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Kask et al.

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(54) **DIAGNOSTIC MARKER FOR NEUROLOGICAL CONDITIONS**

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(52) **U.S. Cl.** **435/7.1**; 435/4

(58) **Field of Search** 435/4, 7.1

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(57) **ABSTRACT**

The invention relates to a human phospholipase C expressed in the brain (B-PLC) and induced in response to ischemic brain tissue. The inventions provides methods and reagents useful for diagnosis and treatment of hypoxic-ischemic brain insult such as stroke.

6 Claims, 11 Drawing Sheets

FIG. 1A

1/1
 ATG CCA ACA GAG AAG AAG ATC AGC AGT GCA AGT GAT TGT ATT AAT TCA ATG GTT GAG GGT
 M P T E K K I S S A S D C I N S M V E G
 61/21
 TCA GAA CTC AAA AAG GTT CGC TCC AAC TCT AGA ATT TAT CAT AGG TAC TTT CTA CTG GAT
 S E L K K V R S N S R I Y H R Y F L L D
 121/41
 GCT GAC ATG CAG AGC CTA AGG TGG GAG CCA TCT AAG AAG GAT TCT GAG AAA GCC AAG ATT
 A D M Q S L R W E P S K K D S E K A K I
 181/61
 GAC ATT AAA TCC ATC AAG GAA GTG AGA ACG GGA AAA AAC ACA GAC ATA TTC CGC AGC AAT
 D I K S I K E V R T G K N T D I F R S N
 241/81
 GGC ATT TCT GAC CAG ATA TCT GAA GAT TGT GCG TTT TCC GTC ATA TAT GGA GAG AAT TAT
 G I S D Q I S E D C A F S V I Y G E N Y
 301/101
 GAG TCA CTG GAT TTG GTT GCC ACT CTC GCA GAT GTT GCA AAC ATC TGG GTT ACA GGA CTG
 E S L D L V A T L A D V A N I W V T G L
 361/121
 CGG TAC CTA ATT TCT TAT GGA AAA CAT ACA CTT GAT ATG TTA GAA AGT AGC CAA GAT AaC
 R Y L I S Y G K H T L D M L E S S Q D N
 421/141
 ATG AGG ACT TCT TGG GTT TCA CAA ATG TTT AGT GAA ATT GAT GTA GAT AAC CTT GGA CAT
 M R T S W V S Q M F S E I D V D N L G H
 481/161
 ATA ACT CTG TGT AAT GCT GTG CAA TGT ATC AGA AAC CTC AAT CCT GGT TTA AAA ACG AGC
 I T L C N A V Q C I R N L N P G L K T S
 541/181
 AAA ATT GAG CTT AAG TTC AAA GAA TTG CAT AAA TCA AAG GAC AAA GCT GGT ACC GAG GTC
 K I E L K F K E L H K S K D K A G T E V
 601/201
 ACA AAG GAA GAA TTT ATT GAG GTT TTT CAT GAG CTT TGT ACT AGA CCT GAA ATT TAT TTC
 T K E E F I E V F H E L C T R P E I Y F
 661/221
 CTT TTA GTT CAG TTT TCA AGC AAT AAA GAA TTC CTT GAT ACC AAG GAC CTT ATG ATG TTT
 L L V Q F S S N K E F L D T K D L M M F
 721/241
 CTT GAG GCA GAA CAG GGT GTG GCA CAT ATA AAT GAG GAA ATA AGC CTT GAA ATT ATT CAC
 L E A E Q G V A H I N E E I S L E I I H
 781/261
 AAA TAT GAA CCA TCC AAA GAG GGT CAG GAA AAG GGC TGG CTC TCC ATA GAC GGG TTC ACT
 K Y E P S K E G Q E K G W L S I D G F T
 841/281
 AAT TAC CTT ATG TCA CCT GAC TGT TAT ATA TTC GAT CCA GAA CAT AAG AAG GTC TGT CAG
 N Y L M S P D C Y I F D P E H K K V C Q
 901/301
 GAT ATG AAG CAA CCT CTG TCT CAT TAC TTT ATA AAC TCA TCT CAT AAT ACA TAC TTA ATA
 D M K Q P L S H Y F I N S S H N T Y L I
 961/321
 GAG GAT CAG TTC CGA GGT CCC TCC GAC ATC ACA GGA TAT ATT CGA GCT CTT AAA ATG GGT
 E D Q F R G P S D I T G Y I R A L K M G
 1021/341
 TGC CGG AGT GTT GAA TTA GAT GTA TGG GAT GGG CCG GAC AAT GAA CCT GTA ATT TAC ACA
 C R S V E L D V W D G P D N E P V I Y T
 1081/361
 GGC CAC ACC ATG ACC TCT CAG ATA GTT TTC CGC AGT GTC ATT GAT ATT ATT AAC AAG TAT
 G H T M T S Q I V F R S V I D I I N K Y
 1141/381
 GCA TTC TTT GCT TCA GAG TAT CCT CTT ATC TTG TGT TTA GAA AAC CAC TGT TCC ATT AAA
 A F F A S E Y P L I L C L E N H C S I K
 1201/401
 CAA CAG AAG GTA ATG GTT CAG CAC ATG AAG AAA CTT TTA GGA GAC AAG CTC TAT ACA ACA
 Q Q K V M V Q H M K K L L G D K L Y T T
 1261/421
 31/11
 AGT GAT TGT ATT AAT TCA ATG GTT GAG GGT
 S D C I N S M V E G
 91/31
 AGA ATT TAT CAT AGG TAC TTT CTA CTG GAT
 R I Y H R Y F L L D
 151/51
 TCT AAG AAG GAT TCT GAG AAA GCC AAG ATT
 S K K D S E K A K I
 211/71
 GGA AAA AAC ACA GAC ATA TTC CGC AGC AAT
 G K N T D I F R S N
 271/91
 GCG TTT TCC GTC ATA TAT GGA GAG AAT TAT
 A F S V I Y G E N Y
 331/111
 GAT GTT GCA AAC ATC TGG GTT ACA GGA CTG
 D V A N I W V T G L
 391/131
 CTT GAT ATG TTA GAA AGT AGC CAA GAT AaC
 L D M L E S S Q D N
 451/151
 AGT GAA ATT GAT GTA GAT AAC CTT GGA CAT
 S E I D V D N L G H
 511/171
 AGA AAC CTC AAT CCT GGT TTA AAA ACG AGC
 R N L N P G L K T S
 571/191
 AAA TCA AAG GAC AAA GCT GGT ACC GAG GTC
 K S K D K A G T E V
 631/211
 GAG CTT TGT ACT AGA CCT GAA ATT TAT TTC
 E L C T R P E I Y F
 691/231
 GAT ACC AAG GAC CTT ATG ATG TTT
 F L D T K D L M M F
 751/251
 AAT GAG GAA ATA AGC CTT GAA ATT ATT CAC
 N E E I S L E I I H
 811/271
 AAG GGC TGG CTC TCC ATA GAC GGG TTC ACT
 K G W L S I D G F T
 871/291
 TTC GAT CCA GAA CAT AAG AAG GTC TGT CAG
 F D P E H K K V C Q
 931/311
 ATA AAC TCA TCT CAT AAT ACA TAC TTA ATA
 I N S S H N T Y L I
 991/331
 ACA GGA TAT ATT CGA GCT CTT AAA ATG GGT
 T G Y I R A L K M G
 1051/351
 GGG CCG GAC AAT GAA CCT GTA ATT TAC ACA
 G P D N E P V I Y T
 1111/371
 CGC AGT GTC ATT GAT ATT ATT AAC AAG TAT
 R S V I D I I N K Y
 1171/391
 TTG TGT TTA GAA AAC CAC TGT TCC ATT AAA
 L C L E N H C S I K
 1231/411
 AAA CTT TTA GGA GAC AAG CTC TAT ACA ACA
 K L L G D K L Y T T
 1291/431

