Gly Arg Gln Arg Val  Gly Pro Glu
    1415                 1420                 1425

Ser Val  Val Ala Lys Thr Ala  Pro Gln Glu Asp Val  Asp Glu Thr
    1430                 1435                 1440

Pro Ser  Pro Thr Glu Leu Gly  Thr Glu Ala Pro Glu  Ser Pro Glu
    1445                 1450                 1455

Glu Pro  Leu Leu Gly Glu Leu  Thr Val Thr Gly Ser  Ser Pro Asp
    1460                 1465                 1470

Ser Leu  Ser Leu Phe Trp Thr  Val Pro Gln Gly Ser  Phe Asp Ser
    1475                 1480                 1485

Phe Thr  Val Gln Tyr Lys Asp  Arg Asp Gly Arg Pro  Arg Ala Val
    1490                 1495                 1500

Arg Val  Gly Gly Lys Glu Ser  Glu Val Thr Val Gly  Gly Leu Glu
    1505                 1510                 1515

Pro Gly  His Lys Tyr Lys Met  His Leu Tyr Gly Leu  His Glu Gly
    1520                 1525                 1530

Gln Arg  Val Gly Pro Val Ser  Ala Val Gly Val Thr  Ala Pro Gln
    1535                 1540                 1545

Gln Glu  Glu Thr Pro Pro Ala  Thr Glu Ser Pro Leu  Glu Pro Arg
    1550                 1555                 1560

Leu Gly  Glu Leu Thr Val Thr  Asp Val Thr Pro Asn  Ser Val Gly
    1565                 1570                 1575

Leu Ser  Trp Thr Val Pro Glu  Gly Gln Phe Asp Ser  Phe Ile Val
    1580                 1585                 1590

Gln Tyr  Lys Asp Lys Asp Gly  Gln Pro Gln Val Val  Pro Val Ala
    1595                 1600                 1605

Ala Asp  Gln Arg Glu Val Thr  Val Tyr Asn Leu Glu  Pro Glu Arg
    1610                 1615                 1620

Lys Tyr  Lys Met Asn Met Tyr  Gly Leu His Asp Gly  Gln Arg Met
    1625                 1630                 1635

Gly Pro  Leu Ser Val Val Ile  Val Thr Ala Pro Ala  Thr Glu Ala
    1640                 1645                 1650

Ser Lys  Pro Pro Leu Glu Pro  Arg Leu Gly Glu Leu  Thr Val Thr
    1655                 1660                 1665

Asp Ile  Thr Pro Asp Ser Val  Gly Leu Ser Trp Thr  Val Pro Glu
    1670                 1675                 1680

Gly Glu  Phe Asp Ser Phe Val  Val Gln Tyr Lys Asp  Arg Asp Gly
    1685                 1690                 1695

Gln Pro  Gln Val Val Pro Val  Ala Ala Asp Gln Arg  Glu Val Thr
    1700                 1705                 1710

Ile Pro  Asp Leu Glu Pro Ser  Arg Lys Tyr Lys Phe  Leu Leu Phe
    1715                 1720                 1725

Gly Ile  Gln Asp Gly Lys Arg  Arg Ser Pro Val Ser  Val Glu Ala
    1730                 1735                 1740

Lys Thr  Val Ala Arg Gly Asp  Ala Ser Pro Gly Ala  Pro Pro Arg
    1745                 1750                 1755

Leu Gly  Glu Leu Trp Val Thr  Asp Pro Thr Pro Asp  Ser Leu Arg
    1760                 1765                 1770
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Leu Ser  Trp Thr Val Pro Glu  Gly Gln Phe Asp Ser  Phe Val Val
    1775                1780                1785

Gln Phe  Lys Asp Lys Asp Gly  Pro Gln Val Val Pro  Val Glu Gly
    1790                1795                1800

His Glu  Arg Ser Val Thr Val  Thr Pro Leu Asp Ala  Gly Arg Lys
    1805                1810                1815

Tyr Arg  Phe Leu Leu Tyr Gly  Leu Leu Gly Lys Lys  Arg His Gly
    1820                1825                1830

Pro Leu  Thr Ala Asp Gly Thr  Thr Glu Ala Arg Ser  Ala Met Asp
    1835                1840                1845

Asp Thr  Gly Thr Lys Arg Pro  Pro Lys Pro Arg Leu  Gly Glu Glu
    1850                1855                1860

Leu Gln  Val Thr Thr Val Thr  Gln Asn Ser Val Gly  Leu Ser Trp
    1865                1870                1875

Thr Val  Pro Glu Gly Gln Phe  Asp Ser Phe Val Val  Gln Tyr Lys
    1880                1885                1890

Asp Arg  Asp Gly Gln Pro Gln  Val Val Pro Val Glu  Gly Ser Leu
    1895                1900                1905

Arg Glu  Val Ser Val Pro Gly  Leu Asp Pro Ala His  Arg Tyr Lys
    1910                1915                1920

Leu Leu  Leu Tyr Gly Leu His  His Gly Lys Arg Val  Gly Pro Ile
    1925                1930                1935

Ser Ala  Val Ala Ile Thr Ala  Gly Arg Glu Glu Thr  Glu Thr Glu
    1940                1945                1950

Thr Thr  Ala Pro Thr Pro Pro  Ala Pro Glu Pro His  Leu Gly Glu
    1955                1960                1965

Leu Thr  Val Glu Glu Ala Thr  Ser His Thr Leu His  Leu Ser Trp
    1970                1975                1980

Met Val  Thr Glu Gly Glu Phe  Asp Ser Phe Glu Ile  Gln Tyr Thr
    1985                1990                1995

Asp Arg  Asp Gly Gln Leu Gln  Met Val Arg Ile Gly  Gly Asp Arg
    2000                2005                2010

Asn Asp  Ile Thr Leu Ser Gly  Leu Glu Ser Asp His  Arg Tyr Leu
    2015                2020                2025

Val Thr  Leu Tyr Gly Phe Ser  Asp Gly Lys His Val  Gly Pro Val
    2030                2035                2040

His Val  Glu Ala Leu Thr Val  Pro Glu Glu Glu Lys  Pro Ser Glu
    2045                2050                2055

Pro Pro  Thr Ala Thr Pro Glu  Pro Pro Ile Lys Pro  Arg Leu Gly
    2060                2065                2070

Glu Leu  Thr Val Thr Asp Ala  Thr Pro Asp Ser Leu  Ser Leu Ser
    2075                2080                2085

Trp Thr  Val Pro Glu Gly Gln  Phe Asp His Phe Leu  Val Gln Tyr
    2090                2095                2100

Arg Asn  Gly Asp Gly Gln Pro  Lys Ala Val Arg Val  Pro Gly His
    2105                2110                2115

Glu Glu  Gly Val Thr Ile Ser  Gly Leu Glu Pro Asp  His Lys Tyr
    2120                2125                2130

Lys Met  Asn Leu Tyr Gly Phe  His Gly Gly Gln Arg  Met Gly Pro
    2135                2140                2145

Val Ser  Val Val Gly Val Thr  Glu Pro Ser Met Glu  Ala Pro Glu
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    2150                 2155                 2160

Pro Ala  Glu Glu Pro Leu Leu  Gly Glu Leu Thr Val  Thr Gly Ser
    2165                 2170                 2175

Ser Pro  Asp Ser Leu Ser Leu  Ser Trp Thr Val Pro  Gln Gly Arg
    2180                 2185                 2190

Phe Asp  Ser Phe Thr Val Gln  Tyr Lys Asp Arg Asp  Gly Arg Pro
    2195                 2200                 2205

Gln Val  Val Arg Val Gly Gly  Glu Glu Ser Glu Val  Thr Val Gly
    2210                 2215                 2220

Gly Leu  Glu Pro Gly Arg Lys  Tyr Lys Met His Leu  Tyr Gly Leu
    2225                 2230                 2235

His Glu  Gly Arg Arg Val Gly  Pro Val Ser Ala Val  Gly Val Thr
    2240                 2245                 2250

Ala Pro  Glu Glu Glu Ser Pro  Asp Ala Pro Leu Ala  Lys Leu Arg
    2255                 2260                 2265

Leu Gly  Gln Met Thr Val Arg  Asp Ile Thr Ser Asp  Ser Leu Ser
    2270                 2275                 2280

Leu Ser  Trp Thr Val Pro Glu  Gly Gln Phe Asp His  Phe Leu Val
    2285                 2290                 2295

Gln Phe  Lys Asn Gly Asp Gly  Gln Pro Lys Ala Val  Arg Val Pro
    2300                 2305                 2310

Gly His  Glu Asp Gly Val Thr  Ile Ser Gly Leu Glu  Pro Asp His
    2315                 2320                 2325

Lys Tyr  Lys Met Asn Leu Tyr  Gly Phe His Gly Gly  Gln Arg Val
    2330                 2335                 2340

Gly Pro  Val Ser Ala Val Gly  Leu Thr Ala Ser Thr  Glu Pro Pro
    2345                 2350                 2355

Thr Pro  Glu Pro Pro Ile Lys  Pro Arg Leu Glu Glu  Leu Thr Val
    2360                 2365                 2370

Thr Asp  Ala Thr Pro Asp Ser  Leu Ser Leu Ser Trp  Thr Val Pro
    2375                 2380                 2385

Glu Gly  Gln Phe Asp His Phe  Leu Val Gln Tyr Lys  Asn Gly Asp
    2390                 2395                 2400

Gly Gln  Pro Lys Ala Thr Arg  Val Pro Gly His Glu  Asp Arg Val
    2405                 2410                 2415

Thr Ile  Ser Gly Leu Glu Pro  Asp Asn Lys Tyr Lys  Met Asn Leu
    2420                 2425                 2430

Tyr Gly  Phe His Gly Gly Gln  Arg Val Gly Pro Val  Ser Ala Ile
    2435                 2440                 2445

Gly Val  Thr Glu Glu Glu Thr  Pro Ser Pro Thr Glu  Pro Ser Met
    2450                 2455                 2460

Glu Ala  Pro Glu Pro Pro Glu  Glu Pro Leu Leu Gly  Glu Leu Thr
    2465                 2470                 2475

Val Thr  Gly Ser Ser Pro Asp  Ser Leu Ser Leu Ser  Trp Thr Val
    2480                 2485                 2490

Pro Gln  Gly Arg Phe Asp Ser  Phe Thr Val Gln Tyr  Lys Asp Arg
    2495                 2500                 2505

Asp Gly  Arg Pro Gln Val Val  Arg Val Gly Gly Glu  Glu Ser Glu
    2510                 2515                 2520

Val Thr  Val Gly Gly Leu Glu  Pro Gly Arg Lys Tyr  Lys Met His
    2525                 2530                 2535
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Leu Tyr  Gly Leu His Glu Gly  Arg Arg Val Gly Pro  Val Ser Thr
    2540                 2545                 2550

Val Gly  Val Thr Ala Pro Gln  Glu Asp Val Asp Glu  Thr Pro Ser
    2555                 2560                 2565

Pro Thr  Glu Pro Gly Thr Glu  Ala Pro Gly Pro Pro  Glu Glu Pro
    2570                 2575                 2580

Leu Leu  Gly Glu Leu Thr Val  Thr Gly Ser Ser Pro  Asp Ser Leu
    2585                 2590                 2595

Ser Leu  Ser Trp Thr Val Pro  Gln Gly Arg Phe Asp  Ser Phe Thr
    2600                 2605                 2610

Val Gln  Tyr Lys Asp Arg Asp  Gly Arg Pro Gln Ala  Val Arg Val
    2615                 2620                 2625

Gly Gly  Gln Glu Ser Lys Val  Thr Val Arg Gly Leu  Glu Pro Gly
    2630                 2635                 2640

Arg Lys  Tyr Lys Met His Leu  Tyr Gly Leu His Glu  Gly Arg Arg
    2645                 2650                 2655

Leu Gly  Pro Val Ser Ala Val  Gly Val Thr Glu Asp  Glu Ala Glu
    2660                 2665                 2670

Thr Thr  Gln Ala Val Pro Thr  Met Thr Pro Glu Pro  Pro Ile Lys
    2675                 2680                 2685

Pro Arg  Leu Gly Glu Leu Thr  Met Thr Asp Ala Thr  Pro Asp Ser
    2690                 2695                 2700

Leu Ser  Leu Ser Trp Thr Val  Pro Glu Gly Gln Phe  Asp His Phe
    2705                 2710                 2715

Leu Val  Gln Tyr Arg Asn Gly  Asp Gly Gln Pro Lys  Ala Val Arg
    2720                 2725                 2730

Val Pro  Gly His Glu Asp Gly  Val Thr Ile Ser Gly  Leu Glu Pro
    2735                 2740                 2745

Asp His  Lys Tyr Lys Met Asn  Leu Tyr Gly Phe His  Gly Gly Gln
    2750                 2755                 2760

Arg Val  Gly Pro Ile Ser Val  Ile Gly Val Thr Glu  Glu Glu Thr
    2765                 2770                 2775

Pro Ser  Pro Thr Glu Leu Ser  Thr Glu Ala Pro Glu  Pro Pro Glu
    2780                 2785                 2790

Glu Pro  Leu Leu Gly Glu Leu  Thr Val Thr Gly Ser  Ser Pro Asp
    2795                 2800                 2805

Ser Leu  Ser Leu Ser Trp Thr  Ile Pro Gln Gly His  Phe Asp Ser
    2810                 2815                 2820

Phe Thr  Val Gln Tyr Lys Asp  Arg Asp Gly Arg Pro  Gln Val Met
    2825                 2830                 2835

Arg Val  Arg Gly Glu Glu Ser  Glu Val Thr Val Gly  Gly Leu Glu
    2840                 2845                 2850

Pro Gly  Arg Lys Tyr Lys Met  His Leu Tyr Gly Leu  His Glu Gly
    2855                 2860                 2865

Arg Arg  Val Gly Pro Val Ser  Thr Val Gly Val Thr  Val Pro Thr
    2870                 2875                 2880

Thr Thr  Pro Glu Pro Pro Asn  Lys Pro Arg Leu Gly  Glu Leu Thr
    2885                 2890                 2895

Val Thr  Asp Ala Thr Pro Asp  Ser Leu Ser Leu Ser  Trp Met Val
    2900                 2905                 2910
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Pro Glu  Gly Gln Phe Asp His  Phe Leu Val Gln Tyr  Arg Asn Gly
    2915                 2920                 2925

Asp Gly  Gln Pro Lys Val Val  Arg Val Pro Gly His  Glu Asp Gly
    2930                 2935                 2940

Val Thr  Ile Ser Gly Leu Glu  Pro Asp His Lys Tyr  Lys Met Asn
    2945                 2950                 2955

Leu Tyr  Gly Phe His Gly Gly  Gln Arg Val Gly Pro  Ile Ser Val
    2960                 2965                 2970

Ile Gly  Val Thr Glu Glu Glu  Thr Pro Ala Pro Thr  Glu Pro Ser
    2975                 2980                 2985

Thr Glu  Ala Pro Glu Pro Pro  Glu Glu Pro Leu Leu  Gly Glu Leu
    2990                 2995                 3000

Thr Val  Thr Gly Ser Ser Pro  Asp Ser Leu Ser Leu  Ser Trp Thr
    3005                 3010                 3015

Ile Pro  Gln Gly Arg Phe Asp  Ser Phe Thr Val Gln  Tyr Lys Asp
    3020                 3025                 3030

Arg Asp  Gly Arg Pro Gln Val  Val Arg Val Arg Gly  Glu Glu Ser
    3035                 3040                 3045

Glu Val  Thr Val Gly Gly Leu  Glu Pro Gly Cys Lys  Tyr Lys Met
    3050                 3055                 3060

His Leu  Tyr Gly Leu His Glu  Gly Gln Arg Val Gly  Pro Val Ser
    3065                 3070                 3075

Ala Val  Gly Val Thr Ala Pro  Lys Asp Glu Ala Glu  Thr Thr Gln
    3080                 3085                 3090

Ala Val  Pro Thr Met Thr Pro  Glu Pro Pro Ile Lys  Pro Arg Leu
    3095                 3100                 3105

Gly Glu  Leu Thr Val Thr Asp  Ala Thr Pro Asp Ser  Leu Ser Leu
    3110                 3115                 3120

Ser Trp  Met Val Pro Glu Gly  Gln Phe Asp His Phe  Leu Val Gln
    3125                 3130                 3135

Tyr Arg  Asn Gly Asp Gly Gln  Pro Lys Ala Val Arg  Val Pro Gly
    3140                 3145                 3150

His Glu  Asp Gly Val Thr Ile  Ser Gly Leu Glu Pro  Asp His Lys
    3155                 3160                 3165