FIG. 1B

TCA CCC AAT GTT GAG GAA TCT TAT CTA CCA TCC CCA GAT GTC CTG AAA GGG AAA ATA CTA
S P N V E E S Y L P S P D V L K G K I L
1321/441 1351/451
ATT AAA GCA AAG AAG CTG TCC TCA AAT TGT TCT GGG GTA GAA GGA GAT GTT ACT GAC GAA
I K A K K L S S N C S G V E G D V T D E
1381/461 1411/471
GAT GAA GGA GCA GAA ATG TCT CAG AGG ATG GGA AAA GAG AAC ATG GAG CAA CCC AAT AAT
D E G A E M S Q R M G K E N M E Q P N N
1441/481 1471/491
GTG CCT GTG AAG CGA TTT CAG CTT TGT AAA GAA CTG TCT GAA CTG GTC AGC ATC TGC AAA
V P V K R P Q L C K E L S E L V S I C K
1501/501 1531/511
TCA GTT CAG TTC AAA GAA TTT CAG GTG TCG TTT CAG GTT CAG AAG TAC TGG GAA GTC TGT
S V Q P K E F Q V S F Q V Q K Y W E V C
1561/521 1591/531
TCC TTT AAT GAA GTG CTT GCC AGC AAG TAC GCC AAT GAA AAT CCA GGG GAC TTT GTA AAT
S F N E V L A S K Y A N E N P G D F V N
1621/541 1651/551
TAC AAC AAA CGT TTT CTT GCT AGG GTT TTT CCC AGT CCA ATG AGA ATT GAT TCC AGT AAC
Y N K R F L A R V F P S P M R I D S S N
1681/561 1711/571
ATG AAT CCT CAA GAT TTT TGG AAA TGT GGT TGC CAA ATT GTA GCC ATG AAC TTT CAG ACA
M N P Q D F W K C G C Q I V A M N F Q T
1741/581 1771/591
CCA GGA CTG ATG ATG GAC CTG AAT ATT GGC TGG TTT AGG CAG AAC GGA AAC TGT GGC TAT
P G L M M D L N I G W F R Q N G N C G Y
1801/601 1831/611
GTC CTC CGG CCA GCC ATC ATG AGG GAG GAG GTC TCC TTC TTC AGC GCC AAT ACA AAA GAC
V L R P A I M R E E V S F F S A N T K D
1861/621 1891/631
TCT GTC CCA GGG GTC TCA CCT CAA CTT CTT CAC ATT AAA ATC ATC AGT GGG CAG AAC TTT
S V P G V S P Q L L H I K I I S G Q N F
1921/641 1951/651
CCC AAG CCC AAA GGA TCA GGT GCC AAA GGT GAT GTA GAT CCT TAT GTC TAT GTT GAA
P K P K G S G A K G D V V D P Y V Y V E
1981/661 2011/671
ATC CAT GGA ATC CCT GCT GAT TGT GCA GAA CAA AGG ACA AAA ACA GTG CAC CAG AAT GAA
I H G I P A D C A E Q R T K T V H Q N G
2041/681 2071/691
GAC GCT CCC ATT TTT GAT GAA AGC TTT GAA TTT CAA ATC AAC CTG CCT GAA CTG GCC ATG
D A P I F D E S F E F Q I N L P E L A M
2101/701 2131/711
GTG CGC TTT GTA GTG CTG GAT GAT GAC TAC ATT GGG GAT GAA TTC ATG GGC CAG TAC ACA
V R F V V L D D D Y I G D E F M G Q Y T
2161/721 2191/731
ATT CCC TTT GAA TGT TTA CAG ACG GGC TAC CGC CAT GTC CCC CTG CAG TCC TTA ACT GGA
I P F E C L Q T G Y R H V P L Q S L T G
2221/741 2251/751
GAG GTC CTT GCA CAT GCT TCT TTA TTT GTC CAC GTG GCT ATT ACT AAC CGA AGA GTA GGA
E V L A H A S L F V H V A I T N R R V G
2281/761 2311/771
GGA AAG CCT CAT AAA AGG GGC CTT TCT GTG AGA AAA GGG AAG AAA TCC AGG GAA TAT GCA
G K P H K R G L S V R K G K K S R E Y A
2341/781 2371/791
TCT TTG AGA ACA CTG TGG ATT AAA ACC GTG GAT GAG GTA TTC AAG AAT GCC CAG CCC CCT
S L R T L W I K T V D E V F K N A Q P P
2401/801 2431/811
ATA CGG GAT GCC ACA GAT CTG AGA GAA AAC ATG CAG AAT GCG GTG GTG TCA TTC AAG GAG
I R D A T D L R E N M Q N A V V S F K E
2461/821 2491/831
CTG TGT GGC CTC TCC TCT GTG GCC CTC ATG CAG TGC ATG TTG GCG GTG TCT CCC CGC
L C G L S S V A N L M Q C M L A V S P R
2521/841 2551/851
TTT CTG GGG CCC GAT AAC ACA CCC CTA GTG GTC CTA AAT CTC AGC GAG CAG TAC CCC ACA
F L G P D N T P L V V L N L S E Q Y P T

FIG. 1C

2581/861
ATG GAG CTG CAG GGA ATT GTG TCG GAG GTT CTG AAG AAG ATC GTA ACA ACT TAT GAC ATG
M E L Q G I V S E V L K K I V T T Y D M

2611/871
CTG AAG AAG ATC GTA ACA ACT TAT GAC ATG

2641/881
ATG ATT CAG TCC CTC AAG GCG TTG ATT GAA AAT GCA GAT GCT GTA TAT GAA AAG ATC GTA
M I Q S L K A L I E N A D A V Y E K I V

2671/891
AAT GCA GAT GCT GTA TAT GAA AAG ATC GTA

2701/901
CAT TGT CAG AAG GCA GCC ATG GAA TTC CAT GAA CAC TTG CAC AGC ATA GGC ACC AAG GAA
H C Q K A A M E F H E H L H S I G T K E

2731/911
GAA CAC TTG CAC AGC ATA GGC ACC AAG GAA

2761/921
GGT TTG AAG GAA AGA AAA CTA CAA AAA GCA GTG GAG AGC TTT ACC TGG AAT ATT ACC ATC
G L K E R K L Q K A V E S F T W N I T I

2791/931
GTG GAG AGC TTT ACC TGG AAT ATT ACC ATC

2821/941
TTA AAG GGA CAA GCA GAT CTT TTG AAA TAT GCT AAG AAT GAG ACA TTG GAG AAC CTG AAA
L K G Q A D L L K Y A K N E T L E N L K

2851/951
GCT AAG AAT GAG ACA TTG GAG AAC CTG AAA

2881/961
CAA ATC CAT TTT GCT GCT GTT TCA TGT GGA CTG AAT AAA CCA GGC ACC GAA AAT GCT GAT
Q I H F A A V S C G L N K P G T E N A D

2911/971
CTG AAT AAA CCA GGC ACC GAA AAT GCT GAT

2941/981
GTC CAG AAG CCA CGC CGG AGC TTG GAA GTC ATA CCC GAA AAA GCA AAC GAT GAA ACT GGA
V Q K P R R S L E V I P E K A N D E T G

2971/991
ATA CCC GAA AAA GCA AAC GAT GAA ACT GGA

3001/1001
GAA TGA
E *

FIG. 2

atgccaacagagaagaagatcagcagtgcaagtgattgtattaattcaatgggtgaggggt
tcagaactcaaaaagggttcgctccaactctagaatttatcataggtactttctactggat
gctgacatgcagagcctaagggtgggagccatctaagaaggattctgagaaagccaagatt
gacattaaatccatcaaggaagtgagaacgggaaaaaacacagacatattccgcagcaat
ggcatttctgaccagatctctgaagattgtgcggtttccgctcatatattggagagaattat
gagtcactggatttgggtgcccactctcgcagatggtgcaaacatctgggttacaggactg
cggtaacctaatctcttatggaaaacatacacttgatatggttagaaagtagccaagataac
atgaggacttcttgggtttcacaaatggttagtgaaattgatgtagataaccttggacat
ataactctgtgtaatgctgtgcaatgtatcagaaaacctcaatcctgggttaaaaaacgagc
aaaattgagcttaagttcaaagaattgcataaatcaaaggacaaagctggtaccgaggtc
acaaaggaagaatttattgaggtttttcatgagctttgtactagacctgaaatttatttc
cttttagttcagttttcaagcaataaagaattccttgataccaaggaccttatgatggtt
cttgaggcagaacaggggtgtggcacatataaatgaggaaataagccttgaaattattcac
aaatattgaacctccaaagaggggtcaggaaaagggctggctctccatagacgggttact
aattaccttatgtcacctgactggttatataattcgatccagaacataagaaggctgtgcag
gatattgaagcaacctctgtctcattactttataaaactcatctcataatacacttaata
gaggatcagttccgaggtccctccgacatcacaggatataattcgagctcttaaaatgggt
tgccggagtggtgaattagatgtatgggatggccggacaatgaacctgtaatttacaca
ggccacaccatgacctctcagatagttttccgcagtgctattgatattattaacaagat
gcattctttgcttcagagtatcctcttatcttggttttagaaaacctggtccattaaa
caacagaaggtaatgggttcagcacatgaagaaacttttaggagacaagctctatacaaca
tcaccaatggttgaggaatcttatctaccatccccagatgtcctgaaagggaaaatacta
attaaagcaaagaagctgtcctcaaattgttctggggtagaaggagatggtactgacgaa
gatgaaggagcagaaatgtctcagaggatgggaaaagagaacatggagcaaccaataat
gtgcctgtgaagcgatttcagctttgtaagaactgtctgaactggctcagcatctgcaaa
tcagttcagttcaaagaatttcaggtgtcgtttcaggttcagaagtactgggaagtctgt
tcctttaatgaagtgcttgccagcaagtagccaatgaaaatccaggggactttgtaaat
tacaacaaacgttttcttgctagggttttccagtcctaatgagaattgattccagtaac
atgaatcctcaagatttttgaaaatgtggttgccaaattgtagccatgaactttcagaca
ccaggactgatgatggacctgaatattggctgggttaggcagaacggaaactgtggctat
gtcctccggccagccatcatgaggaggagggtctccttcttcagcgcctaatacaaaagac
tctgtcccaggggtctcacctcaacttcttcacattaaaatcatcagtgggcagaacttt
cccaagcccaaaggatcaggtgcaaagggtgatgtggttagatccttatgtctatgttgaa
atccatggaatccctgctgattgtgcagaacaaaggacaaaaacagtgaccagaatgga
gacgctcccatttttgatgaaagctttgaatttcaaatacaactgctgaactggccatg
gtgcgctttgtagtgtggatgatgactacattggggatgaattcatgggcccagtagaca
attccctttgaatggttacagacgggctaccgcatgtccccctgcagtccttaactgga
gaggtccttgacatgcttctttatttgtccacgtggctattactaaccgaagagtagga
ggaaagcctcataaaagggcctttctgtgagaaaaggaagaatccaggggaatagca
tctttgagaacactgtggattaaaaccgtggatgaggtattcaagaatgccagccccct
atacgggatgccacagatctgagagaaaacatgcagaatgcggtgggtgtcattcaaggag
ctgtgtggcctctcctctgtggccaatctcatgcagtgcatgttggcgggtgtctccccgc
tttctggggcccgataaacacacccttagtggtcctaaatctcagcagcagtagccccaca
atggagctgcagggaaattgtgtcggaggttctgaagaagatcgtaacaacttatgacatg
atgattcagtcctcaaggcgttgattgaaaatgcagatgctgtatagaaaagatcgta
cattgtcagaaggcagccatggaattccatgaacacttgacagcataggcaccaggaa
ggtttgaaaggaagaaaactacaaaaagcagtgagagctttacctggaatattaccatc
ttaaagggacaagcagatcttttgaaatagctaagaatgagacattggagaacctgaaa
caaatccattttgctgtgtttcatgtggactgaaataaacaggcaccgaaaatgctgat
gtccagaagccagcggagcttggaagtcatacccgaaaaagcaaacgatgaaactgga
aatga (SEQ ID NO: 01)

FIG. 3

TGTTATTAATAAAAATAAAGGGCCAGAATTGTCTCAAAGGATGGGAAAAGAGATTGGGAC
CACCCACCCATGGGCTTGTAAGCGATTTAAGCTTTGCAAAGACCTGTCTTAACTGGC
AGCATCTGTAAGTCAGTCCAGTTCAGAAGTTCAGGTGTCGTTTCAGGTGCAAAAGTAC
TGGGAAGTGTGTTCAATCAATGAAGTGCTAGCCAGTAAATACGCCAATGAGAATCCTGGG
GACTTGTAAATPACAATAAGCGTTTCCTCGCCAGAGTCTTTCCTAGTCCAATGAGAATT
GATTCTAGTAACATGAACCCTCAAGATTTTTGGAAATGTGGCTGTCAAATCGTAGCCATG
AACTTTCAGACTCCAGGGCTAATGATGGATCTGAACATTGGCTGTTTAGGCAGAATGGA
AACTGTGGCTATGTTCTTCGACCAGCCATCATGAGGGAAGAAGTCTCCTTCTTCAGTGCC
AACACAAAGGACTCTGTCCCTGGAGTTTCGCCTCAGTTGCTTACATCAAATCATCAGT
GGCCAGAACTTTCCAAGCCCAAAGGGTCAGGTGCCAAAGGGGATGTGGTGGACCCTT
(SEQ ID NO: 03)

TGSICKSVQFKKFQVSFQVQKYWEVCSFNEVLASKYANENPGDFVNYNKRFLARVFPSPM
RIDSSNMNPQDFWKCGCQIVAMNFQTPGLMMDLNIGWFRQNGNCGYVLRPAIMREEVSFF
SANTDKSVPGVSPQLLHIKIISGQNFPPKPGSGAKGDVVDP (SEQ ID NO: 04)

FIG. 4

GAGCAAACCCACGGCCTGCCCGCCGGAGCACCATCATCAACGATGGCACGAAGCAGAA
AAGAGAGCGGAAGAAGACCGTGTTCATTACAGCAGCATGCCAACAGAGAAGAAGATCAGCAG
TGCAAGCGACTGCATCAACTCAATGGTGGAGGGCTCTGAACTCAAGAAGGTTTCGTTCAA
CTCCAGAATTTACCATCGGTACTTTCTGCTGGACGCCGACATGCAAAGCCTGAGTGGGGA
GCCATCCAAGAAGGATTCTGAGAAAGCCAAGATTGACATCAAGTCCATCAAGGAAGTTAG
AACGGGGAAAAACACAGATATATTTCCCGCAGCAATGGGCATTCTGAGCAAATATCTGAA
AGATTGTGCGTTTTTCAGTCATATATGGAGAAAATATGAGTCACTCCGATTTGGTTGCCAA
TTCTGCAGATGTTGCAACATCTGGGTGACAGGACTCCGGTACCTGATTTCTTATGGGAA
ACATACACTTGATATGTTAGAAAGTAGCCAAGACAACATGAGGACTTGTGGGTTTACA
GATGTTTAGTGAAATGATGTAGATGACCTTGACATATAACTCTGTGTAATGCTGTTCA
GTGTATCAGAAACCTCAATCCTGGCTTAAAAACAAGCAAAATGAGCTTAAGTTCAAAGA
ACTGCATAAATCAAAGGACAAAACCTGGTACTGAAATCACAAGGAAGAATTTGTTGAGGT
TTTTCATGAACTTTGCACTAGACCTGAAATTTACTTCTTTTAGTTTCAAGTTCAGTTTCAAGCAA
TAAAGAATTCCTTGATACCAAGGACCTTATGATGTTTCTTGAGGCAGAACAGGGTGTAGC
ACATATAAATGAGGAAATAAGCCTGAAATTTACCAAAATATGAGCCATCCAAAGAAGG
CCAGGAAAAGGGCTGGCTCTCCATAGATGGGTTCACTAATTACCTGATGTACCTGATG
TTACATCTTTGATCCGGAACATAAGAAGGTCTGTGAGGATATGAAGCAACCTCTGTCTCA
TTACTTCATAAACTCATCTCATAATACATACTTAATAGAGGACCAGTTCCCGGGTCCCTC
TGACATTACAGGATATATCCGTGCTCTTAAATGGGTTGCAGGAGTGTGAGTTGGATGT
GTGGGATGGCCAGATAATGAGCCCGTATTACACAGGCCACACCATGACCTCTCAGAT
AGTCTCCCGCAGTGTTCATCGATATCATTAAACAAGTATGCATTCTTTGCTTCTGAGTATCC
TCTCATCCTGTGTTTAGAAAATCATGTTCTATTAAACAACAAAAGGTGATGGTTCAACA
CATGAAGAAAATTTTAGGAGACAAGCTGTATACCACATCACCCAACATGGAGGAATCTTA
TCTACCATCCCCGATGTCTGAAAGGGAAAATACTAATCAAAGCAAAGAAGCTGTCTTC
AAATGCTCTGGTGTGGAAGGGGATGTTACTGATGAAGATGAAGGGGCAGAAATGTCTCA
GAGGATGGGGAAAGAGAATGTGGAACAACCCAACCATGTGCCTGTGAAGCGATTTAGCT
TTGCAAAGACCTGTCTGAACTGGTCAAGCATCTGTAAGTCAAGTCCAGTTCAAGGAGTTCCA
GGTGTGCTTTCAGGTGCAGAAGTACTGGGAAGTGTGTTCAATCAATGAAGTCTAGCCAG
TAAATACGCCAATGAGAATCCTGGGGACTTTGTAAATTACAATAAGCGTTTCTCGCCAG
AGTCTTTCTAGTCCAATGAGAATTGATTCTAGTAACATGAACCTCAAGATTTTGGAA
ATGTGGCTGTCAAATCGTAGCCATGAACTTTGAGACTCCAGGGCTAATGATGGATCTGAA
CATTGGCTGGTTTAGGCAGAAATGAAACTGGGCGTAGTTCTTCGACCAGCCATCATGAG
GGAAGAAGTCTCCTTCTTCAGTGCCAACACAAAAGGACTCTGTCCCTGGAGTTTCGCCTCA
GTTGCTTACATCAAATCATCAGTGGCCAGAACTTTCCCAAGCCCAAGGGTCAAGGTGC
CAAAGGGGATGTGGTGGACCCCTATGTCTATGTGAAATCCATGGCATTCCTGCTGACTG
CGCAGAACAGAGGACGAAAACCTGTGAACCAGAATGGAGATGCTCCTATGTTGATGAAAG
CTTTGAATTTCAAATCAACCTCCCCGAACTAGCCATGGTGCCTTTTGTAGTGTGGATGA
TGACTACATTTGGCGATGAATTTATTGGCCAGTACACGATTCCCTTTGAATGTTTACAAAC
GGGCTACCGCCATGTGCCTCTGCAGTCTTACTGAGGAGGTCCTTGCCCATGCTTCTCT
GTTGCTCCACGTGGCTATTACTAACAGAAGAGGAGGAGGGAAAGCCTCATAAACGGGCCT
TTCTGTGAGGAAAGGGAAGAAGTCCCGGAATATGCATCTCTGAGAACACTGTGGATTAA
AACTGTAGATGAGGTGTTCAAGAATGCCAGCCCCCATCCGGGATGCCACAGACTGAG
AGAGAACATGCAGAATGCAGTGGTTTCTTTCAAGGAATTATGTGGCCTCTCCTCAGTGGC
CAACCTTATGCAGTGCATGCTGGCCGTCTCCTCGATTCTGGGGCCTGACAATACTCC
CCTGGTGGTCTTGAATCTTAGTGAGCCCTACCCACCATGAACTGCAGGCCATCGTGCC
TGAGGTTCTGAAGAAGATCGTCACAACCTTATGACATGATGATTCAGTCCCTCAAGGCAG
ATTGAAAATGCAGATGCTGTGTATGAAAAGATTGTGCACTGTGAGAAGGCAGCCATGGAA
TTTCATGAACACTTGACAGCATAGGCACCAAGGAGGACTGAAGGAACGGAACTACAG
AAGGCGGTGGAGAGCTTACCTGGAATATTACGATTTTAAAGGGACCTCGTGCCGAATTC
CTGCAGCCCG GGGATCC (SEQ ID NO: 05)