Tyr Lys  Met Asn Leu Tyr Gly  Phe His Gly Gly Gln  Arg Val Gly
    3170                 3175                 3180

Pro Val  Ser Ala Ile Gly Val  Thr Glu Glu Glu Thr  Pro Ser Pro
    3185                 3190                 3195

Thr Glu  Pro Ser Thr Glu Ala  Pro Glu Ala Pro Glu  Glu Pro Leu
    3200                 3205                 3210

Leu Gly  Glu Leu Thr Val Thr  Gly Ser Ser Pro Asp  Ser Leu Ser
    3215                 3220                 3225

Leu Ser  Trp Thr Val Pro Gln  Gly Arg Phe Asp Ser  Phe Thr Val
    3230                 3235                 3240

Gln Tyr  Lys Asp Arg Asp Gly  Gln Pro Gln Val Val  Arg Val Arg
    3245                 3250                 3255

Gly Glu  Glu Ser Glu Val Thr  Val Gly Gly Leu Glu  Pro Gly Arg
    3260                 3265                 3270

Lys Tyr  Lys Met His Leu Tyr  Gly Leu His Glu Gly  Gln Arg Val
    3275                 3280                 3285

Gly Pro  Val Ser Thr Val Gly  Ile Thr Ala Pro Leu  Pro Thr Pro
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    3290                3295                3300

Leu Pro  Val Glu Pro Arg Leu  Gly Glu Leu Ala Val  Ala Ala Val
    3305                3310                3315

Thr Ser  Asp Ser Val Gly Leu  Ser Trp Thr Val Ala  Gln Gly Pro
    3320                3325                3330

Phe Asp  Ser Phe Leu Val Gln  Tyr Arg Asp Ala Gln  Gly Gln Pro
    3335                3340                3345

Gln Ala  Val Pro Val Ser Gly  Asp Leu Arg Ala Val  Ala Val Ser
    3350                3355                3360

Gly Leu  Asp Pro Ala Arg Lys  Tyr Lys Phe Leu Leu  Phe Gly Leu
    3365                3370                3375

Gln Asn  Gly Lys Arg His Gly  Pro Val Pro Val Glu  Ala Arg Thr
    3380                3385                3390

Ala Pro  Asp Thr Lys Pro Ser  Pro Arg Leu Gly Glu  Leu Thr Val
    3395                3400                3405

Thr Asp  Ala Thr Pro Asp Ser  Val Gly Leu Ser Trp  Thr Val Pro
    3410                3415                3420

Glu Gly  Glu Phe Asp Ser Phe  Val Val Gln Tyr Lys  Asp Lys Asp
    3425                3430                3435

Gly Arg  Leu Gln Val Val Pro  Val Ala Ala Asn Gln  Arg Glu Val
    3440                3445                3450

Thr Val  Gln Gly Leu Glu Pro  Ser Arg Lys Tyr Arg  Phe Leu Leu
    3455                3460                3465

Tyr Gly  Leu Ser Gly Arg Lys  Arg Leu Gly Pro Ile  Ser Ala Asp
    3470                3475                3480

Ser Thr  Thr Ala Pro Leu Glu  Lys Glu Leu Pro Pro  His Leu Gly
    3485                3490                3495

Glu Leu  Thr Val Ala Glu Glu  Thr Ser Ser Ser Leu  Arg Leu Ser
    3500                3505                3510

Trp Thr  Val Ala Gln Gly Pro  Phe Asp Ser Phe Val  Val Gln Tyr
    3515                3520                3525

Arg Asp  Thr Asp Gly Gln Pro  Arg Ala Val Pro Val  Ala Ala Asp
    3530                3535                3540

Gln Arg  Thr Val Thr Val Glu  Asp Leu Glu Pro Gly  Lys Lys Tyr
    3545                3550                3555

Lys Phe  Leu Leu Tyr Gly Leu  Leu Gly Gly Lys Arg  Leu Gly Pro
    3560                3565                3570

Val Ser  Ala Leu Gly Met Thr  Ala Pro Glu Glu Asp  Thr Pro Ala
    3575                3580                3585

Pro Glu  Leu Ala Pro Glu Ala  Pro Glu Pro Pro Glu  Glu Pro Arg
    3590                3595                3600

Leu Gly  Val Leu Thr Val Thr  Asp Thr Thr Pro Asp  Ser Met Arg
    3605                3610                3615

Leu Ser  Trp Ser Val Ala Gln  Gly Pro Phe Asp Ser  Phe Val Val
    3620                3625                3630

Gln Tyr  Glu Asp Thr Asn Gly  Gln Pro Gln Ala Leu  Leu Val Asp
    3635                3640                3645

Gly Asp  Gln Ser Lys Ile Leu  Ile Ser Gly Leu Glu  Pro Ser Thr
    3650                3655                3660

Pro Tyr  Arg Phe Leu Leu Tyr  Gly Leu His Glu Gly  Lys Arg Leu
    3665                3670                3675
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Gly Pro Leu Ser Ala Glu Gly Thr Thr Gly Leu Ala Pro Ala Gly
3680 3685 3690

Gln Thr Ser Glu Glu Ser Arg Pro Arg Leu Ser Gln Leu Ser Val
3695 3700 3705

Thr Asp Val Thr Thr Ser Ser Leu Arg Leu Asn Trp Glu Ala Pro
3710 3715 3720

Pro Gly Ala Phe Asp Ser Phe Leu Leu Arg Phe Gly Val Pro Ser
3725 3730 3735

Pro Ser Thr Leu Glu Pro His Pro Arg Pro Leu Leu Gln Arg Glu
3740 3745 3750

Leu Met Val Pro Gly Thr Arg His Ser Ala Val Leu Arg Asp Leu
3755 3760 3765

Arg Ser Gly Thr Leu Tyr Ser Leu Thr Leu Tyr Gly Leu Arg Gly
3770 3775 3780

Pro His Lys Ala Asp Ser Ile Gln Gly Thr Ala Arg Thr Leu Ser
3785 3790 3795

Pro Val Leu Glu Ser Pro Arg Asp Leu Gln Phe Ser Glu Ile Arg
3800 3805 3810

Glu Thr Ser Ala Lys Val Asn Trp Met Pro Pro Pro Ser Arg Ala
3815 3820 3825

Asp Ser Phe Lys Val Ser Tyr Gln Leu Ala Asp Gly Gly Glu Pro
3830 3835 3840

Gln Ser Val Gln Val Asp Gly Gln Ala Arg Thr Gln Lys Leu Gln
3845 3850 3855

Gly Leu Ile Pro Gly Ala Arg Tyr Glu Val Thr Val Val Ser Val
3860 3865 3870

Arg Gly Phe Glu Glu Ser Glu Pro Leu Thr Gly Phe Leu Thr Thr
3875 3880 3885

Val Pro Asp Gly Pro Thr Gln Leu Arg Ala Leu Asn Leu Thr Glu
3890 3895 3900

Gly Phe Ala Val Leu His Trp Lys Pro Pro Gln Asn Pro Val Asp
3905 3910 3915

Thr Tyr Asp Val Gln Val Thr Ala Pro Gly Ala Pro Pro Leu Gln
3920 3925 3930

Ala Glu Thr Pro Gly Ser Ala Val Asp Tyr Pro Leu His Asp Leu
3935 3940 3945

Val Leu His Thr Asn Tyr Thr Ala Thr Val Arg Gly Leu Arg Gly
3950 3955 3960

Pro Asn Leu Thr Ser Pro Ala Ser Ile Thr Phe Thr Thr Gly Leu
3965 3970 3975

Glu Ala Pro Arg Asp Leu Glu Ala Lys Glu Val Thr Pro Arg Thr
3980 3985 3990

Ala Leu Leu Thr Trp Thr Glu Pro Pro Val Arg Pro Ala Gly Tyr
3995 4000 4005

Leu Leu Ser Phe His Thr Pro Gly Gly Gln Asn Gln Glu Ile Leu
4010 4015 4020

Leu Pro Gly Gly Ile Thr Ser His Gln Leu Leu Gly Leu Phe Pro
4025 4030 4035

Ser Thr Ser Tyr Asn Ala Arg Leu Gln Ala Met Trp Gly Gln Ser
4040 4045 4050

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Leu Leu  Pro Pro Val Ser Thr  Ser Phe Thr Thr Gly  Gly Leu Arg
    4055                 4060                 4065

Ile Pro  Phe Pro Arg Asp Cys  Gly Glu Glu Met Gln  Asn Gly Ala
    4070                 4075                 4080

Gly Ala  Ser Arg Thr Ser Thr  Ile Phe Leu Asn Gly  Asn Arg Glu
    4085                 4090                 4095

Arg Pro  Leu Asn Val Phe Cys  Asp Met Glu Thr Asp  Gly Gly Gly
    4100                 4105                 4110

Trp Leu  Val Phe Gln Arg Arg  Met Asp Gly Gln Thr  Asp Phe Trp
    4115                 4120                 4125

Arg Asp  Trp Glu Asp Tyr Ala  His Gly Phe Gly Asn  Ile Ser Gly
    4130                 4135                 4140

Glu Phe  Trp Leu Gly Asn Glu  Ala Leu His Ser Leu  Thr Gln Ala
    4145                 4150                 4155

Gly Asp  Tyr Ser Met Arg Val  Asp Leu Arg Ala Gly  Asp Glu Ala
    4160                 4165                 4170

Val Phe  Ala Gln Tyr Asp Ser  Phe His Val Asp Ser  Ala Ala Glu
    4175                 4180                 4185

Tyr Tyr  Arg Leu His Leu Glu  Gly Tyr His Gly Thr  Ala Gly Asp
    4190                 4195                 4200

Ser Met  Ser Tyr His Ser Gly  Ser Val Phe Ser Ala  Arg Asp Arg
    4205                 4210                 4215

Asp Pro  Asn Ser Leu Leu Ile  Ser Cys Ala Val Ser  Tyr Arg Gly
    4220                 4225                 4230

Ala Trp  Trp Tyr Arg Asn Cys  His Tyr Ala Asn Leu  Asn Gly Leu
    4235                 4240                 4245

Tyr Gly  Ser Thr Val Asp His  Gln Gly Val Ser Trp  Tyr His Trp
    4250                 4255                 4260

Lys Gly  Phe Glu Phe Ser Val  Pro Phe Thr Glu Met  Lys Leu Arg
    4265                 4270                 4275

Pro Arg  Asn Phe Arg Ser Pro  Ala Gly Gly Gly
    4280                 4285


<210> SEQ ID NO 23
<211> LENGTH: 1712
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

Met Gly Arg Asp Gln Arg Ala Val Ala Gly Pro Ala Leu Arg Arg Trp
1               5                   10                  15

Leu Leu Leu Gly Thr Val Thr Val Gly Phe Leu Ala Gln Ser Val Leu
            20                  25                  30

Ala Gly Val Lys Lys Phe Asp Val Pro Cys Gly Gly Arg Asp Cys Ser
        35                  40                  45

Gly Gly Cys Gln Cys Tyr Pro Glu Lys Gly Gly Arg Gly Gln Pro Gly
    50                  55                  60

Pro Val Gly Pro Gln Gly Tyr Asn Gly Pro Pro Gly Leu Gln Gly Phe
65                  70                  75                  80

Pro Gly Leu Gln Gly Arg Lys Gly Asp Lys Gly Glu Arg Gly Ala Pro
                85                  90                  95

Gly Val Thr Gly Pro Lys Gly Asp Val Gly Ala Arg Gly Val Ser Gly
            100                 105                 110
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Phe Pro Gly Ala Asp Gly Ile Pro Gly His Pro Gly Gln Gly Gly Pro
        115                 120                 125

Arg Gly Arg Pro Gly Tyr Asp Gly Cys Asn Gly Thr Gln Gly Asp Ser
    130                 135                 140

Gly Pro Gln Gly Pro Pro Gly Ser Glu Gly Phe Thr Gly Pro Pro Gly
145                 150                 155                 160

Pro Gln Gly Pro Lys Gly Gln Lys Gly Glu Pro Tyr Ala Leu Pro Lys
                165                 170                 175

Glu Glu Arg Asp Arg Tyr Arg Gly Glu Pro Gly Glu Pro Gly Leu Val
            180                 185                 190

Gly Phe Gln Gly Pro Pro Gly Arg Pro Gly His Val Gly Gln Met Gly
        195                 200                 205

Pro Val Gly Ala Pro Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Pro
    210                 215                 220

Lys Gly Gln Gln Gly Asn Arg Gly Leu Gly Phe Tyr Gly Val Lys Gly
225                 230                 235                 240

Glu Lys Gly Asp Val Gly Gln Pro Gly Pro Asn Gly Ile Pro Ser Asp
                245                 250                 255

Thr Leu His Pro Ile Ile Ala Pro Thr Gly Val Thr Phe His Pro Asp
            260                 265                 270

Gln Tyr Lys Gly Glu Lys Gly Ser Glu Gly Glu Pro Gly Ile Arg Gly
        275                 280                 285

Ile Ser Leu Lys Gly Glu Glu Gly Ile Met Gly Phe Pro Gly Leu Arg
    290                 295                 300

Gly Tyr Pro Gly Leu Ser Gly Glu Lys Gly Ser Pro Gly Gln Lys Gly
305                 310                 315                 320

Ser Arg Gly Leu Asp Gly Tyr Gln Gly Pro Asp Gly Pro Arg Gly Pro
                325                 330                 335

Lys Gly Glu Ala Gly Asp Pro Gly Pro Pro Gly Leu Pro Ala Tyr Ser
            340                 345                 350

Pro His Pro Ser Leu Ala Lys Gly Ala Arg Gly Asp Pro Gly Phe Pro
        355                 360                 365

Gly Ala Gln Gly Glu Pro Gly Ser Gln Gly Glu Pro Gly Asp Pro Gly
    370                 375                 380

Leu Pro Gly Pro Pro Gly Leu Ser Ile Gly Asp Gly Asp Gln Arg Arg
385                 390                 395                 400

Gly Leu Pro Gly Glu Met Gly Pro Lys Gly Phe Ile Gly Asp Pro Gly
                405                 410                 415

Ile Pro Ala Leu Tyr Gly Gly Pro Pro Gly Pro Asp Gly Lys Arg Gly
            420                 425                 430

Pro Pro Gly Pro Pro Gly Leu Pro Gly Pro Pro Gly Pro Asp Gly Phe
        435                 440                 445

Leu Phe Gly Leu Lys Gly Ala Lys Gly Arg Ala Gly Phe Pro Gly Leu
    450                 455                 460

Pro Gly Ser Pro Gly Ala Arg Gly Pro Lys Gly Trp Lys Gly Asp Ala
465                 470                 475                 480

Gly Glu Cys Arg Cys Thr Glu Gly Asp Glu Ala Ile Lys Gly Leu Pro
                485                 490                 495

Gly Leu Pro Gly Pro Lys Gly Phe Ala Gly Ile Asn Gly Glu Pro Gly
            500                 505                 510
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Arg Lys Gly Asp Arg Gly Asp Pro Gly Gln His Gly Leu Pro Gly Phe
        515                 520                 525

Pro Gly Leu Lys Gly Val Pro Gly Asn Ile Gly Ala Pro Gly Pro Lys
    530                 535                 540

Gly Ala Lys Gly Asp Ser Arg Thr Ile Thr Thr Lys Gly Glu Arg Gly
545                 550                 555                 560

Gln Pro Gly Val Pro Gly Val Pro Gly Met Lys Gly Asp Asp Gly Ser
                565                 570                 575

Pro Gly Arg Asp Gly Leu Asp Gly Phe Pro Gly Leu Pro Gly Pro Pro
            580                 585                 590

Gly Asp Gly Ile Lys Gly Pro Pro Gly Asp Pro Gly Tyr Pro Gly Ile
        595                 600                 605

Pro Gly Thr Lys Gly Thr Pro Gly Glu Met Gly Pro Pro Gly Leu Gly
    610                 615                 620

Leu Pro Gly Leu Lys Gly Gln Arg Gly Phe Pro Gly Asp Ala Gly Leu
625                 630                 635                 640

Pro Gly Pro Pro Gly Phe Leu Gly Pro Pro Gly Pro Ala Gly Thr Pro
                645                 650                 655

Gly Gln Ile Asp Cys Asp Thr Asp Val Lys Arg Ala Val Gly Gly Asp
            660                 665                 670

Arg Gln Glu Ala Ile Gln Pro Gly Cys Ile Gly Gly Pro Lys Gly Leu
        675                 680                 685

Pro Gly Leu Pro Gly Pro Pro Gly Pro Thr Gly Ala Lys Gly Leu Arg
    690                 695                 700

Gly Ile Pro Gly Phe Ala Gly Ala Asp Gly Gly Pro Gly Pro Arg Gly
705                 710                 715                 720