FIG. 5

MPTEKKISSASDCINSMVEGSELKKVRSNSRIYHRYFLLDADMQSLRWEP SKKDSEKAKI
DIKSIKEVRTGKNTDIFPQQWAFLSKYLKDCAFSVIYGENMSHSDLVANSADVANIWVTG
LRYLISYGKHTLDMLESSQDNMRTCWVSQMFSEIDVDDLGHITLCNAVQCIRNLNPGPKT
SKIELKFKELHKS KDKTGTEITKEEFVEVFHELCTRPEIYFLLVQFSSNKEFLDTKDLMM
FLEAEQGV AHINEEISLEIIHKYEPSKEGQEKWLSIDGFTNYLMSPCYIFDPEHKKVC
QDMKQPLSHYFINSSHNTYLI EDQFPGPSDITGYIRALKMGCRSVELDVWDGPDNEPVIY
TGHTMTSQIVFRSVIDIINKYAFFASEYPLIILCLENHCSIKQQKVMVQHMKKILGDKLYT
TSPNMEESYLPSPDVLKGIKILIKAKKLSSNCSGVEGDVTDEDEGAEMSQRMGKENVEQPN
HVPVKRFQLCKDLSELVSICKSVQFKEFQVSFQVQKYWEVCSFNEVLASKYANENPGDFV
NYNKRFLARVFPSPMRIDSSNMNPQDFWKCGCQIVAMNFQTPGLMMDLNI GWFRQNGNWA
LVLRPAIMREEVSFFSANTKDSVPGVSPQLLHIKII SGQNF PKPKGSGAKGDVVDPYVYV
EIHGIPADCAEQRTKTVNONGDAPMFDESFEFQINLPELAMVRFVVLDDDYIGDEFIQY
TIPFECLQTYRHVPLQSLTGEVLAHASLFVHVAITNRRGGGKPHKRGLSVRKGKKSREY
ASLRTLWIKTVDEVEFKNAQPPIRDATDLRENMQNAVVSFKELCGLSSVANLMQCMLAVSP
RFLGPDNTPLVVLNLSEPYPTMELQAIVPEVLKKIVTTYDMMIQSLKARLKMQLCMKRL
CTVRRQPWNFMNTCTA (SEQ ID NO:09)

FIG. 6

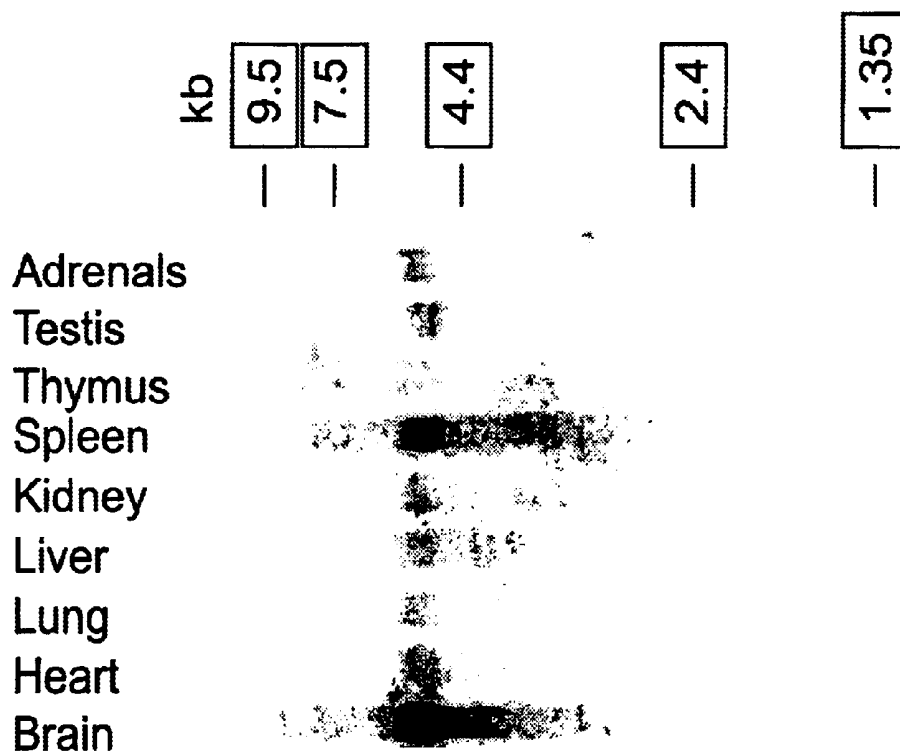


FIG. 7



a) DNA sequence of KIAA1092

CCGCGCGCGCGCCCGAGGCGGGCGGGGACGCGGGGACGCGAGGACGCGGCTTTGTGCAGGCGGGTC
GCGGGGCGCCCATGGCGGAGTGCGGCCGGGGGGCGCCGCGGGCGGGCCCTGCCACCTCCCCGGGGCC
GGCCCTCGGCGCAAGGGCGCCCTGAAAGCCGGAGTGGGGGAAGCGGTGCCGGGGAGGTCCCTCGGC
CACGGGCGGCGCGCTATGACAGCGCGGGGTTTCCAACGGAGACTGCAGCCTCGGCGTGTCCGGGACG
AAGCCCGGGCTAGCCCTACCAGGGGACCCCGCGGCTTGGCGCTCGCCCCGACCCCCAGCGGTCGTCTG
TACCCCTCCCCGGGAGAGCAAGCCGGGCGGCTGCCCGCCGGAGCAGCATCATCAAGGATGGTACAAA
CAGAAGAGGGAACGGAAGAACAGTCTCATTGAGCAGCATGCCAACAGAGAAGAATCAGCAGTGCAA
GTGATTGTATTAATCAATGGTTGAGGGTTGAGAACTCAAAAAGGTTCCGTCACACTAGAAATTTATCA
TAGGTACTTTTTACTGGATGCTGACATGCAGAGCCTAAGGTGGGAGCCATCTAAGAAGGATTCTGAGAAA
GCCAAGATTGACATTAATCCATCAAGGAAGTGAGAACAGGAAAAACACAGACATATCCCGCAGCAATG
GCATTTCTGACCAGATATCTGAAGATTGTGCGTTTTCCGTCATATATGGAGAGAATATGAGTCACTGGA
TTTGGTTGCCAACTCCGCGAGATGTTGCAAAACATCTGGGTTACAGGACTGCGGTACCTAATTTCTTATGGA
AAACATACACTTGATATGTTAGAAAGTAGCCAAGATAACATGAGGACTTCTTGGGTTTCAAAATGTTTA
GTGAAATTGATGTAGATAACCTTGGACATATAACTCTGTGTAATGCTGTGCAATGTATCAGAAACCTCAA
TCCTGGTTTAAAAACGAGCAAAATTGAGCTTAAGTTCAAAGAATTCATATAATCAAAGGACAAAGCTGGT
ACCGAGGTCACAAAGGAAGAAATTTATTGAGGTTTTTCATGAGCTTTGTACTAGACCTGAAATTTATTTCC
TTTATGTTCAAGTTCAGCAATAAAGAAATTCCTTGATACCAAGGACCTTATGATGTTCTTGAGGCAGA
ACAGGTTGTGGCACATATAAATGAGGAAATAAGCCTTGAATTTATCACAATATGAAACCTCAAAGAG
GGTCAGGAAAAGGGCTGGCTCTCCATGACGGGTTCACTAATTACCTTATGTCACCTGACTGTTATATAT
TCGATCCAGAACATAAGAAGGTTCTGTGAGGATATGAAGCAACCTCTGTCTCATTACTTTATAAATCATC
TCATAATACATACTTAATAGAGGATCAGTTCGAGGTCCTCCGACATCAGAGATATATTGAGCTCTT
AAAATGGGTTGCCGGAGTGTGAATTAGATGTATGGGATGGGCCGACAATGAACCTGTAATTTACACAG
GCCACACCATGACCTCTCAGATAGTTTTCCGCACTGTCTATTGATATTATAACAAGTATGCATTTCTTGC
TTCAGAGTATCCTCTTATCTTGTGTTAGAAAACCACTGTTCCATTAACAACAGAAAGGTAATGTTTCAG
CCCCAGATGCTCTGAAAGGGAAAATACTAATTAAGCAAAGAAGCTGTCTCAAATGCTCTGGGGTAGA
AGGAGATGTTACTGACGAAGATGAAGGAGCAGAAATGTCTCAGAGGATGGGAAAAGAGAACATGGAGCAA
CCCAATAATGTGCTGTGAAGCGATTTGAGCTTTGTAAAGAAGTGTCTGAACTGGTCAGCATCTGCAAAAT
CAGTTCAGTTCAAAGAATTTGAGGTGTGTTTTGAGGTTCAAGGACTGAGGAAAGTCTGTTCTTTAATGA
AGTCTTGGCCAGCAAGTACGCCAATGAAAATCCAGGGGACTTTGTAAATTACAACAACGTTTTCTTGTCT
AGGGTTTTTCCAGTCCAATGAGAATTGATCCAGTAACATGAATCCTCAAGATTTTTGGAAATGTGGTT
GCCAAATGTAGCCATGAACTTTCAGACACCAGGACTGATGATGGACCTGAAATATTGGCTGGTTTAGGCA
GAACGGAAAAGCTGTGGCTATGTCCTCCGGCCAGCCATCATGAGGGAGGAGGTTCTCTTCTTCAGCGCCAAT
ACAAAAGACTCTGTCCAGGGTCTCACCTCAACTTCTTACATTAATAATCATCAGTGGCCAGAACTTTC
CCAAGCCCAAAGGATCAGGTGCCAAAGGTGATGTGGTAGATCCTTATGCTATGTTGAAATCCATGGAAT
CCTGTCTGATTTGTGAGAACAAAGGACAAAACAGTGCACCAGAATGGAGACGCTCCCATTTTTGATGAA
AGCTTTGAATTTCAAATCAACTGCCTGAACTGGCCATGGTGGCTTTGTAGTGTGGATGATGACTACA
TTGGGGATGAATTCATCGGCCAGTACACAATCCCTTTGAATGTTTACAGACGGGCTACGCCCATGCCC
CCTGCAGTCTTAACTGGAGAGGTCCTTGCACATGCTTCTTATTATTGTTCCAGTGGCTATTACTAACCGA
AGAGGAGGAGGAAAAGCCTCATAAAAAGGGCCCTTCTGTGAGAAAAGGGAAGAAATCCAGGGAATAATGCAT
CTTTGAGAACACTGTGGATTAACCCGTGGATGAGGTATTCAAGAAATGCCAGCCCCCTATACGGGATGC
CACAGATCTGAGAGAAAACATGCAGAAATGCGGTGGTGTCAATCAAGGAGCTGTGTGGCCTCTCCTCTGTG
GCCAATCTCATGAGTGCATGTTGGCGGTGTCTCCCCGCTTTCTGGGGCCCGATAACACACCCCTAGTGG
TCCTAAATCTCAGCGAGCAGTACCCACAATGGAGCTGCAGGGAATGTGCGGAGGTTCTGAAGAAGAT
CGTAACAACCTATGACATGATGATTGAGTCCCTCAAGGCGTTGATTGAAAATGCAGATGCTGTATATGAA
AAGATCGTACATTTGTCAGAAGGCAGCCATGGAATTCATGAACACTTGCACAGCATAGGCAACCAAGGAAG
GTTTGAAGGAAAAGAAAACCTCAAAAAGCAGTGGAGAGCTTTACCTGGAATATTACCATCTTAAAGGGACA
AGCAGATCTTTGAAATATGCTAAGAATGAGACATTTGGAGAACCTGAAAACAAATCCATTTTGTCTGTGTT
TCATGTGGACTGAATAAACAGGCACCGAAAATGCTGATGTCCAGAAGCCAGCGGAGCTTGGAAATCA
TACCCGAAAAGCAAACGATGAACTGGAGAATGAGGAACTTACAATAAACCATTTATGGAGTTTATAAC
TCTAGGACCAATTTGATGATGAGTGGGACATTTGCTTTCAGTCACTAATGAGAATAATATCGGGATTTT
AAAGCACAACTGGAATAGCTAATTACAGTCTATTAAAACCTGGAATGTATGTAGCAATCCTGCGTGTGAA
GGCAATAAATACTCTTAAAGGCAATTAATTTGCTGGCCAAAATATGCTATATTTGTATACAAAGACAT
CTAACTCAGTTCCAGTATGAAGAAAGATTATTCACTCTAGCTCCACTGAGAAACATTTTCTTAAGTGAAA
ACAATTTCTTAAAGTGAATGGAAATGGATTGGATTGTCAAATTAATTTTATTTGGAGAAAAAACCCTGATCTAC
ACATTTTACTTATATGGGGTTGCCAGAGTCTCTGGGTTCTAGATGATTTTGGTGGCATGCTTGCTGAGC
CATAATTACTAAAGAGAATGTAAGTGGACGGGTTCCCTGAAATCCCCGGGGTCTTGGAGAGCCATCGAGG
AGAATGTGCAATTTGACTGAAGCTCCCTGGCTGAAGATACATGCCGAGTCAGCACATGGGTAGAGATGAT
GTAAGAGCAGCAATCTGAAAACAATACATTTGTAATAGTTTTTCAATGATGAAGTACTGTTTACATTA
AAAAGATGTTTTATGAT