Leu Pro Gly Asp Ala Gly Arg Glu Gly Phe Pro Gly Pro Pro Gly Phe
                725                 730                 735

Ile Gly Pro Arg Gly Ser Lys Gly Ala Val Gly Leu Pro Gly Pro Asp
            740                 745                 750

Gly Ser Pro Gly Pro Ile Gly Leu Pro Gly Pro Asp Gly Pro Pro Gly
        755                 760                 765

Glu Arg Gly Leu Pro Gly Glu Val Leu Gly Ala Gln Pro Gly Pro Arg
    770                 775                 780

Gly Asp Ala Gly Val Pro Gly Gln Pro Gly Leu Lys Gly Leu Pro Gly
785                 790                 795                 800

Asp Arg Gly Pro Pro Gly Phe Arg Gly Ser Gln Gly Met Pro Gly Met
                805                 810                 815

Pro Gly Leu Lys Gly Gln Pro Gly Leu Pro Gly Pro Ser Gly Gln Pro
            820                 825                 830

Gly Leu Tyr Gly Pro Pro Gly Leu His Gly Phe Pro Gly Ala Pro Gly
        835                 840                 845

Gln Glu Gly Pro Leu Gly Leu Pro Gly Ile Pro Gly Arg Glu Gly Leu
    850                 855                 860

Pro Gly Asp Arg Gly Asp Pro Gly Asp Thr Gly Ala Pro Gly Pro Val
865                 870                 875                 880

Gly Met Lys Gly Leu Ser Gly Asp Arg Gly Asp Ala Gly Phe Thr Gly
                885                 890                 895

Glu Gln Gly His Pro Gly Ser Pro Gly Phe Lys Gly Ile Asp Gly Met
            900                 905                 910

Pro Gly Thr Pro Gly Leu Lys Gly Asp Arg Gly Ser Pro Gly Met Asp
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        915                 920                 925

Gly Phe Gln Gly Met Pro Gly Leu Lys Gly Arg Pro Gly Phe Pro Gly
    930                 935                 940

Ser Lys Gly Glu Ala Gly Phe Phe Gly Ile Pro Gly Leu Lys Gly Leu
945                 950                 955                 960

Ala Gly Glu Pro Gly Phe Lys Gly Ser Arg Gly Asp Pro Gly Pro Pro
                965                 970                 975

Gly Pro Pro Pro Val Ile Leu Pro Gly Met Lys Asp Ile Lys Gly Glu
            980                 985                 990

Lys Gly Asp Glu Gly Pro Met Gly  Leu Lys Gly Tyr Leu  Gly Ala Lys
        995                 1000                 1005

Gly Ile  Gln Gly Met Pro Gly  Ile Pro Gly Leu Ser  Gly Ile Pro
    1010                 1015                 1020

Gly Leu  Pro Gly Arg Pro Gly  His Ile Lys Gly Val  Lys Gly Asp
    1025                 1030                 1035

Ile Gly  Val Pro Gly Ile Pro  Gly Leu Pro Gly Phe  Pro Gly Val
    1040                 1045                 1050

Ala Gly  Pro Pro Gly Ile Thr  Gly Phe Pro Gly Phe  Ile Gly Ser
    1055                 1060                 1065

Arg Gly  Asp Lys Gly Ala Pro  Gly Arg Ala Gly Leu  Tyr Gly Glu
    1070                 1075                 1080

Ile Gly  Ala Thr Gly Asp Phe  Gly Asp Ile Gly Asp  Thr Ile Asn
    1085                 1090                 1095

Leu Pro  Gly Arg Pro Gly Leu  Lys Gly Glu Arg Gly  Thr Thr Gly
    1100                 1105                 1110

Ile Pro  Gly Leu Lys Gly Phe  Phe Gly Glu Lys Gly  Thr Glu Gly
    1115                 1120                 1125

Asp Ile  Gly Phe Pro Gly Ile  Thr Gly Val Thr Gly  Val Gln Gly
    1130                 1135                 1140

Pro Pro  Gly Leu Lys Gly Gln  Thr Gly Phe Pro Gly  Leu Thr Gly
    1145                 1150                 1155

Pro Pro  Gly Ser Gln Gly Glu  Leu Gly Arg Ile Gly  Leu Pro Gly
    1160                 1165                 1170

Gly Lys  Gly Asp Asp Gly Trp  Pro Gly Ala Pro Gly  Leu Pro Gly
    1175                 1180                 1185

Phe Pro  Gly Leu Arg Gly Ile  Arg Gly Leu His Gly  Leu Pro Gly
    1190                 1195                 1200

Thr Lys  Gly Phe Pro Gly Ser  Pro Gly Ser Asp Ile  His Gly Asp
    1205                 1210                 1215

Pro Gly  Phe Pro Gly Pro Pro  Gly Glu Arg Gly Asp  Pro Gly Glu
    1220                 1225                 1230

Ala Asn  Thr Leu Pro Gly Pro  Val Gly Val Pro Gly  Gln Lys Gly
    1235                 1240                 1245

Asp Gln  Gly Ala Pro Gly Glu  Arg Gly Pro Pro Gly  Ser Pro Gly
    1250                 1255                 1260

Leu Gln  Gly Phe Pro Gly Ile  Thr Pro Pro Ser Asn  Ile Ser Gly
    1265                 1270                 1275

Ala Pro  Gly Asp Lys Gly Ala  Pro Gly Ile Phe Gly  Leu Lys Gly
    1280                 1285                 1290

Tyr Arg  Gly Pro Pro Gly Pro  Pro Gly Ser Ala Ala  Leu Pro Gly
    1295                 1300                 1305
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Ser Lys  Gly Asp Thr Gly Asn  Pro Gly Ala Pro Gly  Thr Pro Gly
    1310                 1315                 1320

Thr Lys  Gly Trp Ala Gly Asp  Ser Gly Pro Gln Gly  Arg Pro Gly
    1325                 1330                 1335

Val Phe  Gly Leu Pro Gly Glu  Lys Gly Pro Arg Gly  Glu Gln Gly
    1340                 1345                 1350

Phe Met  Gly Asn Thr Gly Pro  Thr Gly Ala Val Gly  Asp Arg Gly
    1355                 1360                 1365

Pro Lys  Gly Pro Lys Gly Asp  Pro Gly Phe Pro Gly  Ala Pro Gly
    1370                 1375                 1380

Thr Val  Gly Ala Pro Gly Ile  Ala Gly Ile Pro Gln  Lys Ile Ala
    1385                 1390                 1395

Val Gln  Pro Gly Thr Val Gly  Pro Gln Gly Arg Arg  Gly Pro Pro
    1400                 1405                 1410

Gly Ala  Pro Gly Glu Met Gly  Pro Gln Gly Pro Pro  Gly Glu Pro
    1415                 1420                 1425

Gly Phe  Arg Gly Ala Pro Gly  Lys Ala Gly Pro Gln  Gly Arg Gly
    1430                 1435                 1440

Gly Val  Ser Ala Val Pro Gly  Phe Arg Gly Asp Glu  Gly Pro Ile
    1445                 1450                 1455

Gly His  Gln Gly Pro Ile Gly  Gln Glu Gly Ala Pro  Gly Arg Pro
    1460                 1465                 1470

Gly Ser  Pro Gly Leu Pro Gly  Met Pro Gly Arg Ser  Val Ser Ile
    1475                 1480                 1485

Gly Tyr  Leu Leu Val Lys His  Ser Gln Thr Asp Gln  Glu Pro Met
    1490                 1495                 1500

Cys Pro  Val Gly Met Asn Lys  Leu Trp Ser Gly Tyr  Ser Leu Leu
    1505                 1510                 1515

Tyr Phe  Glu Gly Gln Glu Lys  Ala His Asn Gln Asp  Leu Gly Leu
    1520                 1525                 1530

Ala Gly  Ser Cys Leu Ala Arg  Phe Ser Thr Met Pro  Phe Leu Tyr
    1535                 1540                 1545

Cys Asn  Pro Gly Asp Val Cys  Tyr Tyr Ala Ser Arg  Asn Asp Lys
    1550                 1555                 1560

Ser Tyr  Trp Leu Ser Thr Thr  Ala Pro Leu Pro Met  Met Pro Val
    1565                 1570                 1575

Ala Glu  Asp Glu Ile Lys Pro  Tyr Ile Ser Arg Cys  Ser Val Cys
    1580                 1585                 1590

Glu Ala  Pro Ala Ile Ala Ile  Ala Val His Ser Gln  Asp Val Ser
    1595                 1600                 1605

Ile Pro  His Cys Pro Ala Gly  Trp Arg Ser Leu Trp  Ile Gly Tyr
    1610                 1615                 1620

Ser Phe  Leu Met His Thr Ala  Ala Gly Asp Glu Gly  Gly Gly Gln
    1625                 1630                 1635

Ser Leu  Val Ser Pro Gly Ser  Cys Leu Glu Asp Phe  Arg Ala Thr
    1640                 1645                 1650

Pro Phe  Ile Glu Cys Asn Gly  Gly Arg Gly Thr Cys  His Tyr Tyr
    1655                 1660                 1665

Ala Asn  Lys Tyr Ser Phe Trp  Leu Thr Thr Ile Pro  Glu Gln Ser
    1670                 1675                 1680
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Phe Gln  Gly Ser Pro Ser Ala  Asp Thr Leu Lys Ala  Gly Leu Ile
    1685                 1690                 1695

Arg Thr  His Ile Ser Arg Cys  Gln Val Cys Met Lys  Asn Leu
    1700                 1705                 1710


<210> SEQ ID NO 24
<211> LENGTH: 1691
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

Met Lys Leu Arg Gly Val Ser Leu Ala Ala Gly Leu Phe Leu Leu Ala
1               5                   10                  15

Leu Ser Leu Trp Gly Gln Pro Ala Glu Ala Ala Ala Cys Tyr Gly Cys
            20                  25                  30

Ser Pro Gly Ser Lys Cys Asp Cys Ser Gly Ile Lys Gly Glu Lys Gly
        35                  40                  45

Glu Arg Gly Phe Pro Gly Leu Glu Gly His Pro Gly Leu Pro Gly Phe
    50                  55                  60

Pro Gly Pro Glu Gly Pro Pro Gly Pro Arg Gly Gln Lys Gly Asp Asp
65                  70                  75                  80

Gly Ile Pro Gly Pro Pro Gly Pro Lys Gly Ile Arg Gly Pro Pro Gly
                85                  90                  95

Leu Pro Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Met Pro Gly His
            100                 105                 110

Asp Gly Ala Pro Gly Pro Gln Gly Ile Pro Gly Cys Asn Gly Thr Lys
        115                 120                 125

Gly Glu Arg Gly Phe Pro Gly Ser Pro Gly Phe Pro Gly Leu Gln Gly
    130                 135                 140

Pro Pro Gly Pro Pro Gly Ile Pro Gly Met Lys Gly Glu Pro Gly Ser
145                 150                 155                 160

Ile Ile Met Ser Ser Leu Pro Gly Pro Lys Gly Asn Pro Gly Tyr Pro
                165                 170                 175

Gly Pro Pro Gly Ile Gln Gly Leu Pro Gly Pro Thr Gly Ile Pro Gly
            180                 185                 190

Pro Ile Gly Pro Pro Gly Pro Pro Gly Leu Met Gly Pro Pro Gly Pro
        195                 200                 205

Pro Gly Leu Pro Gly Pro Lys Gly Asn Met Gly Leu Asn Phe Gln Gly
    210                 215                 220

Pro Lys Gly Glu Lys Gly Glu Gln Gly Leu Gln Gly Pro Pro Gly Pro
225                 230                 235                 240

Pro Gly Gln Ile Ser Glu Gln Lys Arg Pro Ile Asp Val Glu Phe Gln
                245                 250                 255

Lys Gly Asp Gln Gly Leu Pro Gly Asp Arg Gly Pro Pro Gly Pro Pro
            260                 265                 270

Gly Ile Arg Gly Pro Pro Gly Pro Pro Gly Gly Glu Lys Gly Glu Lys
        275                 280                 285

Gly Glu Gln Gly Glu Pro Gly Lys Arg Gly Lys Pro Gly Lys Asp Gly
    290                 295                 300

Glu Asn Gly Gln Pro Gly Ile Pro Gly Leu Pro Gly Asp Pro Gly Tyr
305                 310                 315                 320

Pro Gly Glu Pro Gly Arg Asp Gly Glu Lys Gly Gln Lys Gly Asp Thr
                325                 330                 335
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Gly Pro Pro Gly Pro Pro Gly Leu Val Ile Pro Arg Pro Gly Thr Gly
            340                 345                 350

Ile Thr Ile Gly Glu Lys Gly Asn Ile Gly Leu Pro Gly Leu Pro Gly
        355                 360                 365

Glu Lys Gly Glu Arg Gly Phe Pro Gly Ile Gln Gly Pro Pro Gly Leu
    370                 375                 380

Pro Gly Pro Pro Gly Ala Ala Val Met Gly Pro Pro Gly Pro Pro Gly
385                 390                 395                 400

Phe Pro Gly Glu Arg Gly Gln Lys Gly Asp Glu Gly Pro Pro Gly Ile
                405                 410                 415

Ser Ile Pro Gly Pro Pro Gly Leu Asp Gly Gln Pro Gly Ala Pro Gly
            420                 425                 430

Leu Pro Gly Pro Pro Gly Pro Ala Gly Pro His Ile Pro Pro Ser Asp
        435                 440                 445

Glu Ile Cys Glu Pro Gly Pro Pro Gly Pro Pro Gly Ser Pro Gly Asp
    450                 455                 460

Lys Gly Leu Gln Gly Glu Gln Gly Val Lys Gly Asp Lys Gly Asp Thr
465                 470                 475                 480

Cys Phe Asn Cys Ile Gly Thr Gly Ile Ser Gly Pro Pro Gly Gln Pro
                485                 490                 495

Gly Leu Pro Gly Leu Pro Gly Pro Pro Gly Ser Leu Gly Phe Pro Gly
            500                 505                 510

Gln Lys Gly Glu Lys Gly Gln Ala Gly Ala Thr Gly Pro Lys Gly Leu
        515                 520                 525

Pro Gly Ile Pro Gly Ala Pro Gly Ala Pro Gly Phe Pro Gly Ser Lys
    530                 535                 540

Gly Glu Pro Gly Asp Ile Leu Thr Phe Pro Gly Met Lys Gly Asp Lys
545                 550                 555                 560

Gly Glu Leu Gly Ser Pro Gly Ala Pro Gly Leu Pro Gly Leu Pro Gly
                565                 570                 575

Thr Pro Gly Gln Asp Gly Leu Pro Gly Leu Pro Gly Pro Lys Gly Glu
            580                 585                 590

Pro Gly Gly Ile Thr Phe Lys Gly Glu Arg Gly Pro Pro Gly Asn Pro
        595                 600                 605

Gly Leu Pro Gly Leu Pro Gly Asn Ile Gly Pro Met Gly Pro Pro Gly
    610                 615                 620

Phe Gly Pro Pro Gly Pro Val Gly Glu Lys Gly Ile Gln Gly Val Ala
625                 630                 635                 640

Gly Asn Pro Gly Gln Pro Gly Ile Pro Gly Pro Lys Gly Asp Pro Gly
                645                 650                 655

Gln Thr Ile Thr Gln Pro Gly Lys Pro Gly Leu Pro Gly Asn Pro Gly
            660                 665                 670

Arg Asp Gly Asp Val Gly Leu Pro Gly Asp Pro Gly Leu Pro Gly Gln
        675                 680                 685

Pro Gly Leu Pro Gly Ile Pro Gly Ser Lys Gly Glu Pro Gly Ile Pro
    690                 695                 700

Gly Ile Gly Leu Pro Gly Pro Pro Gly Pro Lys Gly Phe Pro Gly Ile
705                 710                 715                 720

Pro Gly Pro Pro Gly Ala Pro Gly Thr Pro Gly Arg Ile Gly Leu Glu
                725                 730                 735
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Gly Pro Pro Gly Pro Pro Gly Phe Pro Gly Pro Lys Gly Glu Pro Gly
            740                 745                 750

Phe Ala Leu Pro Gly Pro Pro Gly Pro Pro Gly Leu Pro Gly Phe Lys
        755                 760                 765

Gly Ala Leu Gly Pro Lys Gly Asp Arg Gly Phe Pro Gly Pro Pro Gly
    770                 775                 780

Pro Pro Gly Arg Thr Gly Leu Asp Gly Leu Pro Gly Pro Lys Gly Asp
785                 790                 795                 800

Val Gly Pro Asn Gly Gln Pro Gly Pro Met Gly Pro Pro Gly Leu Pro
                805                 810                 815

Gly Ile Gly Val Gln Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly Pro
            820                 825                 830