FIG. 8A

FIG. 8B

B) Protein sequence of KIAA1092

PRAAARGGGGDAGTRGRGFVQAGRGAPMAECGRGGAAGGALPTSPGPALGAKGALKAGVGEAGGGGGRLG
HGRARYDSGGVSNDCSLGVSDEARASPTRGPRGVALAPTPSAVVCTLPRESKPGGLPRRSIIKDGTK
OKRERKKTVSFSSMPTEKKISSASDCINSMVEGSELKKVRSNSRIYHRYFLLDADMQSLRWEPSSKDKSEK
AKIDIKSIKEVRTGKNTDI PRSNGISDQISEDCAF SVIYGENYESLDLVANSADVANIWVTGLRYLISYG
KHTLDMLESSQDNMRTSWVSQMFSEIDVDNLGHITLCNAVQCIRNLNPLKTSKIELKFKELHKSCKD KAG
TEVTKEEFIEVPHELCTRPEIYFLLVQFSSNKEFLDTKDLMMFLEAEQGVVAHINEEISLEIIHKYEPSKE
GQEKGWSIDGFTNYLMSPCYIFDPEHKKVCQDMKQPLSHYFINSSHNTYLI EDQFRG PSDITGYIRAL
KMGCRSVELDVWDGPDNEPVIYTGHTMTSQIVFRSVIDIINKYAFFASEYPLIILCLENHCSIKQOKVMVQ
HMKLLGDKLYTTPNVEESYLPSPDVLK GKILIKAKLSSNCSGVEGDVTDEDEGAEMSQRMGKENMEQ
PNNVPVKRFQLCKELSELVSIKSVQFKFQVVFQVQKYWEVCSFNEVLASKYANENPGDFVNYNKRFLA
RVFSPMRIDSSNMNPQDFWKCGCQIVAMNFQTPGLMMDLNI GWFRQNGNCGYVLRPAIMREEVSFFSAN
TKDSVPGVSPQLLHIKII SGQNFPPKPKGSGAKGDVVDPYVYVEIHGIPADCAEQRTKTVHQNGDAPIFDE
SFEFQINLPELANVRFVVLDDDYIGDEFIGQYTI PFECLOTGYRHVPLQSLTGEVLAHASLFVHVAITNR
RGGGKPHKRGLSVRKGKKSREYASLRTLWIKTVDEVFKNAQPPIRDATDLRENMQNAVVSFKELCGLSSV
ANLMQCM LAVSPRFLGPDNTPLVVLNLSEQYPTMELQGI VPEVLK KIVTTYDMMIQSLKAL IENADAVYE
KIVHCQKAAMEFHEHLHSIGTKEGLKERK LQKAVESFTWNTILKGQADLLKYAKNETLENLQIHFAAV
SCGLNKPGTENADVQKPRRSLEVIPEKANDETGE

DIAGNOSTIC MARKER FOR NEUROLOGICAL CONDITIONS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. provisional patent application No. 60/159,622 (filed Oct. 14, 1999) the disclosure of which is expressly incorporated herein by reference, in its entirety and for all purposes.

FIELD OF THE INVENTION

The invention relates to a human phospholipase C expressed in the brain (B-PLC), and to compositions and methods useful for diagnosing and treating physiologic pathologic conditions mediated by B-PLC. The invention finds application in the medical sciences.

BACKGROUND OF THE INVENTION

Intracellular signaling in the central nervous system (CNS) occurs predominantly by chemical signaling in which neurotransmitter molecules are released from one cell upon a challenge and are received and translated in the other into an appropriate pattern of response by specialized, cell membrane spanning polypeptides termed receptors. Some cellular responses are mediated by G-protein coupled receptors (GPCRs), members of a large family of transmembrane receptors. Upon their activation by neurotransmitters, GPCRs stimulate the GTPase activity of bound G-proteins and the latter are released and can activate several intracellular effector systems within the cell, including phospholipase C.

Phospholipase C (PLC) is an enzyme that breaks down phosphatidylinositol, a component of plasma membrane highly enriched in the CNS, to two important intracellular signaling molecules: diacylglycerol (DAG) and inositol-1, 4,5-phosphate (IP₃). Both DAG and IP₃ can trigger numerous signaling cascades in response to extracellular stimuli to maintain normal cellular homeostasis in the case of normal neuronal activity, or, when the stimulus is associated with a neuropathologic challenge, to manage the balance between cell death and cell survival, repair and regeneration. DAGs activate an important intracellular kinase, protein kinase C, in Ca²⁺-dependent manner, while IP₃ activates specific receptors on the endoplasmic reticulum to release Ca²⁺ from intracellular stores, as well as IP₃-dependent kinase (IP₃-K). Via these pathways, the PLC-mediated signaling impacts such cellular phenomena as neurotransmitter release, receptor desensitization, transcriptional activation.

Proteins with homology to PLCs, but apparently lacking lipase activity, are also known. Like PLCs, these proteins bind inositol-1,4,5-phosphate, and are believed to play roles in regulation of activities mediated by IP₃. See, e.g., Kanematsu et al., 1996, *Biochem J* 313:319-25.

SUMMARY OF THE INVENTION

In one aspect, the invention provides an isolated, substantially pure, or recombinant B-PLC polypeptide, or immunogenic fragment thereof, for example, a polypeptide having an amino acid sequence exactly or substantially (e.g., at least about 80% or about 90%) identical to SEQ ID NO:2 or SEQ ID NO:4 or a fragment of the full-length sequence (e.g., a fragment having at least about 20 contiguous amino acid residues exactly identical to SEQ ID NO:2). In one embodiment, the invention provides a fusion protein having a sequence of a B-PLC polypeptide. In embodiment, the

polypeptide has IP₃ binding activity. In embodiments, the polypeptide has PLC catalytic activity.

In another aspect, the invention provides an isolated polynucleotide that encodes, or is complementary to a sequence that encodes, a B-PLC polypeptide (e.g., having a sequence of SEQ ID NO:2 or a fragment thereof). In embodiments, the isolated polynucleotide has at least 15, at least 50, or at least 100 or more contiguous bases identical or exactly complementary to SEQ ID NO:1. In one embodiment, the invention provides an isolated polynucleotide that selectively hybridizes under stringent hybridization conditions to a polynucleotide sequence of SEQ ID NO:1. The polynucleotides of the invention may be operably linked to a promoter. The invention further provides a recombinant vector (such as an expression vector) containing a B-PLC polynucleotide, as well as cells (e.g., eukaryotic, mammalian or human cells) that contain the vector.

In another aspect, the invention provides an antibody (e.g., a monoclonal antibody), or fragment thereof, wherein the antibody or antibody fragment specifically binds to a B-PLC polypeptide.

In one aspect, the invention provides a method of detecting an B-PLC gene product in a sample by (a) contacting the sample with a probe that specifically binds the gene product, wherein the probe and the gene product form a complex, and detecting the formation of the complex; or (b) specifically amplifying the gene product in the biological sample, wherein said gene product is a polynucleotide, and detecting the amplification product; where the formation of the complex or presence of the amplification product is correlated with the presence of the B-PLC gene product in the biological sample. In this assay, the sample may be from human. The gene product may be, in various embodiments, a protein or RNA, and the probe may be an antibody or polynucleotide.