Ile Gly Gln Pro Gly Leu His Gly Ile Pro Gly Glu Lys Gly Asp Pro
        835                 840                 845

Gly Pro Pro Gly Leu Asp Val Pro Gly Pro Pro Gly Glu Arg Gly Ser
    850                 855                 860

Pro Gly Ile Pro Gly Ala Pro Gly Pro Ile Gly Pro Pro Gly Ser Pro
865                 870                 875                 880

Gly Leu Pro Gly Lys Ala Gly Ala Ser Gly Phe Pro Gly Thr Lys Gly
                885                 890                 895

Glu Met Gly Met Met Gly Pro Pro Gly Pro Pro Gly Pro Leu Gly Ile
            900                 905                 910

Pro Gly Arg Ser Gly Val Pro Gly Leu Lys Gly Asp Asp Gly Leu Gln
        915                 920                 925

Gly Gln Pro Gly Leu Pro Gly Pro Thr Gly Glu Lys Gly Ser Lys Gly
    930                 935                 940

Glu Pro Gly Leu Pro Gly Pro Pro Gly Pro Met Asp Pro Asn Leu Leu
945                 950                 955                 960

Gly Ser Lys Gly Glu Lys Gly Glu Pro Gly Leu Pro Gly Ile Pro Gly
                965                 970                 975

Val Ser Gly Pro Lys Gly Tyr Gln Gly Leu Pro Gly Asp Pro Gly Gln
            980                 985                 990

Pro Gly Leu Ser Gly Gln Pro Gly  Leu Pro Gly Pro Pro  Gly Pro Lys
        995                 1000                 1005

Gly Asn  Pro Gly Leu Pro Gly  Gln Pro Gly Leu Ile  Gly Pro Pro
    1010                 1015                 1020

Gly Leu  Lys Gly Thr Ile Gly  Asp Met Gly Phe Pro  Gly Pro Gln
    1025                 1030                 1035

Gly Val  Glu Gly Pro Pro Gly  Pro Ser Gly Val Pro  Gly Gln Pro
    1040                 1045                 1050

Gly Ser  Pro Gly Leu Pro Gly  Gln Lys Gly Asp Lys  Gly Asp Pro
    1055                 1060                 1065

Gly Ile  Ser Ser Ile Gly Leu  Pro Gly Leu Pro Gly  Pro Lys Gly
    1070                 1075                 1080

Glu Pro  Gly Leu Pro Gly Tyr  Pro Gly Asn Pro Gly  Ile Lys Gly
    1085                 1090                 1095

Ser Val  Gly Asp Pro Gly Leu  Pro Gly Leu Pro Gly  Thr Pro Gly
    1100                 1105                 1110

Ala Lys  Gly Gln Pro Gly Leu  Pro Gly Phe Pro Gly  Thr Pro Gly
    1115                 1120                 1125

Pro Pro  Gly Pro Lys Gly Ile  Ser Gly Pro Pro Gly  Asn Pro Gly
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1130 1135 1140

Leu Pro Gly Glu Pro Gly Pro Val Gly Gly Gly Gly His Pro Gly
1145 1150 1155

Gln Pro Gly Pro Pro Gly Glu Lys Gly Lys Pro Gly Gln Asp Gly
1160 1165 1170

Ile Pro Gly Pro Ala Gly Gln Lys Gly Glu Pro Gly Gln Pro Gly
1175 1180 1185

Phe Gly Asn Pro Gly Pro Pro Gly Leu Pro Gly Leu Ser Gly Gln
1190 1195 1200

Lys Gly Asp Gly Gly Leu Pro Gly Ile Pro Gly Asn Pro Gly Leu
1205 1210 1215

Pro Gly Pro Lys Gly Glu Pro Gly Phe His Gly Phe Pro Gly Val
1220 1225 1230

Gln Gly Pro Pro Gly Pro Pro Gly Ser Pro Gly Pro Ala Leu Glu
1235 1240 1245

Gly Pro Lys Gly Asn Pro Gly Pro Gln Gly Pro Pro Gly Arg Pro
1250 1255 1260

Gly Pro Thr Gly Phe Gln Gly Leu Pro Gly Pro Glu Gly Pro Pro
1265 1270 1275

Gly Leu Pro Gly Asn Gly Gly Ile Lys Gly Glu Lys Gly Asn Pro
1280 1285 1290

Gly Gln Pro Gly Leu Pro Gly Leu Pro Gly Leu Lys Gly Asp Gln
1295 1300 1305

Gly Pro Pro Gly Leu Gln Gly Asn Pro Gly Arg Pro Gly Leu Asn
1310 1315 1320

Gly Met Lys Gly Asp Pro Gly Leu Pro Gly Val Pro Gly Phe Pro
1325 1330 1335

Gly Met Lys Gly Pro Ser Gly Val Pro Gly Ser Ala Gly Pro Glu
1340 1345 1350

Gly Glu Pro Gly Leu Ile Gly Pro Pro Gly Pro Pro Gly Leu Pro
1355 1360 1365

Gly Pro Ser Gly Gln Ser Ile Ile Ile Lys Gly Asp Ala Gly Pro
1370 1375 1380

Pro Gly Ile Pro Gly Gln Pro Gly Leu Lys Gly Leu Pro Gly Pro
1385 1390 1395

Gln Gly Pro Gln Gly Leu Pro Gly Pro Thr Gly Pro Pro Gly Asp
1400 1405 1410

Pro Gly Arg Asn Gly Leu Pro Gly Phe Asp Gly Ala Gly Gly Arg
1415 1420 1425

Lys Gly Asp Pro Gly Leu Pro Gly Gln Pro Gly Thr Arg Gly Leu
1430 1435 1440

Asp Gly Pro Pro Gly Pro Asp Gly Leu Gln Gly Pro Pro Gly Pro
1445 1450 1455

Pro Gly Thr Ser Ser Val Ala His Gly Phe Leu Ile Thr Arg His
1460 1465 1470

Ser Gln Thr Thr Asp Ala Pro Gln Cys Pro Gln Gly Thr Leu Gln
1475 1480 1485

Val Tyr Glu Gly Phe Ser Leu Leu Tyr Val Gln Gly Asn Lys Arg
1490 1495 1500

Ala His Gly Gln Asp Leu Gly Thr Ala Gly Ser Cys Leu Arg Arg
1505 1510 1515

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Phe Ser  Thr Met Pro Phe Met  Phe Cys Asn Ile Asn  Asn Val Cys
    1520                 1525                 1530

Asn Phe  Ala Ser Arg Asn Asp  Tyr Ser Tyr Trp Leu  Ser Thr Pro
    1535                 1540                 1545

Glu Pro  Met Pro Met Ser Met  Gln Pro Leu Lys Gly  Gln Ser Ile
    1550                 1555                 1560

Gln Pro  Phe Ile Ser Arg Cys  Ala Val Cys Glu Ala  Pro Ala Val
    1565                 1570                 1575

Val Ile  Ala Val His Ser Gln  Thr Ile Gln Ile Pro  His Cys Pro
    1580                 1585                 1590

Gln Gly  Trp Asp Ser Leu Trp  Ile Gly Tyr Ser Phe  Met Met His
    1595                 1600                 1605

Thr Ser  Ala Gly Ala Glu Gly  Ser Gly Gln Ala Leu  Ala Ser Pro
    1610                 1615                 1620

Gly Ser  Cys Leu Glu Glu Phe  Arg Ser Ala Pro Phe  Ile Glu Cys
    1625                 1630                 1635

His Gly  Arg Gly Thr Cys Asn  Tyr Tyr Ala Asn Ser  Tyr Ser Phe
    1640                 1645                 1650

Trp Leu  Ala Thr Val Asp Val  Ser Asp Met Phe Ser  Lys Pro Gln
    1655                 1660                 1665

Ser Glu  Thr Leu Lys Ala Gly  Asp Leu Arg Thr Arg  Ile Ser Arg
    1670                 1675                 1680

Cys Gln  Val Cys Met Lys Arg  Thr
    1685                 1690


<210> SEQ ID NO 25
<211> LENGTH: 730
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

Met Ala Gly Leu Thr Ala Ala Ala Pro Arg Pro Gly Val Leu Leu Leu
1               5                   10                  15

Leu Leu Ser Ile Leu His Pro Ser Arg Pro Gly Gly Val Pro Gly Ala
            20                  25                  30

Ile Pro Gly Gly Val Pro Gly Gly Val Phe Tyr Pro Gly Ala Gly Leu
        35                  40                  45

Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro Gly Gly Lys Pro Leu Lys
    50                  55                  60

Pro Val Pro Gly Gly Leu Ala Gly Ala Gly Leu Gly Ala Gly Leu Gly
65                  70                  75                  80

Ala Phe Pro Ala Val Thr Phe Pro Gly Ala Leu Val Pro Gly Gly Val
                85                  90                  95

Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala Lys Ala Gly Ala Gly Leu
            100                 105                 110

Gly Gly Val Pro Gly Val Gly Gly Leu Gly Val Ser Ala Gly Ala Val
        115                 120                 125

Val Pro Gln Pro Gly Ala Gly Val Lys Pro Gly Lys Val Pro Gly Val
    130                 135                 140

Gly Leu Pro Gly Val Tyr Pro Gly Gly Val Leu Pro Gly Ala Arg Phe
145                 150                 155                 160

Pro Gly Val Gly Val Leu Pro Gly Val Pro Thr Gly Ala Gly Val Lys
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                165                 170                 175

Pro Lys Ala Pro Gly Val Gly Gly Ala Phe Ala Gly Ile Pro Gly Val
            180                 185                 190

Gly Pro Phe Gly Gly Pro Gln Pro Gly Val Pro Leu Gly Tyr Pro Ile
        195                 200                 205

Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly Leu Pro Tyr Thr Thr Gly
    210                 215                 220

Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly Val Ala Gly Ala Ala Gly
225                 230                 235                 240

Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val Gly Pro Gln Ala Ala Ala
                245                 250                 255

Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe Gly Ala Gly Ala Ala Gly
            260                 265                 270

Val Leu Pro Gly Val Gly Gly Ala Gly Val Pro Gly Val Pro Gly Ala
        275                 280                 285

Ile Pro Gly Ile Gly Gly Ile Ala Gly Val Gly Thr Pro Ala Ala Ala
    290                 295                 300

Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Ala
305                 310                 315                 320

Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val Val Gly Val
                325                 330                 335

Pro Gly Ala Gly Val Pro Gly Val Gly Val Pro Gly Ala Gly Ile Pro
            340                 345                 350

Val Val Pro Gly Ala Gly Ile Pro Gly Ala Ala Val Pro Gly Val Val
        355                 360                 365

Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys Tyr Gly
    370                 375                 380

Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly Val Gly
385                 390                 395                 400

Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile Pro Gly
                405                 410                 415

Val Ala Gly Val Pro Ser Val Gly Gly Val Pro Gly Val Gly Gly Val
            420                 425                 430

Pro Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala Ala Ala Lys
        435                 440                 445

Ala Ala Lys Tyr Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Lys Ala
    450                 455                 460

Ala Ala Lys Ala Ala Gln Phe Ala Leu Leu Asn Leu Ala Gly Leu Val
465                 470                 475                 480

Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly
                485                 490                 495

Val Ala Pro Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala Pro Gly
            500                 505                 510

Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly
        515                 520                 525

Gly Val Ala Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala
    530                 535                 540

Gln Leu Arg Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly
545                 550                 555                 560

Val Gly Val Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly
                565                 570                 575
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Leu Gly Val Gly Ala Gly Val Pro Gly Phe Gly Ala Val Pro Gly Ala
            580                 585                 590

Leu Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val
        595                 600                 605

Leu Gly Gly Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val
    610                 615                 620

Val Gly Ala Gly Pro Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala
625                 630                 635                 640

Lys Ala Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu
                645                 650                 655

Gly Val Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile
            660                 665                 670

Pro Pro Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu
        675                 680                 685

Gly Gly Val Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala
    690                 695                 700

Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys
705                 710                 715                 720

Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys
                725                 730


<210> SEQ ID NO 26
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 26

Thr Gly Gly Ile Ser Val Pro Gly Pro Met Gly Pro Ser Gly Pro Arg
1               5                   10                  15


<210> SEQ ID NO 27
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 27

Gly Leu Pro Gly Pro Pro Gly Ala Pro Gly Pro Gln Gly
1               5                   10


<210> SEQ ID NO 28
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 28

Gly Leu Pro Gly Pro Pro Gly Ala Pro Gly Pro Gln Gly Phe
1               5                   10


<210> SEQ ID NO 29
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 29

Pro Gly Glu Pro Gly Glu Pro Gly Ala Ser Gly Pro Met Gly Pro Arg
1               5                   10                  15

Gly Pro Pro Gly Pro Pro Gly Lys
            20


<210> SEQ ID NO 30
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 30

Gly Ala Ser Gly Pro Met Gly Pro Arg Gly Pro Pro Gly Pro Pro Gly
1               5                   10                  15

Lys


<210> SEQ ID NO 31
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 31

Lys Pro Gly Arg Pro Gly Glu Arg Gly Pro Pro Gly Pro Gln Gly Ala
1               5                   10                  15

Arg


<210> SEQ ID NO 32
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 32

Gly Pro Pro Gly Pro Gln Gly Ala Arg Gly Leu Pro Gly Thr Ala Gly
1               5                   10                  15

Leu Pro Gly Met
            20


<210> SEQ ID NO 33
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 33

Ala Gly Pro Gln Gly Pro Arg
1               5


<210> SEQ ID NO 34
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence
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```
<400> SEQUENCE: 34

Gly Ala Pro Gly Ile Ala Gly Ala Pro Gly Phe Pro Gly Ala Arg
1               5                   10                  15


<210> SEQ ID NO 35
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 35

Pro Gly Ile Ala Gly Ala Pro Gly Phe Pro Gly Ala Arg Gly Pro Ser
1               5                   10                  15

Gly Pro Gln Gly Pro Gly Gly Pro Pro Gly Pro Lys
            20                  25


<210> SEQ ID NO 36
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 36

Ile Ala Gly Ala Pro Gly Phe Pro Gly Ala Arg Gly Pro Ser Gly Pro
1               5                   10                  15

Gln Gly Pro Gly Gly Pro Pro Gly Pro Lys
            20                  25


<210> SEQ ID NO 37
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 37

Gly Phe Pro Gly Ala Arg Gly Pro Ser Gly Pro Gln Gly Pro Gly Gly
1               5                   10                  15

Pro Pro Gly Pro Lys
            20


<210> SEQ ID NO 38
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 38

Gly Pro Ser Gly Pro Gln Gly Pro Gly Gly
1               5                   10


<210> SEQ ID NO 39
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 39
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```
Gly Asp Thr Gly Ala Lys Gly Glu Pro
1               5


<210> SEQ ID NO 40
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 40

Val Gln Gly Pro Pro Gly Pro Ala Gly Glu Glu Gly Lys
1               5                   10


<210> SEQ ID NO 41
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 41

Gly Glu Pro Gly Pro Thr Gly Leu Pro Gly Pro Pro Gly
1               5                   10


<210> SEQ ID NO 42
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 42

Gly Glu Pro Gly Pro Thr Gly Leu Pro Gly Pro Pro Gly Glu Arg Gly
1               5                   10                  15

Gly Pro Gly Ser
            20


<210> SEQ ID NO 43
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 43

Thr Gly Leu Pro Gly Pro Pro Gly Glu Arg
1               5                   10


<210> SEQ ID NO 44
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 44

Leu Pro Gly Pro Pro Gly Glu Arg
1               5


<210> SEQ ID NO 45
<211> LENGTH: 10
<212> TYPE: PRT
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-continued

```
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 45

Ala Gly Pro Lys Gly Pro Ala Gly Glu Arg
1               5                   10


<210> SEQ ID NO 46
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 46

Gly Ser Pro Gly Pro Ala Gly Pro Lys Gly Ser Pro Gly Glu Ala Gly
1               5                   10                  15

Arg Pro Gly Glu Ala Gly
            20


<210> SEQ ID NO 47
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 47

Pro Gly Glu Ala Gly Arg Pro Gly Glu Ala Gly Leu Pro Gly Ala Lys
1               5                   10                  15

Gly Leu Thr Gly Ser Pro Gly Ser Pro Gly Pro Asp Gly Lys
            20                  25                  30


<210> SEQ ID NO 48
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 48

Leu Thr Gly Ser Pro Gly Ser Pro Gly Pro Asp Gly Lys
1               5                   10


<210> SEQ ID NO 49
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 49

Thr Gly Pro Pro Gly Pro Ala Gly Gln Asp Gly Arg Pro Gly Pro Pro
1               5                   10                  15

Gly Pro Pro Gly Ala Arg Gly
            20


<210> SEQ ID NO 50
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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```
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 50

Pro Gly Ala Val Gly Pro Ala Gly Lys Asp Gly Glu Ala Gly Ala Gln
1               5                   10                  15

Gly Pro Pro Gly Pro Ala Gly Pro Ala Gly Glu Arg
            20                  25


<210> SEQ ID NO 51
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 51

Gly Glu Ala Gly Ala Gln Gly Pro Pro Gly Pro Ala Gly Pro Ala Gly
1               5                   10                  15

Glu Arg


<210> SEQ ID NO 52
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 52

Glu Ala Gly Ala Gln Gly Pro Pro Gly Pro Ala Gly Pro Ala Gly Glu
1               5                   10                  15

Arg


<210> SEQ ID NO 53
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 53

Val Gln Gly Pro Pro Gly Pro Ala Gly Pro Arg
1               5                   10


<210> SEQ ID NO 54
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 54

Gln Gly Pro Pro Gly Pro Ala Gly Pro Arg
1               5                   10


<210> SEQ ID NO 55
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 55
```

```
Gly Pro Pro Gly Pro Ala Gly Pro Arg
1               5
```

<210> SEQ ID NO 56
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 56

```
Ala Asn Gly Ala Pro Gly Asn Asp Gly Ala Lys Gly Asp Ala Gly Ala
1               5                   10                  15

Pro Gly Ala Pro Gly Ser Gln Gly Ala Pro Gly Leu Gln Gly Met Pro
            20                  25                  30

Gly Glu Arg
        35
```

<210> SEQ ID NO 57
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 57

```
Leu Gln Gly Met Pro Gly Glu Arg
1               5
```

<210> SEQ ID NO 58
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 58

```
Leu Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Asp
1               5                   10                  15

Lys
```

<210> SEQ ID NO 59
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 59

```
Ile Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Asp Lys
1               5                   10
```

<210> SEQ ID NO 60
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 60

```
Lys Gly Glu Ser Gly Pro Ser Gly Pro Ala Gly Pro Thr Gly Ala Arg
1               5                   10                  15
```

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```
<210> SEQ ID NO 61
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 61

Pro Gly Asp Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Phe Ala
1               5                   10                  15

Gly Pro Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys
            20                  25


<210> SEQ ID NO 62
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 62

Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Phe
1               5                   10


<210> SEQ ID NO 63
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 63

Phe Ala Gly Pro Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys
1               5                   10


<210> SEQ ID NO 64
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 64

Ala Gly Pro Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys
1               5                   10


<210> SEQ ID NO 65
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 65

Arg Val Gly Pro Pro Gly Pro Ser Gly Asn Ala Gly Pro Pro Gly Pro
1               5                   10                  15

Pro Gly Pro Ala Gly Lys
            20


<210> SEQ ID NO 66
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 66

Val Gly Pro Pro Gly Pro Ser Gly Asn Ala Gly Pro Pro Gly Pro Pro
1               5                   10                  15

Gly Pro Ala Gly Lys Glu Gly Gly
            20


<210> SEQ ID NO 67
<211> LENGTH: 38
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 67

Glu Val Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Glu Lys Gly Ser
1               5                   10                  15

Pro Gly Ala Asp Gly Pro Ala Gly Ala Pro Gly Thr Pro Gly Pro Gln
            20                  25                  30

Gly Ile Ala Gly Gln Arg
        35


<210> SEQ ID NO 68
<211> LENGTH: 34
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 68

Pro Gly Pro Pro Gly Pro Ala Gly Glu Lys Gly Ser Pro Gly Ala Asp
1               5                   10                  15

Gly Pro Ala Gly Ala Pro Gly Thr Pro Gly Pro Gln Gly Ile Ala Gly
            20                  25                  30

Gln Arg


<210> SEQ ID NO 69
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 69

Gly Ser Pro Gly Ala Asp Gly Pro Ala Gly Ala Pro Gly Thr Pro Gly
1               5                   10                  15

Pro Gln Gly


<210> SEQ ID NO 70
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 70

Gly Pro Ala Gly Ala Pro Gly Thr Pro Gly Pro Gln Gly Ile Ala Gly
1               5                   10                  15
```

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```
Gln Arg


<210> SEQ ID NO 71
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 71

Val Val Gly Leu Pro Gly Gln Arg
1               5


<210> SEQ ID NO 72
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 72

Leu Ala Gly Pro Pro Gly Glu Ser Gly Arg
1               5                   10


<210> SEQ ID NO 73
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 73

Glu Thr Gly Pro Ala Gly Pro Pro Gly Ala Pro Gly Ala Pro Gly Ala
1               5                   10                  15

Pro Gly Pro Val Gly Pro Ala Gly Lys Ser Gly Asp Arg
            20                  25


<210> SEQ ID NO 74
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 74

Arg Gly Glu Thr Gly Pro Ala Gly Pro Ala Gly Pro Val Gly Pro Val
1               5                   10                  15

Gly Ala Arg


<210> SEQ ID NO 75
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 75

Pro Ala Gly Pro Val Gly Pro Val Gly Ala Arg
1               5                   10


<210> SEQ ID NO 76
<211> LENGTH: 8
<212> TYPE: PRT
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 76

Pro Val Gly Pro Val Gly Ala Arg
1               5


<210> SEQ ID NO 77
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 77

Ser Pro Gly Glu Gln Gly Pro Ser Gly Ala Ser Gly Pro Ala Gly Pro
1               5                   10                  15

Arg


<210> SEQ ID NO 78
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 78

Pro Gly Glu Gln Gly Pro Ser Gly Ala Ser Gly Pro Ala Gly Pro Arg
1               5                   10                  15


<210> SEQ ID NO 79
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 79

Gly Pro Ser Gly Ala Ser Gly Pro Ala Gly Pro Arg
1               5                   10


<210> SEQ ID NO 80
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 80

Ala Ser Gly Pro Ala Gly Pro Arg
1               5


<210> SEQ ID NO 81
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 81

Gly Pro Pro Gly Ser Ala Gly Ala Pro Gly Lys Asp
1               5                   10
```

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```
<210> SEQ ID NO 82
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 82

Pro Pro Gly Ser Ala Gly Ala Pro Gly Lys Asp Gly Leu Asn Gly Leu
1               5                   10                  15

Pro Gly Pro Ile Gly Pro Pro Gly Pro Arg
            20                  25


<210> SEQ ID NO 83
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 83

Leu Pro Gln Pro Pro Gln Glu Lys
1               5


<210> SEQ ID NO 84
<211> LENGTH: 39
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 84

Gly Leu Met Gly Pro Arg Gly Pro Pro Gly Ala Ala Gly Ala Pro Gly
1               5                   10                  15

Pro Gln Gly Phe Gln Gly Pro Ala Gly Glu Pro Gly Glu Pro Gly Gln
            20                  25                  30

Thr Gly Pro Ala Gly Ala Arg
        35


<210> SEQ ID NO 85
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 85

Phe Gln Gly Pro Ala Gly Glu Pro Gly Glu Pro Gly Gln Thr Gly Pro
1               5                   10                  15

Ala Gly Ala Arg
            20


<210> SEQ ID NO 86
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 86

Gln Gly Pro Ala Gly Glu Pro Gly Glu Pro Gly Gln Thr Gly Pro Ala
1               5                   10                  15
```

```
Gly Ala Arg


<210> SEQ ID NO 87
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 87

Glu Asp Gly His Pro Gly Lys Pro Gly Arg Pro Gly Glu Arg Gly Val
1               5                   10                  15

Val Gly Pro Gln Gly Ala Arg
            20


<210> SEQ ID NO 88
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 88

Pro Ala Gly Ala Arg Gly Ser Asp Gly Ser Val Gly Pro Val Gly Pro
1               5                   10                  15

Ala Gly Pro Ile Gly Ser Ala Gly Pro Pro Gly Phe Pro Gly Ala Pro
            20                  25                  30

Gly Pro Lys
        35


<210> SEQ ID NO 89
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 89

Asp Gly Ser Val Gly Pro Val Gly Pro Ala Gly Pro Ile Gly Ser Ala
1               5                   10                  15

Gly Pro Pro Gly Phe Pro Gly Ala Pro Gly Pro Lys
            20                  25


<210> SEQ ID NO 90
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 90

Pro Gly Ala Pro Gly Pro Lys Gly Glu Ile Gly Ala Val Gly Asn Ala
1               5                   10                  15

Gly Pro Ala Gly Pro Ala Gly Pro Arg
            20                  25


<210> SEQ ID NO 91
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 91

Gly Pro Ala Gly Pro Ala Gly Pro Arg
1               5


<210> SEQ ID NO 92
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 92

Pro Ala Gly Pro Ala Gly Pro Arg
1               5


<210> SEQ ID NO 93
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 93

Arg Gly Glu Val Gly Leu Pro Gly Leu Ser Gly Pro Val Gly Pro Pro
1               5                   10                  15

Gly Asn Pro Gly Ala Asn Gly Leu Thr Gly Ala Lys
            20                  25


<210> SEQ ID NO 94
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 94

Gly Ala Pro Gly Leu Pro Gly Pro Arg
1               5


<210> SEQ ID NO 95
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 95

Pro Asn Gly Glu Ala Gly Ser Ala Gly Pro Pro Gly Pro Pro Gly Leu
1               5                   10                  15

Arg


<210> SEQ ID NO 96
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 96

Gly Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly
1               5                   10                  15
```

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Lys

<210> SEQ ID NO 97
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 97

```
Gly Arg Pro Gly Pro Ile Gly Pro Ala Gly Ala Arg
1               5                   10
```

<210> SEQ ID NO 98
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 98

```
Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly
1               5                   10
```

<210> SEQ ID NO 99
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 99

```
Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro Gly
1               5                   10                  15

Val Val Gly Ala Val Gly Thr Ala Gly Pro Ser
            20                  25
```

<210> SEQ ID NO 100
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 100

```
Gly Pro Ser Gly Leu Pro Gly Glu Arg
1               5
```

<210> SEQ ID NO 101
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 101

```
Gly Ala Val Gly Ala Pro Gly Pro Ala Gly Ala Thr Gly Asp Arg Gly
1               5                   10                  15

Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Arg
            20                  25                  30
```

<210> SEQ ID NO 102

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```
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 102

Val Gly Ala Pro Gly Pro Ala Gly Ala Thr Gly Asp Arg Gly Glu Ala
1               5                   10                  15

Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Arg
            20                  25


<210> SEQ ID NO 103
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 103

Pro Gly Pro Ala Gly Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala
1               5                   10                  15

Gly Pro Ala Gly Pro Ala Gly Pro Arg
            20                  25


<210> SEQ ID NO 104
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 104

Asn Gly Val Val Gly Pro Thr Gly Pro Val Gly Ala Ala Gly Pro Ala
1               5                   10                  15

Gly Pro Asn Gly Pro Pro Gly Pro Ala Gly Ser Arg
            20                  25


<210> SEQ ID NO 105
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 105

Gly Pro Pro Gly Pro Ala Gly Ser Arg
1               5


<210> SEQ ID NO 106
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 106

Pro Gly Pro Ala Gly Ser Arg Gly Asp Gly Gly Pro Pro Gly Met Thr
1               5                   10                  15

Gly Phe Pro Gly Ala Ala Gly Arg
            20
```

-continued

<210> SEQ ID NO 107
<211> LENGTH: 36
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 107

Gly Asp Gly Gly Pro Pro Gly Met Thr Gly Phe Pro Gly Ala Ala Gly
1   5   10   15

Arg Thr Gly Pro Pro Gly Pro Ser Gly Ile Ser Gly Pro Pro Gly Pro
            20   25   30

Pro Gly Pro Ala
        35

<210> SEQ ID NO 108
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 108

Ile Ser Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Lys
1   5   10

<210> SEQ ID NO 109
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 109

Gly Pro Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly
1   5   10   15

Pro Gln Gly Leu
            20

<210> SEQ ID NO 110
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 110

Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg
1   5   10

<210> SEQ ID NO 111
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 111

Ile Ala Gly Pro Pro Gly Ala Arg
1   5

<210> SEQ ID NO 112
<211> LENGTH: 28

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 112

Pro Gly Asn Ile Gly Pro Val Gly Ala Ala Gly Ala Pro Gly Pro His
1               5                   10                  15

Gly Pro Val Gly Pro Ala Gly Lys His Gly Asn Arg
            20                  25


<210> SEQ ID NO 113
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 113

Val Gly Pro Ala Gly Ala Val Gly Pro Arg
1               5                   10


<210> SEQ ID NO 114
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 114

Gln Gly Ala Pro Gly Ser Val Gly Pro Ala Gly Pro Arg
1               5                   10


<210> SEQ ID NO 115
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 115

Gly Pro Ala Gly Pro Ser Gly Pro Ala Gly Lys Asp
1               5                   10


<210> SEQ ID NO 116
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 116

Gly Thr Val Gly Pro Ala Gly Ile Arg
1               5


<210> SEQ ID NO 117
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 117

Gly Pro Gln Gly Pro Lys Gly Asp Pro Gly Pro Pro Gly Ile Pro Gly
```

-continued

```
1               5                   10                  15

Arg


<210> SEQ ID NO 118
<211> LENGTH: 45
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 118

Pro Gly Thr Ser Gly His Pro Gly Ser Pro Gly Ser Pro Gly Tyr Gln
1               5                   10                  15

Gly Pro Pro Gly Glu Pro Gly Gln Ala Gly Pro Ser Gly Pro Pro Gly
            20                  25                  30

Pro Pro Gly Ala Ile Gly Pro Ser Gly Pro Ala Gly Lys
        35                  40                  45


<210> SEQ ID NO 119
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 119

Gly Leu Pro Gly Pro Pro Gly Ile Lys Gly Pro Ala Gly
1               5                   10


<210> SEQ ID NO 120
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 120

Gly Glu Val Gly Pro Ala Gly Ser Pro Gly Ser Asn Gly Ala Pro Gly
1               5                   10                  15

Gln Arg Gly Glu Pro Gly Pro Gln Gly His Ala Gly
            20                  25


<210> SEQ ID NO 121
<211> LENGTH: 37
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 121

Gly Glu Pro Gly Pro Gln Gly His Ala Gly Ala Gln Gly Pro Pro Gly
1               5                   10                  15

Pro Pro Gly Ile Asn Gly Ser Pro Gly Gly Lys Gly Glu Met Gly Pro
            20                  25                  30

Ala Gly Ile Pro Gly
        35


<210> SEQ ID NO 122
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 122

Gly Glu Met Gly Pro Ala Gly Ile Pro Gly Ala Pro Gly Leu Met Gly
1               5                   10                  15

Ala Arg Gly Pro Pro Gly Pro Ala Gly
            20                  25


<210> SEQ ID NO 123
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 123

Gly Ile Pro Gly Ala Pro Gly Leu Met Gly Ala Arg
1               5                   10


<210> SEQ ID NO 124
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 124

Gly Ala Pro Gly Leu Met Gly Ala Arg Gly Pro Pro Gly Pro Ala Gly
1               5                   10                  15

Ala Asn Gly Ala Pro Gly Leu Arg
            20


<210> SEQ ID NO 125
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 125

Pro Ala Gly Glu Arg Gly Ala Pro Gly Pro Ala Gly Pro Arg
1               5                   10


<210> SEQ ID NO 126
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 126

Gly Ala Pro Gly Pro Ala Gly Pro Arg Gly Ala Ala Gly Glu Pro
1               5                   10                  15


<210> SEQ ID NO 127
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 127
```

```
Gly Glu Pro Gly Arg Asp Gly Val Pro Gly Gly Pro Gly Met Arg
1               5                   10                  15


<210> SEQ ID NO 128
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 128

Asp Gly Lys Pro Gly Pro Pro Gly Ser Gln Gly Glu Ser Gly Arg Pro
1               5                   10                  15

Gly Pro Pro Gly Pro Ser Gly Pro Arg
            20                  25


<210> SEQ ID NO 129
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 129

Gly Lys Pro Gly Pro Pro Gly Ser Gln Gly Glu Ser Gly Arg Pro Gly
1               5                   10                  15

Pro Pro Gly Pro Ser Gly Pro Arg
            20


<210> SEQ ID NO 130
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 130

Gly Arg Pro Gly Pro Pro Gly Pro Ser Gly Pro Arg
1               5                   10


<210> SEQ ID NO 131
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 131

Gly Pro Pro Gly Pro Ser Gly Pro Arg
1               5


<210> SEQ ID NO 132
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 132

Gln Gly Pro Pro Gly Lys Asn Gly Glu Thr Gly Pro Gln Gly Pro Pro
1               5                   10                  15