In a different aspect, the invention provides a method of treating an B-PLC mediated condition in a mammal by modulating (e.g., increasing or reducing) the activity or expression of B-PLC in a cell or tissue in the mammal.

The invention further provides methods for the diagnosis of a neurological condition in an animal, such as a human patient, by obtaining a biological sample from the animal and detecting an increased level of B-PLC in the sample compared to the level in a healthy animal, wherein said increased level is diagnostic of a neurological condition in the animal. In an embodiment the biological sample is blood. In an embodiment, the method of claim 17 wherein the increased level of B-PLC is detected using an immunoassay. The neurological condition that can be diagnosed may be hypoxic-ischemic brain insult (e.g., stroke), a neuroinflammatory disease, or other conditions.

Any method of detection can be used. In an embodiment, the increased level of B-PLC is detected using a detectably labeled polynucleotide probe comprising the sequence of SEQ ID NO:1 or 6 or a fragment thereof. In a different embodiment the the increased level of B-PLC is detected using an antibody that specifically binds the polypeptide of SEQ ID NO: 2 or 7.

In another aspect, the invention provides a method of treating a condition characterized by increased B-PLC expression in a mammal comprising modulating the activity or expression of B-PLC in a cell or tissue in the mammal. Examples of conditions susceptible to treatment include hypoxic-ischemic brain insult (e.g., stroke).

In another aspect, the invention provides a method of identifying an agent that modulates of B-PLC activity com-

prising contacting a cell or composition comprising a B-PLC protein encoded by a B-PLC polynucleotide and detecting a difference in protein activity in the presence of the agent compared to the absence of the agent. In embodiment the activity is IP3-binding activity.

A method of identifying an agent that modulates of B-PLC expression in a cell, comprising contacting a cell that expresses the B-PLC protein of SEQ ID NO:2 or a naturally occurring allele thereof, and detecting a change in B-PLC expression in the presence of the agent compared to the absence of the agent.

The invention also provides a method for identifying an agent for treatment or prevention of a neurological condition (e.g., hypoxic-ischemic brain insult), by determining whether a compound or treatment is a modulator of activity or expression of a B-PLC. In an embodiment, the activity is IP₃-binding activity.

BRIEF DESCRIPTION OF THE FIGURES

FIGS. 1a, 1b, 1c show the nucleotide sequence for a human B-PLC (SEQ. ID NO:1) coding region and the predicted amino acid sequence of the human B-PLC polypeptide (SEQ. ID NO:2).

FIG. 2 shows the nucleotide sequence for a full-length human B-PLC cDNA (SEQ ID NO:8).

FIG. 3 shows the nucleotide (SEQ. ID NO:3) of a portion of a partial rat B-PLC cDNA, as determined from an expressed sequence tag (EST) from a library of ESTs enriched for sequences overexpressed in ischemic brain. The conceptual amino acid sequence (SEQ. ID NO:4) is also shown.

FIG. 4 shows the nucleotide sequence (SEQ. ID NO:5) of a nearly full-length clone of rat B-PLC corresponding to the EST clone of SEQ. ID. NO.:3 (with the boundaries of the EST sequence indicated).

FIG. 5 shows the conceptual translation of the polynucleotide shown in FIG. 4 (SEQ ID NO:9).

FIG. 6 shows the hybridization pattern of hB-PLC specific cDNA to the panel of mRNAs from various tissues.

FIG. 7 shows the result of in situ hybridization of a B-PLC probe to rat brain. In situ hybridization of brain slices from control rats (upper left panel) and rats undergone ischemic preconditioning (3 min global ischemic pulse) (lower left panel), damaging ischemic pulse (10 min global ischemia) (upper right panel) and ischemic damage preceded by ischemic preconditioning (lower right panel). Note the higher intensity of the signal in the hippocampal region (arrow) in upper right panel (damaging ischemia).

FIG. 8a shows the nucleotide sequence and

FIG. 8b shows the amino acid sequence of Clone KIAA1092 (Genbank ID AB029015).

DETAILED DESCRIPTION

I. Definitions

The following definitions are provided to assist the reader in the practice of the invention.

The terms "allele" or "allelic sequence," as used herein, refer to a naturally-occurring alternative form of a gene encoding the B-PLC polypeptide (i.e., a polynucleotide encoding an B-PLC polypeptide). Alleles result from mutations (i.e., changes in the nucleic acid sequence), and generally produce altered and/or differently regulated mRNAs or polypeptides whose structure and/or function

may or may not be altered. Common mutational changes that give rise to alleles are generally ascribed to natural deletions, additions, or substitutions of nucleotides that may or may not affect the encoded amino acids. Each of these types of changes may occur alone, in combination with the others, or one or more times within a given gene, chromosome or other cellular polynucleotide. Any given gene may have no, one or many allelic forms. As used herein, the term "allele" refers to either or both a gene or an mRNA transcribed from the gene.

As used herein, the term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, i.e., an α -carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid.

The term "antisense sequences" refers to polynucleotides having sequence complementary to a RNA sequence. These terms specifically encompass nucleic acid sequences that bind to mRNA or portions thereof to block transcription of mRNA by ribosomes. Antisense methods are generally well known in the art (see, e.g., PCT publication WO 94/12633, and Nielsen et al., 1991, *Science* 254:1497; OLIGONUCLEOTIDES AND ANALOGUES, A PRACTICAL APPROACH, edited by F. Eckstein, IRL Press at Oxford University Press (1991); ANTISENSE RESEARCH AND APPLICATIONS (1993, CRC Press)).

The term "conservative substitution," when describing a polypeptide, refers to a change in the amino acid composition of the polypeptide that does not substantially alter the activity of the polypeptide, i.e., substitution of amino acids with other amino acids having similar properties such that the substitutions of even critical amino acids does not substantially alter activity. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following six groups each contain amino acids that are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W) (see also, Creighton, 1984, *Proteins*, W. H. Freeman and Company).

In addition to the above-defined conservative substitutions, other type of conservative modification of amino acid residues can result in "conservatively modified variants." For example, one may regard all charged amino acids as substitutions for each other whether they are positive or negative. In addition, conservatively modified variants can also result from individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids, e.g., often less than 5%, in an encoded sequence can also be. Further, a conservatively modified variant can be made from a recombinant polypep-

tide by substituting a codon for an amino acid employed by the native or wild-type gene with a different codon for the same amino acid.

The terms "control elements" or "regulatory sequences" include enhancers, promoters, transcription terminators, origins of replication, chromosomal integration sequences, 5' and 3' untranslated regions, with which polypeptides or other biomolecules interact to carry out transcription and translation. For eukaryotic cells, the control sequences will include a promoter and preferably an enhancer, e.g., derived from immunoglobulin genes, SV40, cytomegalovirus, and a polyadenylation sequence, and may include splice donor and acceptor sequences. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used.

As used herein, a "derivatized" polynucleotide, oligonucleotide, or nucleic acid refers to oligo- and polynucleotides that comprise a derivatized substituent. In some embodiments, the substituent is substantially non-interfering with respect to hybridization to complementary polynucleotides. Derivatized oligo- or polynucleotides that have been modified with appended chemical substituents (e.g., by modification of an already synthesized oligo- or polynucleotide, or by incorporation of a modified base or backbone analog during synthesis) may be introduced into a metabolically active eukaryotic cell to hybridize with an B-PLC DNA, RNA, or protein where they produce an alteration or chemical modification to a local DNA, RNA, or protein. Alternatively, the derivatized oligo or polynucleotides may interact with and alter B-PLC polypeptides, or proteins that interact with B-PLC DNA or B-PLC gene products, or alter or modulate expression or function of B-PLC DNA, RNA or protein. Illustrative attached chemical substituents include: europium (III) texaphyrin, cross-linking agents, psoralen, metal chelates (e.g., iron/EDTA chelate for iron catalyzed cleavage), topoisomerases, endonucleases, exonucleases, ligases, phosphodiesterases, photodynamic porphyrins, chemotherapeutic drugs (e.g., adriamycin, doxorubicin), intercalating agents, base-modification agents, immunoglobulin chains, and oligonucleotides. Iron/EDTA chelates are chemical substituents often used where local cleavage of a nucleic acid sequence is desired (Hertzberg et al., 1982, *J. Am. Chem. Soc.* 104: 313; Hertzberg and Dervan, 1984, *Biochemistry* 23: 3934; Taylor et al., 1984, *Tetrahedron* 40: 457; Dervan, 1986, *Science* 232: 464). Illustrative attachment chemistries include: direct linkage, e.g., via an appended reactive amino group (Corey and Schultz, 1988, *Science* 238: 1401, which is incorporated herein by reference) and other direct linkage chemistries, although streptavidin/biotin and digoxigenin/anti-digoxigenin antibody linkage methods can also be used. Methods for linking chemical substituents are provided in U.S. Pat. Nos. 5,135,720, 5,093,245, and 5,055,556, which are incorporated herein by reference. Other linkage chemistries may be used at the discretion of the practitioner.

As used herein, a "detectable label" has the ordinary meaning in the art and refers to an atom (e.g., radionuclide), molecule (e.g., fluorescein), or complex, that is or can be used to detect (e.g., due to a physical or chemical property), indicate the presence of a molecule or to enable binding of another molecule to which it is covalently bound or otherwise associated. The term "label" also refers to covalently bound or otherwise associated molecules (e.g., a biomolecule such as an enzyme) that act on a substrate to produce a detectable atom, molecule or complex. Detectable labels suitable for use in the present invention include any com-

position detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical, chemical means and the like.