Gly Pro Thr Gly Pro Gly Gly Asp Lys
            20                  25
```

<210> SEQ ID NO 133
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 133

Gly Asp Ala Gly Ala Pro Gly Glu Arg Gly Pro
1   5   10

<210> SEQ ID NO 134
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 134

Leu Gln Gly Met Pro Gly Glu Arg
1   5

<210> SEQ ID NO 135
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 135

Gly Glu Gly Gly Pro Pro Gly Val Ala Gly Pro Pro Gly Gly Ser Gly
1   5   10   15

Pro Ala Gly Pro Pro Gly Pro Gln Gly Val
            20   25

<210> SEQ ID NO 136
<211> LENGTH: 39
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 136

Gly Ser Asn Gly Asn Pro Gly Pro Pro Gly Pro Ser Gly Ser Pro Gly
1   5   10   15

Lys Asp Gly Pro Pro Gly Pro Ala Gly Asn Thr Gly Ala Pro Gly Ser
            20   25   30

Pro Gly Val Ser Gly Pro Lys
        35

<210> SEQ ID NO 137
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 137

Asn Gly Asn Pro Gly Pro Pro Gly Pro Ser Gly Ser Pro Gly Lys
1   5   10   15

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<210> SEQ ID NO 138
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 138

Gly Ser Pro Gly Ala Gln Gly Pro Pro
1               5


<210> SEQ ID NO 139
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 139

Gly Asn Pro Gly Ser Asp Gly Leu Pro Gly Arg
1               5                   10


<210> SEQ ID NO 140
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 140

Glu Asn Gly Ser Pro Gly Ala Pro Gly Ala Pro Gly His Pro Gly Pro
1               5                   10                  15

Pro Gly Pro Val Gly Pro Ala Gly Lys
            20                  25


<210> SEQ ID NO 141
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 141

Pro Gly Ala Pro Gly Ala Pro Gly His Pro Gly Pro Pro Gly Pro Val
1               5                   10                  15

Gly Pro Ala Gly Lys
            20


<210> SEQ ID NO 142
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 142

Arg Gly Glu Ser Gly Pro Ala Gly Pro Ala Gly Ala Pro Gly Pro Ala
1               5                   10                  15

Gly Ser Arg


<210> SEQ ID NO 143
<211> LENGTH: 12
<212> TYPE: PRT
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 143

Gly Glu Ser Gly Pro Ala Gly Pro Ala Gly Ala Pro
1               5                   10


<210> SEQ ID NO 144
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 144

Pro Gly Ala Pro Gly Ser Pro Gly Pro Ala Gly Gln Gln Gly Ala Ile
1               5                   10                  15

Gly Ser Pro Gly Pro Ala Gly Pro Arg
            20                  25


<210> SEQ ID NO 145
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 145

Gly Gln Gln Gly Ala Ile Gly Ser Pro Gly Pro Ala Gly Pro Arg Gly
1               5                   10                  15

Pro Val Gly Pro Ser Gly Pro Pro Gly Lys
            20                  25


<210> SEQ ID NO 146
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 146

Gln Gly Ala Ile Gly Ser Pro Gly Pro Ala Gly Pro Arg
1               5                   10


<210> SEQ ID NO 147
<211> LENGTH: 49
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 147

Gly Ser Glu Gly Ser Pro Gly His Pro Gly Gln Pro Gly Pro Pro Gly
1               5                   10                  15

Pro Pro Gly Ala Pro Gly Pro Cys Cys Gly Gly Val Gly Ala Ala Ala
            20                  25                  30

Ile Ala Gly Ile Gly Gly Glu Lys Ala Gly Gly Phe Ala Pro Tyr Tyr
        35                  40                  45

Gly
```

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<210> SEQ ID NO 148
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 148

Gly Pro Gln Gly Phe Gln Gly Asn Pro Gly Glu Pro Gly Glu Pro Gly
1               5                   10                  15

Val Ser Gly Pro Met Gly Pro Arg Gly Pro Pro Gly Pro Pro Gly Lys
            20                  25                  30

Pro Gly Asp Asp Gly Glu Ala Gly Lys Pro Gly Lys
        35                  40


<210> SEQ ID NO 149
<211> LENGTH: 36
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 149

Gly Ala Ala Gly Ala Arg Gly Asn Asp Gly Gln Pro Gly Pro Ala Gly
1               5                   10                  15

Pro Pro Gly Pro Val Gly Pro Ala Gly Gly Pro Gly Phe Pro Gly Ala
            20                  25                  30

Pro Gly Ala Lys
        35


<210> SEQ ID NO 150
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 150

Ala Ala Gly Ala Arg Gly Asn Asp Gly Gln Pro Gly Pro Ala Gly Pro
1               5                   10                  15

Pro Gly Pro Val Gly Pro Ala Gly Gly Pro Gly Phe Pro Gly Ala Pro
            20                  25                  30

Gly Ala Lys
        35


<210> SEQ ID NO 151
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 151

Pro Gly Ala Lys Gly Ser Ala Gly Ala Pro Gly Ile Ala Gly Ala Pro
1               5                   10                  15

Gly Phe Pro Gly Pro Arg
            20


<210> SEQ ID NO 152
<211> LENGTH: 18
<212> TYPE: PRT
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 152

Gly Pro Arg Gly Pro Pro Gly Pro Gln Gly Ala Thr Gly Pro Leu Gly
1               5                   10                  15

Pro Lys


<210> SEQ ID NO 153
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 153

Asp Gly Leu Ala Gly Pro Lys
1               5


<210> SEQ ID NO 154
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 154

Pro Gln Gly Lys Val Gly Pro Ser Gly Ala Pro Gly Glu Asp Gly Arg
1               5                   10                  15

Pro Gly Pro Pro Gly Pro Gln Gly Ala Arg
            20                  25


<210> SEQ ID NO 155
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 155

Gly Phe Pro Gly Pro Lys Gly Ala Asn Gly Glu Pro Gly Lys
1               5                   10


<210> SEQ ID NO 156
<211> LENGTH: 33
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 156

Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Glu Gly Gly Lys Pro Gly
1               5                   10                  15

Asp Gln Gly Val Pro Gly Glu Ala Gly Ala Pro Gly Leu Val Gly Pro
            20                  25                  30

Arg


<210> SEQ ID NO 157
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 157

Gly Pro Pro Gly Glu Gly Gly Lys Pro Gly Asp Gln Gly Val Pro Gly
1               5                   10                  15

Glu Ala Gly Ala Pro Gly Leu Val Gly Pro Arg
            20                  25


<210> SEQ ID NO 158
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 158

Leu Gln Gly Met Pro Gly Glu Arg
1               5


<210> SEQ ID NO 159
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 159

Gly Arg Gly Leu Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly Ala
1               5                   10                  15

Asn Gly Glu Lys
            20


<210> SEQ ID NO 160
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 160

Gly Leu Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly Ala Asn Gly
1               5                   10                  15

Glu Lys Gly Glu Val Gly Pro Pro
            20


<210> SEQ ID NO 161
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 161

Gly Leu Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly Ala Asn Gly
1               5                   10                  15

Glu Lys Gly Glu Val Gly Pro Pro Gly Pro Ala Gly Ser Ala Gly
            20                  25                  30


<210> SEQ ID NO 162
<211> LENGTH: 32
<212> TYPE: PRT
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 162

Leu Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly Ala Asn Gly Glu
1               5                   10                  15

Lys Gly Glu Val Gly Pro Pro Gly Pro Ala Gly Ser Ala Gly Ala Arg
            20                  25                  30


<210> SEQ ID NO 163
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 163

Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly Ala Asn Gly Glu Lys
1               5                   10                  15

Gly Glu Val Gly Pro Pro Gly Pro Ala Gly Ser Ala Gly Ala Arg
            20                  25                  30


<210> SEQ ID NO 164
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 164

Phe Ala Gly Pro Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys
1               5                   10


<210> SEQ ID NO 165
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 165

Ala Gly Pro Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys
1               5                   10


<210> SEQ ID NO 166
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 166

Ser Gly Pro Pro Gly Arg Ala Gly Glu Pro Gly Leu Gln Gly Pro Ala
1               5                   10                  15

Gly Pro Pro Gly Glu Lys
            20


<210> SEQ ID NO 167
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 167

Gly Pro Pro Gly Arg Ala Gly Glu Pro Gly Leu Gln Gly Pro Ala Gly
1               5                   10                  15

Pro Pro Gly Glu Lys
            20


<210> SEQ ID NO 168
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 168

Pro Pro Gly Leu Thr Gly Pro Ala Gly Glu Pro Gly Arg Glu Gly Ser
1               5                   10                  15

Pro Gly Ala Asp Gly Pro Pro Gly Arg
            20                  25


<210> SEQ ID NO 169
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 169

Pro Gly Pro Gly Ile Asp Met Ser Ala Phe Ala Gly Leu Gly Pro Arg
1               5                   10                  15

Glu Lys


<210> SEQ ID NO 170
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 170

Ile Glu Trp His Leu Asn Ala Phe
1               5


<210> SEQ ID NO 171
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 171

Ala Ile Thr Gly Pro Pro Thr Glu Leu Ile Thr Ser Glu Val Thr Ala
1               5                   10                  15

Arg


<210> SEQ ID NO 172
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence
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<400> SEQUENCE: 172

Ala Ile Tyr Ala His Thr Ala Ser Glu Gly Leu Arg
1               5                   10


<210> SEQ ID NO 173
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 173

Leu Tyr Asp Val Thr Glu Asn Ser Met Arg
1               5                   10


<210> SEQ ID NO 174
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 174

Tyr Leu Ile Leu Tyr Ala Pro Leu Thr Glu Gly Leu Ala Gly Asp Glu
1               5                   10                  15

Lys Glu Met Lys
            20


<210> SEQ ID NO 175
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 175

Tyr Ala Pro Leu Thr Glu Gly Leu Ala Gly Asp Glu Lys
1               5                   10


<210> SEQ ID NO 176
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 176

His Val Glu Met Thr Ser Leu Cys Ala His
1               5                   10


<210> SEQ ID NO 177
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 177

Ser Ile Gln Gly Met Pro Gly Met Pro Gly Glu Lys Gly Glu Lys
1               5                   10                  15


<210> SEQ ID NO 178
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<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 178

Gln Val Cys Glu Gln Leu Ile Gln Ser His
1               5                   10


<210> SEQ ID NO 179
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 179

Glu Pro Gly Arg Pro Gly Ser Pro Gly Ala Pro Gly Glu Gln Gly Pro
1               5                   10                  15

Pro Gly Thr Pro Gly Phe Pro Gly Asn Ala Gly Val Pro Gly Thr Pro
            20                  25                  30

Gly Glu Arg
        35


<210> SEQ ID NO 180
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 180

Gly Gly Ser Thr Asn Thr Gly Lys Ala Met Thr Tyr Val Arg Glu
1               5                   10                  15


<210> SEQ ID NO 181
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 181

Pro Lys Val Met Ile Leu Ile Thr Asp Gly Lys
1               5                   10


<210> SEQ ID NO 182
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 182

Pro Asp Asp Thr His Ala Tyr Asn Val Ala Asp Phe Glu Ser Leu Ser
1               5                   10                  15

Arg


<210> SEQ ID NO 183
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 183

Ser Val Val Glu Asp Glu Tyr Ser Glu Pro Leu Lys
1               5                   10


<210> SEQ ID NO 184
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 184

Ser Glu Thr Ser Thr Ser Leu Lys Asp
1               5


<210> SEQ ID NO 185
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 185

Leu Lys Pro Asp Thr Pro Tyr Thr Ile Thr Val Ser Ser Leu Tyr Pro
1               5                   10                  15

Asp Gly Glu Gly Gly Arg Met Thr Gly
            20                  25


<210> SEQ ID NO 186
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 186

Pro Gly Pro Ala Gly Gly Pro Gly Ala Lys
1               5                   10


<210> SEQ ID NO 187
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 187

Gly Arg Thr Gly Thr Pro Gly Leu Pro Gly Pro Pro Gly Pro Met Gly
1               5                   10                  15

Pro Pro Gly Asp Arg
            20


<210> SEQ ID NO 188
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 188
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Thr Pro Gly Leu Pro Gly Pro Pro Gly Pro Met Gly Pro Pro Gly Asp
1 5 10 15

Arg Gly Phe Thr Gly Lys
20

<210> SEQ ID NO 189
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 189

Gly Phe Pro Gly Thr Pro Gly Met Gln Gly Pro Pro Gly Glu Arg Gly
1 5 10 15

Leu Pro Gly Glu Lys
20

<210> SEQ ID NO 190
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 190

Gln Gly Pro Pro Gly Glu Arg
1 5

<210> SEQ ID NO 191
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 191

Pro Arg Gly Leu Pro Gly Pro Pro Gly Pro Gln Gly Glu Ser Arg
1 5 10 15

<210> SEQ ID NO 192
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 192

Pro Pro Ser Leu Gly Arg Pro Trp Ala Pro Leu Thr Gly Pro Ser Val
1 5 10 15

Pro Pro Pro Ser Ser Gly Arg
20

<210> SEQ ID NO 193
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 193

Pro Gly Glu Asp Gly Lys Pro Gly Asp Thr Gly Pro Gln Gly Phe Pro
1 5 10 15

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```
Gly Thr Pro Gly Asp Val Gly Pro Lys Gly Asp Lys
            20                  25


<210> SEQ ID NO 194
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 194

Pro Gly Leu Pro Gly Glu Pro Gly Arg
1               5


<210> SEQ ID NO 195
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 195

Gly Arg Glu Gly Pro Pro Gly Phe Pro Gly Leu Pro Gly Pro Pro Gly
1               5                   10                  15

Pro Pro Gly Arg
            20


<210> SEQ ID NO 196
<211> LENGTH: 33
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 196

Gln Asp Gly Ser Val Leu Ser Val Pro Gly Pro Glu Gly Arg Pro Gly
1               5                   10                  15

Phe Ala Gly Phe Pro Gly Pro Ala Gly Pro Lys Gly Asn Leu Gly Ser
            20                  25                  30

Lys


<210> SEQ ID NO 197
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 197

Ala Glu Ser Ser Arg Pro Gly Pro Pro Gly Leu Pro Gly Asn Gln Gly
1               5                   10                  15

Pro Pro Gly Pro Lys
            20


<210> SEQ ID NO 198
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 198
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```
Gly Pro Pro Gly Pro Lys Gly Ala Lys
1               5


<210> SEQ ID NO 199
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 199

Pro Gly Pro Pro Gly Pro Pro Gly Thr Met Gly Ala Ser Ser Gly Val
1               5                   10                  15

Arg


<210> SEQ ID NO 200
<211> LENGTH: 34
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 200

Arg Leu Pro Glu Pro Gln Pro Tyr Pro Gly Ala Pro His His Ser Ser
1               5                   10                  15

Tyr Val His Leu Arg Pro Ala Arg Pro Thr Ser Pro Pro Ala His Ser
            20                  25                  30

His Arg


<210> SEQ ID NO 201
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 201

Leu Pro Glu Pro Gln Pro Tyr Pro Gly Ala Pro His His Ser Ser Tyr
1               5                   10                  15


<210> SEQ ID NO 202
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 202

Asn Ser Pro Leu Ser Gly Gly Met Arg
1               5


<210> SEQ ID NO 203
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 203

Pro Ser Leu Gly Arg Pro Trp Ala Pro Leu Thr Gly Pro Ser Val Pro
1               5                   10                  15
```

```
Pro Pro Ser Ser Glu Arg
            20


<210> SEQ ID NO 204
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 204

Gly Ala Arg Gly Val Ser Gly Phe Pro Gly Ala Asp Gly Ile Pro Gly
1               5                   10                  15

His Pro Gly Gln Gly Gly Pro Arg
            20


<210> SEQ ID NO 205
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 205

Gly Gly Pro Lys Gly Leu Pro Gly Leu Pro Gly Pro Pro Gly Pro Thr
1               5                   10                  15

Gly Ala Lys


<210> SEQ ID NO 206
<211> LENGTH: 33
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 206

Gly Pro Pro Gly Leu His Gly Phe Pro Gly Ala Pro Gly Gln Glu Gly
1               5                   10                  15

Pro Leu Gly Leu Pro Gly Ile Pro Gly Arg Glu Gly Leu Pro Gly Asp
            20                  25                  30

Arg


<210> SEQ ID NO 207
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 207

Ala Pro Gly Arg Pro Gly Ser Pro Gly Leu Pro Gly Met Pro Gly Arg
1               5                   10                  15


<210> SEQ ID NO 208
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 208

Leu Tyr Cys Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg
```

```
1               5                   10


<210> SEQ ID NO 209
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 209

Leu Met His Thr Ala Ala Gly Asp Glu Gly Gly Gly Gln Ser Leu Val
1               5                   10                  15