The term "epitope" has its ordinary meaning of a site on an antigen recognized by an antibody. Epitopes are typically segments of amino acids which are a small portion of the whole polypeptide. Epitopes may be conformational (i.e., discontinuous). That is, they may be formed from amino acids encoded by noncontiguous parts of a primary sequence that have been juxtaposed by protein folding.

The term "fusion protein," refers to a composite polypeptide, i.e., a single contiguous amino acid sequence, made up of two (or more) distinct, heterologous polypeptides which are not normally fused together in a single amino acid sequence. Thus, a fusion protein may include a single amino acid sequence that contains two entirely distinct amino acid sequences or two similar or identical polypeptide sequences, provided that these sequences are not normally found together in the same configuration in a single amino acid sequence found in nature. Fusion proteins may generally be prepared using either recombinant nucleic acid methods, i.e., as a result of transcription and translation of a recombinant gene fusion product, which fusion comprises a segment encoding a polypeptide of the invention and a segment encoding a heterologous polypeptide, or by chemical synthesis methods well known in the art.

The term "gene product" refers to an RNA molecule transcribed from a gene, or a polypeptide encoded by the gene or translated from the RNA.

The term "high affinity" for an IgG antibody, as used herein, refers to an association constant (K_a) of at least about $10^6 M^{-1}$, preferably at least about $10^8 M^{-1}$, more preferably at least about $10^9 M^{-1}$ or greater, e.g., up to $10^{12} M^{-1}$ or greater. However, "high affinity" binding can vary for other antibody isotypes.

The terms "immunogen" and "immunogenic" have their ordinary meaning in the art, i.e., an immunogen is a molecule, such as a polypeptide or other antigen, that can elicit an adaptive immune response upon injection into a person or an animal.

The terms "nucleic acid" and "polynucleotide" are used interchangeably and refer to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. Unless specifically limited, the disclosure of a polynucleotide sequence is also intended to refer to the complementary sequence. As used herein, the term "polynucleotide" includes oligonucleotides (i.e., short polynucleotides, e.g., typically at least about 7 bases).

The terms "oligonucleotides" or "oligomers" refer to a nucleic acid sequence of approximately 7 nucleotides or greater, and as many as approximately 100 nucleotides, which can be used as a primer or probe. Oligonucleotides are often between about 10 and about 50 nucleotides in length, more often between about 12 and about 50 nucleotides, very often between about 15 and about 25 nucleotides.

The term "operably linked" refers to a functional relationship between two or more polynucleotide (e.g., DNA) segments: for example, a promoter or enhancer is operably linked to a coding sequence if it stimulates the transcription of the sequence in an appropriate host cell or other expression system. Generally, sequences that are operably linked are contiguous, and in the case of a signal sequence both contiguous and in reading phase. However, enhancers need not be located in close proximity to the coding sequences whose transcription they enhance. The terms "peptidomimetic" and "mimetic" refer to a synthetic chemical com-

pound which has substantially the same structural and functional characteristics of the B-PLC polypeptides of the invention. Peptide analogs are commonly used in the pharmaceutical industry as non-peptide drugs with properties analogous to those of the template peptide. These types of non-peptide compound are termed "peptide mimetics" or "peptidomimetics" (Fauchere, J. Adv. Drug Res. 15:29 (1986); Veber and Freidinger TINS p.392 (1985); and Evans et al. J. Med. Chem. 30:1229 (1987), which are incorporated herein by reference). Peptide mimetics that are structurally similar to therapeutically useful peptides may be used to produce an equivalent or enhanced therapeutic or prophylactic effect. Generally, peptidomimetics are structurally similar to a paradigm polypeptide (i.e., a polypeptide that has a biological or pharmacological activity), such as a phospholipase C polypeptide, but have one or more peptide linkages optionally replaced by a linkage selected from the group consisting of, e.g., $-\text{CH}_2\text{NH}-$, $-\text{CH}_2\text{S}-$, $-\text{CH}_2-\text{CH}_2-$, $-\text{CH}=\text{CH}-$ (cis and trans), $-\text{COCH}_2-$, $-\text{CH}(\text{OH})\text{CH}_2-$, and $-\text{CH}_2\text{SO}-$.

The mimetic can be either entirely composed of synthetic, non-natural analogues of amino acids, or, is a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity. For example, a mimetic composition is within the scope of the invention if it is capable of carrying out the enzymatic activities of B-PLC.

The term "polypeptide" is used interchangeably herein with the term "protein," and refers to a polymer composed of amino acid residues linked by amide linkages, including synthetic, naturally-occurring and non-naturally occurring analogs thereof (amino acids and linkages). Peptides are examples of polypeptides.

As used herein, a "probe" refers to a molecule that specifically binds another molecule. One example of a probe is a "nucleic acid probe," which can be a DNA, RNA, or other polynucleotide. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid that specifically binds (e.g., anneals or hybridizes) to a substantially complementary nucleic acid. Another example of a probe is an "antibody probe" that specifically binds to a corresponding antigen or epitope.

The term "recombinant" refers to a polynucleotide synthesized or otherwise manipulated in vitro (e.g., "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. Thus, a "recombinant" polynucleotide is defined either by its method of production or its structure. In reference to its method of production, the process is use of recombinant nucleic acid techniques, e.g., involving human intervention in the nucleotide sequence, typically selection or production. Alternatively, it can be a polynucleotide made by generating a sequence comprising fusion of two fragments which are not naturally contiguous to each other, but is meant to exclude products of nature. Thus, for example, products made by transforming cells with any non-naturally occurring vector is encompassed, as are polynucleotides comprising sequence derived using any synthetic oligonucleotide process. Similarly, a "recombinant" polypeptide is one expressed from a recombinant polynucleotide.

The phrase "selectively hybridizing to" refers to a polynucleotide probe that hybridizes, duplexes or binds to a particular target DNA or RNA sequence when the target sequences are present in a preparation of total cellular DNA or RNA.

The phrase "specifically immunoreactive," or "specifically binds" when referring to the interaction between an antibody and a protein or polypeptide, refers to an antibody that specifically recognizes and binds with relatively high affinity to the protein of interest, e.g., B-PLC, such that this binding is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular polypeptide and do not bind in a significant amount to other polypeptides present in the sample. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular polypeptide. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a polypeptide. See, Harlow, 1988, ANTIBODIES, A LABORATORY MANUAL, Cold Spring Harbor Publications, New York (hereinafter, "Harlow"), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

As used herein, the "substantially sequence identity," refers to two or more sequences or subsequences that have at least 60%, preferably 80%, most preferably 90%, 95%, 98%, or 99% nucleotide or amino acid residue identity, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection. Two sequence (amino acid or nucleotide) can be compared over their full-length (e.g., the length of the shorter of the two, if they are of substantially different lengths) or over a subsequence such as at least about 50, about 100, about 200, about 500 or about 1000 contiguous nucleotides or at least about 10, about 20, about 30, about 50 or about 100 contiguous amino acid residues.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, Proc. Natl. Acad. Sci. USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by visual inspection (see generally Ausubel et al., Current Protocols In Molecular Biology, Greene Publishing and Wiley-Interscience, New York (supplemented through 1999). Each of these references and algorithms is incorporated by reference herein in its entirety. When using any of the aforementioned algorithms, the default parameters for "Window" length, gap penalty, etc., are used.

One example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the

BLAST algorithm, which is described in Altschul et al., *J. Mol. Biol.*, 215:403410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al, supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a wordlength (W) of 11, the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, $M=5$, $N=-4$, and a comparison of both strands.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Natl. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

Alignments may also be carried out using CLUSTAL (Higgins et al., *CLUSTAL V: multiple alignment of DNA and protein sequences. Methods Mol Biol* 1994; 25:307-18) using the default parameters.

A further indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions.

Another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions. Substantial identity exists when the segments will hybridize under stringent hybridization conditions to a strand, or its complement, typically using a sequence of at least about 50 contiguous nucleotides derived from the probe nucleotide sequences. "Stringent hybridization conditions" refers to conditions in a range from about 5° C. to about 20° C. or 25° C. below the melting temperature (T_m) of the target sequence and a probe with exact or nearly exact complementarity to the target. As used herein, the melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half-dissociated into single strands. Methods for calculating the T_m of nucleic acids are well known in the art (see, e.g., Berger and Kimmel (1987) *Methods In*

Enzymology, Vol. 152: Guide To Molecular Cloning Techniques, San Diego: Academic Press, Inc. and Sambrook et al., et al., 1989, *MOLECULAR CLONING: A LABORATORY MANUAL*, (2nd ed.) Vols. 1-3, Cold Spring Harbor Laboratory. As indicated by standard references, a simple estimate of the T_m value may be calculated by the equation: $T_m=81.5+0.41(\% G+C)$, when a nucleic acid is in aqueous solution at 1 M NaCl (see e.g., Anderson and Young, "Quantitative Filter Hybridization" in *Nucleic Acid Hybridization* (1985)). Other references include more sophisticated computations which take structural as well as sequence characteristics into account for the calculation of T_m . The melting temperature of a hybrid (and thus the conditions for stringent hybridization) is affected by various factors such as the length and nature (DNA, RNA, base composition) of the probe and nature of the target (DNA, RNA, base composition, present in solution or immobilized, and the like), and the concentration of salts and other components (e.g., the presence or absence of formamide, dextran sulfate, polyethylene glycol). The effects of these factors are well known and are discussed in standard references in the art, see e.g., Sambrook, supra, and Ausubel, supra. Typically, stringent hybridization conditions are salt concentrations less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion at pH 7.0 to 8.3, and temperatures at least about 30° C. for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C. for long probes (e.g., greater than 50 nucleotides). As noted, stringent conditions may also be achieved with the addition of destabilizing agents such as formamide, in which case lower temperatures may be employed.