Ser Pro Gly Ser Cys Leu Glu Asp Phe Arg
            20                  25


<210> SEQ ID NO 210
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 210

Glu Pro Gly Pro Pro Gly Leu Pro Gly Ser Val Gly Ser Pro Gly Val
1               5                   10                  15

Pro Gly Ile Gly Pro Pro Gly Ala Arg
            20                  25


<210> SEQ ID NO 211
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 211

Pro Gly Val Pro Gly Ile Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly
1               5                   10                  15

Gly Gln Gly Pro Pro Gly Leu Ser Gly Pro Pro Gly Ile Lys
            20                  25                  30


<210> SEQ ID NO 212
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 212

Pro Pro Gly Gly Gln Gly Pro Pro Gly Leu Ser Gly Pro Pro Gly Ile
1               5                   10                  15

Lys Gly Glu Lys
            20


<210> SEQ ID NO 213
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 213
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Asp Pro Gly Phe Gln Gly Met Pro Gly Ile Gly Gly Ser Pro Gly Ile
1               5                   10                  15

Thr Gly Ser Lys
            20


<210> SEQ ID NO 214
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 214

Lys Gly Gln Gln Gly Val Thr Gly Leu Val Gly Ile Pro Gly Pro Pro
1               5                   10                  15

Gly Ile Pro Gly Phe Asp Gly Ala Pro Gly Gln Lys
            20                  25


<210> SEQ ID NO 215
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 215

Ser Leu Leu Tyr Val Gln Gly Asn Glu Arg
1               5                   10


<210> SEQ ID NO 216
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 216

Leu Phe Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg
1               5                   10


<210> SEQ ID NO 217
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 217

Val Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala
1               5                   10                  15

Ser Pro Gly Ser Cys Leu Glu Glu Phe Arg
            20                  25


<210> SEQ ID NO 218
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 218

Arg Ser Ala Pro Phe Ile Glu Cys His Gly Arg
1               5                   10
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<210> SEQ ID NO 219
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 219

Ser Phe Trp Leu Ala Thr Ile Glu Arg
1               5


<210> SEQ ID NO 220
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 220

Trp Leu Ala Thr Ile Glu Arg
1               5


<210> SEQ ID NO 221
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 221

Asp Gly Ile Pro Gly Pro Pro Gly Pro Lys
1               5                   10


<210> SEQ ID NO 222
<211> LENGTH: 46
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 222

Lys Gly Asn Pro Gly Tyr Pro Gly Pro Pro Gly Ile Gln Gly Leu Pro
1               5                   10                  15

Gly Pro Thr Gly Ile Pro Gly Pro Ile Gly Pro Pro Gly Pro Pro Gly
            20                  25                  30

Leu Met Gly Pro Pro Gly Pro Pro Gly Leu Pro Gly Pro Lys
        35                  40                  45


<210> SEQ ID NO 223
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 223

Pro His Ile Pro Pro Ser Asp Glu Ile Cys Glu Pro Gly Pro Pro Gly
1               5                   10                  15

Pro Pro Gly Ser Pro Gly Asp Lys
            20
```

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<210> SEQ ID NO 224
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 224

Gly Leu Pro Gly Leu Pro Gly Pro Pro Gly Ser Leu Gly Phe Pro Gly
1               5                   10                  15

Gln Lys


<210> SEQ ID NO 225
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 225

Pro Lys Gly Glu Pro Gly Gly Ile Thr Phe Lys
1               5                   10


<210> SEQ ID NO 226
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 226

Thr Pro Gly Arg Ile Gly Leu Glu Gly Pro Pro Gly Pro Pro Gly Phe
1               5                   10                  15

Pro Gly Pro Lys
            20


<210> SEQ ID NO 227
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 227

Gly Pro Pro Gly Arg Thr Gly Leu Asp Gly Leu Pro Gly Pro Lys
1               5                   10                  15


<210> SEQ ID NO 228
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 228

Ala Pro Gly Pro Ile Gly Pro Pro Gly Ser Pro Gly Leu Pro Gly Lys
1               5                   10                  15


<210> SEQ ID NO 229
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence
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<400> SEQUENCE: 229

Lys Gly Glu Pro Gly Leu Pro Gly Pro Pro Gly Pro Met Asp Pro Asn
1               5                   10                  15

Leu Leu Gly Ser Lys
            20


<210> SEQ ID NO 230
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 230

Pro Gly Glu Pro Gly Pro Val Gly Gly Gly Gly His Pro Gly Gln Pro
1               5                   10                  15

Gly Pro Pro Gly Glu Lys
            20


<210> SEQ ID NO 231
<211> LENGTH: 43
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 231

Pro Ala Leu Glu Gly Pro Lys Gly Asn Pro Gly Pro Gln Gly Pro Pro
1               5                   10                  15

Gly Arg Pro Gly Pro Thr Gly Phe Gln Gly Leu Pro Gly Pro Glu Gly
            20                  25                  30

Pro Pro Gly Leu Pro Gly Asn Gly Gly Ile Lys
        35                  40


<210> SEQ ID NO 232
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 232

Gly Pro Pro Gly Pro Pro Gly Leu Pro Gly Pro Ser Gly Gln Ser Ile
1               5                   10                  15

Ile Ile Lys


<210> SEQ ID NO 233
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 233

Val Asp Gly Ala Thr Gly Leu Pro Gly Met Lys
1               5                   10


<210> SEQ ID NO 234
<211> LENGTH: 34
<212> TYPE: PRT
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 234

Lys Gly Gln Ala Gly Pro Pro Gly Val Met Gly Pro Pro Gly Pro Pro
1               5                   10                  15

Gly Pro Pro Gly Pro Pro Gly Pro Gly Cys Thr Met Gly Leu Gly Phe
            20                  25                  30

Glu Asp


<210> SEQ ID NO 235
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 235

Lys Leu Gln Leu Gly Glu Leu Ile Pro Ile Pro Ala Asp Ser Pro Pro
1               5                   10                  15

Pro Pro


<210> SEQ ID NO 236
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 236

Ala Trp Arg Thr Ala Asp Thr Ala Val Thr Gly Leu Ala Ser Pro Leu
1               5                   10                  15

Ser Thr Gly Lys
            20


<210> SEQ ID NO 237
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 237

Ala Val Thr Gly Leu Ala Ser Pro Leu Ser Thr Gly Lys Ile Leu Asp
1               5                   10                  15

Gln Lys


<210> SEQ ID NO 238
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 238

Gly Val Glu Asp Ala Asp Glu Gly Ala Leu Lys Glu Ile Ala Ser Glu
1               5                   10                  15

Pro Leu Asn Met His Met Phe Asn Leu Glu Asn Phe Thr Ser Leu His
            20                  25                  30
```

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```
Asp Ile Val Gly Asn Leu Val Ser Cys Val His Ser Ser Val Ser Pro
        35                  40                  45

Glu Arg
    50


<210> SEQ ID NO 239
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 239

Asn Asn Leu Phe Thr Ser Ser Ala Gly Tyr Arg
1               5                   10


<210> SEQ ID NO 240
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 240

Ala Ala Pro Leu Gln Gly Met Leu Pro Gly Leu Leu Ala Pro Leu Arg
1               5                   10                  15


<210> SEQ ID NO 241
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 241

Ile Gly Asp Leu His Pro Gln Ile Val Asn
1               5                   10


<210> SEQ ID NO 242
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 242

Gly Pro Gln Gly Asp Gln Gly Arg
1               5


<210> SEQ ID NO 243
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 243

Thr Asp Pro Ala His Asp Val Arg
1               5


<210> SEQ ID NO 244
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 244

Phe Ser Asp Gly Asn Ser Gln Gly Ala Thr Pro Ala Ala Ile Glu Lys
1   5   10   15

<210> SEQ ID NO 245
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 245

Gln Val Asn Glu Pro His Ile Arg
1   5

<210> SEQ ID NO 246
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 246

Gly Val Phe His Gln Thr Val Ser Arg
1   5

<210> SEQ ID NO 247
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 247

Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys Leu Gly Thr Ala Val
1   5   10   15

Pro Ser Thr Gly Ala Ser Lys
            20

<210> SEQ ID NO 248
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 248

Ala Leu Val Cys Thr Cys Tyr Gly Gly Ser Arg
1   5   10

<210> SEQ ID NO 249
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 249

Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg
1   5   10

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<210> SEQ ID NO 250
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 250

Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg
1               5                   10                  15


<210> SEQ ID NO 251
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 251

Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser Lys
1               5                   10                  15


<210> SEQ ID NO 252
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 252

Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg
1               5                   10                  15


<210> SEQ ID NO 253
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 253

Ser Asp Thr Val Pro Ser Pro Arg Asp Leu Gln Phe Val Glu Val Thr
1               5                   10                  15

Asp Val Lys


<210> SEQ ID NO 254
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 254

Val Asp Val Ile Pro Val Asn Leu Pro Gly Glu His Gly Gln Arg
1               5                   10                  15


<210> SEQ ID NO 255
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 255
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Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro Leu Thr Ala Gln
1   5   10   15

Gln Thr Thr Lys
            20

<210> SEQ ID NO 256
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 256

Leu Gly Val Arg Pro Ser Gln Gly Gly Glu Ala Pro Arg
1   5   10

<210> SEQ ID NO 257
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 257

Asp Ala Pro Ile Val Asn Lys Val Val Thr Pro Leu Ser Pro Pro Thr
1   5   10   15

Asn Leu His

<210> SEQ ID NO 258
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 258

Thr Pro Asp Ile Thr Gly Tyr Arg
1   5

<210> SEQ ID NO 259
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 259

Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln His
1   5   10   15

Glu Ser Thr Pro Leu Arg
            20

<210> SEQ ID NO 260
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 260

Thr Gly Leu Asp Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala
1   5   10   15

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```
Asn Ser Phe Thr Val His
            20


<210> SEQ ID NO 261
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 261

Thr Val His Trp Ile Ala Pro Arg
1               5


<210> SEQ ID NO 262
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 262

Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys
1               5                   10


<210> SEQ ID NO 263
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 263

Val Val Ser Val Tyr Ala Gln Asn Pro Ser Gly Glu Ser Gln Pro Leu
1               5                   10                  15

Val Gln Thr Ala Val Thr Asn Ile Asp Arg Pro Lys
            20                  25


<210> SEQ ID NO 264
<211> LENGTH: 37
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 264

Arg Pro Gly Ser Glu Tyr Thr Val Ser Val Val Ala Leu His Asp Asp
1               5                   10                  15

Met Glu Ser Gln Pro Leu Ile Gly Thr Gln Ser Thr Ala Ile Pro Ala
            20                  25                  30

Pro Thr Asp Leu Lys
        35


<210> SEQ ID NO 265
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 265

Tyr Glu Val Ser Val Tyr Ala Leu Lys
```

```
1               5


<210> SEQ ID NO 266
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 266

Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg
1               5                   10


<210> SEQ ID NO 267
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 267

Ser Leu Leu Val Ser Trp Gln Pro Pro Arg
1               5                   10


<210> SEQ ID NO 268
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 268

Tyr Glu Lys Pro Gly Ser Pro Pro Arg
1               5


<210> SEQ ID NO 269
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 269

Thr Pro Phe Val Thr His Pro Gly
1               5


<210> SEQ ID NO 270
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 270

Thr Pro Phe Val Thr His Pro Gly Tyr Asp Thr
1               5                   10


<210> SEQ ID NO 271
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 271
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```
Thr Pro Phe Val Thr His Pro Gly Tyr Asp Thr Gly Asn Gly Ile Gln
1               5                   10                  15

Leu Pro Gly Thr Ser Gly Gln Gln Pro Ser Val Gly Gln Gln Met
            20                  25                  30


<210> SEQ ID NO 272
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 272

Gln Asp Thr Ser Glu Tyr Ile Ile Ser Cys His Pro Val Gly Thr Asp
1               5                   10                  15

Glu Glu Pro Leu Gln Phe Arg
            20


<210> SEQ ID NO 273
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 273

Val Pro Gly Thr Ser Thr Ser Ala Thr Leu Thr Gly Leu Thr Arg Gly
1               5                   10                  15

Ala Thr Tyr Asn Ile Ile Val Glu Ala Leu Lys
            20                  25


<210> SEQ ID NO 274
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 274

Val Arg Glu Glu Val Val Thr Val Gly Asn
1               5                   10


<210> SEQ ID NO 275
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 275

Ser Val Asn Glu Gly Leu Asn Gln Pro Thr Asp Asp Ser Cys Phe Asp
1               5                   10                  15

Pro Tyr Thr Val Ser His Tyr Ala Val Gly Asp Glu Trp Glu Arg
            20                  25                  30


<210> SEQ ID NO 276
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence
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<400> SEQUENCE: 276

Leu Gly Phe Gly Ser Gly His Phe Arg
1               5


<210> SEQ ID NO 277
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 277

Ala Cys Glu Asp Ile Asp Glu Cys Ser Leu Pro Asn Ile Cys Val Phe
1               5                   10                  15

Gly Thr Cys His Asn Leu Pro Gly Leu Phe Arg
            20                  25


<210> SEQ ID NO 278
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 278

Thr Gly Leu Pro Val Asp Ile Asp Glu Cys Arg
1               5                   10


<210> SEQ ID NO 279
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 279

Pro Val Asp Ile Asp Glu Cys Arg
1               5


<210> SEQ ID NO 280
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 280

Glu Ile Pro Gly Val Cys Asn Gly Val Cys Ile Asn His Val Gly Ser
1               5                   10                  15

Phe Arg


<210> SEQ ID NO 281
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 281

Glu Ile Pro Gly Val Cys Glu Asn Gly Val Cys Ile Asn Met Val Gly
1               5                   10                  15

Ser Phe Arg
```

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<210> SEQ ID NO 282
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 282

Leu Leu Val Cys Glu Asp Ile Asp Glu Cys Gln Asn Gly Pro Val Cys
1 5 10 15

Gln Arg

<210> SEQ ID NO 283
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 283

Thr Cys Val Asp Ile Asn Glu Cys Leu Leu Glu Pro Arg
1 5 10

<210> SEQ ID NO 284
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 284

Gly Glu Gly Trp Gly Asp Pro Cys Glu Leu Cys Pro Thr Glu Pro Asp
1 5 10 15

Glu Ala Phe Arg
20

<210> SEQ ID NO 285
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 285

Cys Thr Asp Tyr Thr Ala Glu Cys Lys Pro Gln Val Thr Arg
1 5 10

<210> SEQ ID NO 286
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 286

Ile Tyr Ile Ser Gly Met Ala Pro Arg Pro Ser
1 5 10

<210> SEQ ID NO 287
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 287

Thr Cys Glu Pro Ile Gln Ser Val Phe Phe Phe Ser Gly Asp Lys
1               5                   10                  15


<210> SEQ ID NO 288
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 288

Ser Ile Ala Gln Tyr Trp Leu Gly Cys Pro Ala Pro Gly His
1               5                   10


<210> SEQ ID NO 289
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 289

Trp Leu Gly Cys Pro Ala Pro Gly His Leu
1               5                   10


<210> SEQ ID NO 290
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 290

Cys Asn Ser Asp Leu Val Ile Arg
1               5


<210> SEQ ID NO 291
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 291

Leu Gln Asp Gly Leu Leu His Ile Thr Thr Cys
1               5                   10


<210> SEQ ID NO 292
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 292

Ser Phe Val Ala Pro Trp Asn Ser Leu Ser Leu Ala Gln Arg
1               5                   10


<210> SEQ ID NO 293
<211> LENGTH: 10
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 293

Ser Asp Asp Gly Trp Val Asn Leu Asn Arg
1               5                   10


<210> SEQ ID NO 294
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 294

Ser Tyr Gln Cys Pro Gln Gly Gln Val Ile Val Ala Val Arg
1               5                   10


<210> SEQ ID NO 295
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 295

Ser Leu Gly Glu Pro Thr Glu Cys Trp Trp Glu Glu Ile Asn Arg
1               5                   10                  15


<210> SEQ ID NO 296
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 296

Ser Asn Asn Gly Leu Val Ala Gly Phe Gln Ser Arg
1               5                   10


<210> SEQ ID NO 297
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 297

Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg
1               5                   10


<210> SEQ ID NO 298
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 298

Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys
1               5                   10
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<210> SEQ ID NO 299
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 299

Met Ala Ala Asp Gly Asp Phe Lys
1               5


<210> SEQ ID NO 300
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 300

Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro Ser Ala Met Tyr
1               5                   10                  15

Cys Asp Glu Leu Lys
            20


<210> SEQ ID NO 301
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 301

Arg Asn Asn Gln Ile Asp His Ile Asp Glu Lys
1               5                   10


<210> SEQ ID NO 302
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 302

Asn Asn Gln Ile Asp His Ile Asp Glu
1               5


<210> SEQ ID NO 303
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 303

Ile Leu Asp His Asn Leu Leu Glu Asn Ser Lys
1               5                   10


<210> SEQ ID NO 304
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 304
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```
Ser Leu Glu Asp Leu Gln Leu Thr His
1               5


<210> SEQ ID NO 305
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 305

Ile His Leu Gln His Asn Arg
1               5


<210> SEQ ID NO 306
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 306

Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser Lys
1               5                   10


<210> SEQ ID NO 307
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 307

Glu Val Pro Ser Ala Leu Pro Arg
1               5


<210> SEQ ID NO 308
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 308

Arg Leu Ser Gln Asn His Ile Ser Arg
1               5


<210> SEQ ID NO 309
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 309

Arg Leu Ser Gln Asn His Ile Ser Arg Ile Pro Pro Gly Val Phe Ser
1               5                   10                  15

Lys


<210> SEQ ID NO 310
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 310

Leu Ser Asp Gly Val Phe Lys Pro Asp Thr
1               5                   10


<210> SEQ ID NO 311
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 311

Asn Leu Ala His Asn Ile Leu Arg
1               5


<210> SEQ ID NO 312
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 312

Leu Ala His Asn Ile Leu Arg
1               5


<210> SEQ ID NO 313
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 313

Leu Asp Ser Asn Lys Ile Glu Thr Ile Pro Asn Gly Tyr Phe Lys Ser
1               5                   10                  15

Phe Pro Asn Leu Ala Phe Ile Arg
            20


<210> SEQ ID NO 314
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 314

Ile Glu Thr Ile Pro Asn Gly Tyr Phe Lys Ser Phe Pro Asn Leu Ala
1               5                   10                  15


<210> SEQ ID NO 315
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 315

Ser Phe Pro Asn Leu Ala Phe Ile Arg Leu Asn Tyr Asn
1               5                   10
```

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<210> SEQ ID NO 316
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 316

Leu Asn Asn Asn Ser Ile Glu Lys
1               5


<210> SEQ ID NO 317
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 317

Asp Leu Val Ala Phe His Asp Phe Ser Ser Asp Leu Glu Asn Val Pro
1               5                   10                  15

His Leu Arg


<210> SEQ ID NO 318
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 318

Glu Leu Glu Pro Gly Val Glu Tyr Phe Ile Arg
1               5                   10


<210> SEQ ID NO 319
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 319

Thr Val Ser Ile Tyr Gly Val Ile Gln Gly Tyr Arg
1               5                   10


<210> SEQ ID NO 320
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 320

Thr Val Thr Leu His Gly Glu Val Arg
1               5


<210> SEQ ID NO 321
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 321
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Phe Arg Ile Thr Tyr Val Pro Ile Thr Gly Gly Thr Pro Ser Met Val
1               5                   10                  15

Thr Val Asp Gly Thr Lys
            20


<210> SEQ ID NO 322
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 322

Trp Arg Pro Gln Pro Pro Ala Glu Gly Pro Gly Gly Glu Leu Thr Val
1               5                   10                  15

Pro Gly Thr Thr Arg Thr Val Ser
            20


<210> SEQ ID NO 323
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 323

Phe Asp Ser Phe Thr Val Gln Tyr Lys
1               5


<210> SEQ ID NO 324
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 324

Gly Glu Glu Ser Glu Val Thr Val Gly Gly Leu Glu Pro Gly Arg
1               5                   10                  15


<210> SEQ ID NO 325
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 325

Glu Pro Pro Asn Lys Pro Arg
1               5


<210> SEQ ID NO 326
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 326

Gly Phe Glu Glu Ser Glu Pro Leu Thr Gly Phe Leu Thr Thr Val Pro
1               5                   10                  15

Asp Gly Pro Thr Gln
```

```
            20


<210> SEQ ID NO 327
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 327

Ile Ser Cys Thr Ile Ala Asn Arg
1               5


<210> SEQ ID NO 328
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 328

Leu Phe Ser Asp Gly Asn Ser Gln Gly Ala Thr Pro Ala Ala Ile Glu
1               5                   10                  15

Lys Ala


<210> SEQ ID NO 329
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 329

Arg Gly Val Phe His Gln Thr Val Ser Arg Lys
1               5                   10


<210> SEQ ID NO 330
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 330

Arg Gln Val Asn Glu Pro His Ile Arg Val
1               5                   10


<210> SEQ ID NO 331
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 331

Arg Thr Asp Pro Ala His Asp Val Arg Val
1               5                   10


<210> SEQ ID NO 332
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence
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<400> SEQUENCE: 332

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Asp Ala Pro Ile Val Asn Lys
1               5
```

<210> SEQ ID NO 333
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 333

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Ser Glu Pro Leu Ile Gly Arg
1               5
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<210> SEQ ID NO 334
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 334

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Ala Thr Ile Thr Gly Tyr Arg
1               5
```

<210> SEQ ID NO 335
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 335

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Ala Gln Ile Thr Gly Tyr Arg
1               5
```

<210> SEQ ID NO 336
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 336

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Ser Asp Thr Val Pro Ser Pro Arg
1               5
```

<210> SEQ ID NO 337
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 337

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Val Phe Ala Val Ser His Gly Arg
1               5
```

<210> SEQ ID NO 338
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 338

Ile Ser Cys Thr Ile Ala Asn Arg Cys
1               5


<210> SEQ ID NO 339
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 339

Pro Leu Thr Ala Gln Gln Thr Thr Lys
1               5


<210> SEQ ID NO 340
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 340

Tyr Glu Val Ser Val Tyr Ala Leu Lys
1               5


<210> SEQ ID NO 341
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 341

Gln Tyr Asn Val Gly Pro Ser Val Ser Lys
1               5                   10


<210> SEQ ID NO 342
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 342

Gly Ala Thr Tyr Asn Ile Ile Val Glu Ala Leu Lys
1               5                   10


<210> SEQ ID NO 343
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 343

Asp Leu Gln Phe Val Glu Val Thr Asp Val Lys
1               5                   10


<210> SEQ ID NO 344
<211> LENGTH: 13
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 344

Leu Gly Val Arg Pro Ser Gln Gly Gly Glu Ala Pro Arg
1               5                   10


<210> SEQ ID NO 345
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 345

Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg
1               5                   10


<210> SEQ ID NO 346
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 346

Val Pro Gly Thr Ser Thr Ser Ala Thr Leu Thr Gly Leu Thr Arg
1               5                   10                  15


<210> SEQ ID NO 347
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 347

Val Asp Val Ile Pro Val Asn Leu Pro Gly Glu His Gly Gln Arg
1               5                   10                  15


<210> SEQ ID NO 348
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 348

Lys Ala Cys Glu Asp Ile Asp Glu Cys Ser Leu Pro Asn Ile Cys Val
1               5                   10                  15

Phe Gly Thr Cys His Asn Leu Pro Gly Leu Phe Arg Cys
            20                  25


<210> SEQ ID NO 349
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 349

Tyr Thr Gly Leu Pro Val Asp Ile Asp Glu Cys Arg Glu
```

```
1               5                   10


<210> SEQ ID NO 350
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 350

Leu Pro Val Asp Ile Asp Glu Cys Arg Glu
1               5                   10


<210> SEQ ID NO 351
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 351

Arg Glu Ile Pro Gly Val Cys Glu Asn Gly Val Cys Ile Asn Met Val
1               5                   10                  15

Gly Ser Phe Arg Cys
            20


<210> SEQ ID NO 352
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 352

Lys Leu Leu Val Cys Glu Asp Ile Asp Glu Cys Gln Asn Gly Pro Val
1               5                   10                  15

Cys Gln Arg Asn
            20


<210> SEQ ID NO 353
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 353

Arg Thr Cys Val Asp Ile Asn Glu Cys Leu Leu Glu Pro Arg Lys
1               5                   10                  15


<210> SEQ ID NO 354
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 354

Lys Gly Glu Gly Trp Gly Asp Pro Cys Glu Leu Cys Pro Thr Glu Pro
1               5                   10                  15

Asp Glu Ala Phe Arg Gln
            20
```

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<210> SEQ ID NO 355
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic amino acid sequence

<400> SEQUENCE: 355

Asn Pro Gly Ala Pro Gly Pro Arg
1               5
```

What is claimed is:

1. A method for detecting an unstable arteriosclerotic plaque in an individual, the method comprising detecting in a biological sample from the individual an enzymatic cleavage product of a protein component of an arteriosclerotic plaque.

2. The method of claim **1**, wherein the protein component is a structural protein.

3. The method of claim **1**, wherein the protein component is a non-enzymatic protein.

4. The method of claim **1**, wherein the individual is asymptomatic with respect to an arterial occlusive event.

5. The method of claim **1**, wherein the subject is an apparently healthy human subject.

6. The method of claim **1**, wherein the individual has experienced one or more typical symptoms of cardiovascular disease.

7. The method of claim **1**, wherein the individual has experienced an atypical symptom of cardiovascular disease.

8. The method of claim **1**, wherein the biological sample is blood or a blood fraction.

9. The method of claim **6**, wherein the blood fraction is serum or plasma.

10. The method of claim **1**, wherein the level of the one or more enzymatic cleavage products is determined by an immunological method.

11. The method of claim **1**, wherein the protein component is fibrillin, vitronectin, fibronectin, tenascin, prolargin, dermatopontin, vascular collagen, metalloproteinase inhibitor-1, galectin-1, or tenascin-X.

12. The method of claim **11**, where the collagen is collagen alpha-1 (I) chain, collagen alpha-1 (II) chain, collagen alpha-1 (IV) chain, collagen alpha-1 (VI) chain, collagen alpha-1 (XII), collagen alpha-1 (XIV) chain, collagen alpha-1 (XV) chain, collagen alpha-1 (XVIII), collagen alpha-1 (XIX), collagen alpha-2 (I) chain, collagen alpha-3 (VI), collagen alpha-2 (IV), or collagen alpha-5 (IV).

13. The method of claim **1**, wherein the enzymatic cleavage product has a molecular weight in a range of from about 0.5 kDa to about 50 kDa.

14. The method of claim **1**, wherein the enzymatic cleavage product has a length in a range of from about 5 amino acids to about 500 amino acids.

15. The method of claim **1**, wherein said detecting further comprises processing the enzymatic cleavage product in vitro.

16. The method of claim **15**, wherein said processing comprises trypsin digestion.

17. The method of claim **1**, wherein the enzymatic cleavage product is a cleavage product of a matrix metalloproteinase (MMP).

18. The method of claim **17**, wherein the MMP is secreted by a macrophage.

19. The method of claim **17**, wherein the MMP is MMP1, MMP2, MMP3, MMP7, MMP8, MMP9, MMP10, MMP11, MMP12, or MMP13.

20. The method of claim **1**, wherein the enzymatic cleavage product is a cleavage product of a cathepsin.

21. The method of claim **1**, wherein the method comprises generating a report providing an indication of the risk that the individual will experience an occlusive vascular event.

22. A method for determining a risk that an individual will develop an occlusive vascular event, the method comprising:

a) assaying the level, in a biological sample from the individual, of an enzymatic cleavage product of a protein component of an arteriosclerotic plaque;

b) identifying the individual as being at risk of developing an occlusive vascular event when the level of the enzymatic cleavage product is higher than a normal control level.

23. The method of claim **22**, wherein the protein component is fibrillin, vitronectin, fibronectin, tenascin, prolargin, dermatopontin, vascular collagen, metalloproteinase inhibitor-1, galectin-1, or tenascin-X.

24. The method of claim **22**, wherein the level of the one or more enzymatic cleavage products is determined by an immunological method.

25. The method of claim **22**, wherein the biological sample is blood, serum, or plasma.

26. The method of claim **22**, wherein the subject is an apparently healthy human subject.

27. The method of claim **22**, wherein the individual does not have a history of having an occlusive vascular event.

28. The method of claim **22**, further comprising outputting a report indicating a risk assessment based on said identifying to facilitate a treatment decision by a clinician.

29. A kit for detecting an unstable arteriosclerotic plaque in an individual, the kit comprising:

a) a binding reagent that specifically binds an enzymatic cleavage product of a protein component of an arteriosclerotic plaque;

b) a control that provides for quantitation of the enzymatic product.

30. The kit of claim **29**, wherein the reagent that specifically binds an enzymatic cleavage product of a protein component of an arteriosclerotic plaque is an antibody.

31. The kit of claim **30**, wherein the antibody is a monoclonal antibody, or an antigen-binding fragment.

32. The kit of claim **29**, wherein the antibody is immobilized on an insoluble support.

33. The kit of claim **29**, wherein the antibody comprises a detectable label.

34. The kit of claim **29**, further comprising one or more reagents for developing a detectable label.

35. An assay device for use in detecting, in a liquid biological sample obtained from an individual, an enzymatic cleavage product of a protein component of an arteriosclerotic plaque, the device comprising a matrix defining an axial flow path, the matrix comprising:

i) a sample receiving zone at an upstream end of the flow path that receives the liquid sample;

ii) one or more test zones positioned within the flow path and downstream from the sample receiving zone, each of said one or more test zones comprising an antibody specific for an enzymatic cleavage product of a protein component of an arteriosclerotic plaque immobilized in each of said test zones, wherein each of said immobilized antibodies is capable of binding different enzymatic cleavage product present in said liquid sample, to form an immobilized antibody/enzymatic cleavage product complex; and

iii) one or more control zones positioned within the flow path and downstream from the sample receiving zone.

36. The assay device of claim **35**, wherein the one or more control zones are positioned between the test zones when two or more test zones are present.

37. The assay device of claim **35**, wherein the test zones and control zones are positioned in an alternating format within the flow path beginning with a test zone positioned upstream of any control zone.

38. The assay device of claim **35**, further comprising a label zone positioned upstream of a test zone, wherein the label zone comprises a labeled antibody specific for an enzymatic cleavage product of a protein component of an arteriosclerotic plaque, wherein the labeled antibody is capable of binding an enzymatic cleavage product present in an immobilized antibody/enzymatic cleavage product complex to form a labeled immobilized antibody/enzymatic cleavage product complex, and wherein the labeled antibody is mobilizable in the presence of the liquid sample.

39. The assay device of claim **38**, wherein the labeled antibody comprises a label component selected from the group consisting of a chemiluminescent agent, a particulate label, a colorimetric agent, an energy transfer agent, an enzyme, a fluorescent agent, and a radioisotope.

40. The assay device of claim **35**, wherein the matrix is positioned within a housing comprising a support and optionally a cover, wherein the housing contains an application aperture and one or more observation ports.

41. The assay device of claim **35**, wherein the device is a test strip.

42. The assay device of claim **35**, wherein the device is a dipstick assay device.

43. The assay device of claim **35**, wherein the liquid sample is blood, serum, or plasma.

44. A panel of purified enzymatic cleavage products of a protein component of an arteriosclerotic plaque.

45. The panel of claim **44**, wherein the panel comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 10-15, 15-20, 20-25, 25-30, 30-35, 35-40, 40-45, 45-50, or more than 50, different enzymatic cleavage products.

46. The panel of claim **44**, wherein the protein component is fibrillin, vitronectin, fibronectin, tenascin, prolargin, dermatopontin, vascular collagen, metalloproteinase inhibitor-1, galectin-1, or tenascin-X.

47. The panel of claim **44**, wherein each enzymatic cleavage product has a length in a range of from about 5 amino acids to about 500 amino acids.

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专利名称(译)	用于检测不稳定动脉硬化斑块的组合物和方法		
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摘要(译)

本公开内容提供了检测个体中不稳定的动脉硬化斑块的方法，包括在来自个体的生物样品中检测动脉硬化斑块的蛋白质组分的酶促裂解产物。本公开提供了评估个体发生闭塞性血管事件的风险的方法。本公开还提供了用于实施主题方法的试剂盒。

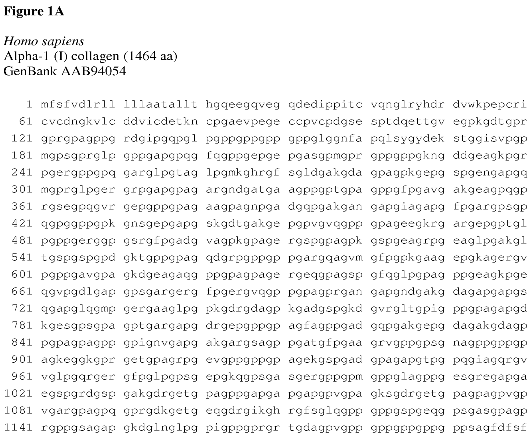

Figure 1A

Homo sapiens
Alpha-1 (I) collagen (1464 aa)
GenBank AAB94054

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 121 gprgpagppg rdgipgqpgl pgppgppgpp gppglggnfa pqlsygydek stggisvpgp
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