The terms "substantially pure" or "isolated," when referring to proteins and polypeptides, e.g., B-PLC, denote those polypeptides that are separated from proteins or other contaminants with which they are naturally associated. A protein or polypeptide is considered substantially pure when that protein makes up greater than about 50% of the total protein content of the composition containing that protein, and typically, greater than about 60% of the total protein content. More typically, a substantially pure or isolated protein or polypeptide will make up at least 75%, more preferably, at least 90%, of the total protein. Preferably, the protein will make up greater than about 90%, and more preferably, greater than about 95% of the total protein in the composition. When referring to polynucleotides, the terms "substantially pure" or "isolated" generally refer to the polynucleotide separated from contaminants with which it is generally associated, e.g., lipids, proteins and other polynucleotides. The substantially pure or isolated polynucleotides of the present invention will be greater than about 50% pure. Typically, these polynucleotides will be more than about 60% pure, more typically, from about 75% to about 90% pure and preferably from about 95% to about 98% pure.

The following sections provide guidance for making and using the compositions of the invention, and carrying out the methods of the invention.

II. Introduction

The mammalian brain has a limited capacity to survive long periods of hypoxia and ischemia (lack of oxygen and blood supply). Following exposure to hypoxia-ischemia, neurons affected by this treatment die by rapid or slow mechanisms of cell death (necrosis or apoptosis). Hypoxic-ischemic brain insults, such as stroke, neonatal asphyxia, heart failure (resulting in prolonged lack of blood supply to the brain), or drowning, can cause severe permanent brain

damage. On the other hand, brief, sublethal periods of hypoxia-ischemia can lead to a transient phase in the brain when neurons become protected from subsequent injury and death. This treatment, generally referred to as ischemic tolerance, or ischemic preconditioning, can provide the basis for and lead to an understanding of intrinsic protective mechanisms and pathways through endogenous proteins or factors that provide for this effect. The present invention relates to a phospholipase C expressed in brain (e.g., hippocampus and cerebral cortex, the regions of brain containing neurons most vulnerable in ischemic stroke) in response to ischemic preconditioning.

The specificity and selectivity of the activation of a particular PLC in a given cell is determined by the presence in the cell of G protein coupled receptors (GPCR), the subset of G-proteins capable of conveying the extracellular stimulus from the GPCR to the PLC, and expression of the particular PLC. The present invention provides B-PLC polynucleotides and polypeptides useful for diagnosis and treatment of pathological conditions in humans and non-human animals. "B-PLC" refers to a phospholipase C-like protein expressed in brain as further described herein.

In one embodiment, the invention provides a novel B-PLC polynucleotides and polypeptides (including human and rodent homologs) discovered by the inventors as described in Examples 1 and 2 (e.g., SEQ ID NOS:1-5, 8, and 9 and related molecules and variants thereof). Further, as shown in Example 4, *infra*, it has been discovered by the present inventors that increased expression of the B-PLC of the invention occurs under conditions of ischemia. It will be recognized from this discovery that detection of such increased expression is useful in diagnosis and prognosis of ischemia (or other neuronal damage) in a patient or model animal. Reagents useful in the methods of the invention (e.g., detection, diagnostic, and therapeutic methods) include the B-PLC molecules specifically exemplified in Examples 1 and 2, *infra*, and Clone KIAA1092 (a longer variant of B-PLC).

III. B-PLC Polypeptides

The present invention provides isolated, substantially pure, or recombinant B-PLC polypeptides and immunogenic fragments of mammalian B-PLC polypeptides. In one embodiment, the B-PLC polypeptide or fragment has an amino acid sequence identical to, or substantially identical to, the sequence set forth in SEQ ID NO:2 or a subsequence thereof. In another embodiment, the B-PLC polypeptide or fragment has an amino acid sequence identical to, or substantially identical to, the sequence set forth in FIG. 5 (SEQ ID NO:9) or a subsequence thereof (e.g., SEQ ID NO:4). In one embodiment, a polypeptide having a sequence of SEQ ID NO:7 is used in the methods of the invention (e.g., diagnostic, therapeutic, and screening methods), in preparation pharmaceutical compositions, and the like.

The various protein domains present in the B-PLC polypeptide (e.g., SEQ ID NO:2) serve different functional purposes. Two domains termed the X and Y regions are present in PLCs and they associate tightly to form the active catalytic center of the enzyme. The pleckstrin homology (PH) domain in the N-terminus of B-PLC is known to attach the members of PLC family to membranous phosphoinositols (PIP2) prior to their actual cleavage by PLC activity. The EF-hand Ca^{2+} -binding domain as well as two essential histidine residues in the catalytic active site domain X mediate the Ca^{2+} -dependence of the enzymatic reaction. The C2 domain in the C-terminal half of B-PLC has been

suggested to be involved in the Ca^{2+} -dependent binding of PLCs to lipid vesicles as well as in interactions with signaling G-proteins. B-PLC and other known PLCs (except PLC γ) lack SH2 or SH3 domains, which participate in protein-protein interactions with members of the PLC γ family.

PLCs are members of a superfamily of PLCs that has been divided into different classes: PLC- α , PLC- β , PLC- γ , PLC- δ and PLC- ϵ . Although B-PLC displays sequence similarity to PLC- δ throughout its protein coding sequence except in the elongated C-terminus which bears more resemblance to PLC- β , it is likeliest that B-PLC may form a family together PLC- ϵ , with which it shares about 66% identity at the amino acid level.

The following functional domains were detected in the predicted protein sequence using PROSITE database of protein motifs (Henikoff et al. 1991, *Nucleic Acids Res.* 19: 6565-72). (The numbering refers to the amino acid sequence):

- a.a. 15-127 pleckstrin homology domain
- a.a. 146-209 EF-hand Ca^{2+} -binding domain
- a.a. 300-444 PIP2-dependent phospholipase C catalytic region X
- a.a. 419-608 PIP2-dependent phospholipase C catalytic region Y
- a.a. 615-711 C2-domain

In an embodiment, the B-PLC polypeptides of the invention have IP_3 -binding activity. IP_3 -binding of a protein can be detected using any of a variety routine assays known in the art (including assays described *infra*). In an embodiment, a B-PLC polypeptide of the invention has phospholipase catalytic activity. Catalytic activity can be detected using any of a variety routine assays known in the art (including assays listed *infra*). Two residues involved in catalytic activity (His356, Tyr552) are absent in B-PLC polypeptide. The invention therefor contemplates variants of the exemplified sequences in which residues Thr(360) and Phe(550) of SEQ ID NO:2 (or corresponding residues in other B-PLCs) are mutated (using standard mean, see, e.g., Ausubel, *supra*) to His and Tyr, respectively.

B-PLC is expressed at high levels in brain in many cell types including the majority of forebrain neurons as well as glial cells. Its activity there can thus be activated by many types of neurotransmitters and modulators (glutamate, acetylcholine, noradrenaline, dopamine, serotonin, bioactive lipids, various neuropeptides and chemotactic cytokines) which are released to the synaptic cleft during normal and abnormal brain activity to elicit responses at their respective GPCRs. Most probably the signals from GPCRs to B-PLC are conveyed by G_q or G_{11} . The two main cellular signaling pathways whose engagement depends on PLC, most probably also in cells harboring B-PLC, are the DAG/PKC and IP_3 /intracellular Ca^{2+} release pathways. Both of these pathways have been linked excitotoxic and apoptotic cellular phenomena in neurons, hence the modulation of B-PLC activity (e.g., IP_3 -binding activity) will alleviate the negative impact of above-mentioned events to the fate of neurons exposed to challenge. Furthermore, chemotaxis of microglia/monocytes to the locus of damage induced upon injury or challenge by chemokines is known to be accompanied by elevated intracellular Ca^{2+} levels as a result of increased PLC activity, probably that of B-PLC, in those cells. Thus, modulators of B-PLC activity are useful to circumvent undesired consequences of what the action of microglia/monocytes might do to neurons or to any others cells in the damaged area or its proximity if left uncontrolled.

PLC domains, activities, and interactions are discussed in Rhee et al. *J Biol Chem.* 1997 (272) 15045–8, and Singer et al. *Annu Rev Biochem.* 1997;66:475–509, incorporated herein by reference.

A. B-PLC Polypeptides and Variants

The invention provides substantially pure, isolated, or recombinant B-PLC polypeptides. In some embodiments, the B-PLC polypeptide has an amino acid sequence identical or substantially identical to the amino acid sequence shown in SEQ ID NO:2. In other embodiments, the B-PLC polypeptides are variants and mutants characterized by conservative substitutions of amino acid residues of SEQ ID NO:2.

The polypeptide of the invention may be full-length (e.g., containing about 1000 amino acids for the species shown in FIGS. 1 and 4) or may encode a fragment of the full-length protein. In various embodiments, the fragments may have at least about 16, at least about 25, at least about 35, or at least about 50 residues identical to a region of SEQ ID NO: 2, 5, or 9. The full length B-PLC polypeptides of the invention typically have a calculated molecular weight of from about 110 to about 120 kDa. Also provided by the invention are B-PLC polypeptides that are modified, relative to the amino acid sequence of SEQ ID NO:2, in some manner, e.g., truncated, mutated, derivatized, or fused to other sequences (e.g., to form a fusion protein). Some B-PLC polypeptides comprise insertions, deletions or substitutions of amino acid residues relative to SEQ ID NO:2, or SEQ ID NO:9. For example, some conservative amino acid substitutions can be made, i.e., substitution of selected amino acids with different amino acids having similar structural characteristics, e.g., net charge, hydrophobicity, and the like.

The modified B-PLC polypeptides of the invention can have some or all of the biological activities of naturally-occurring, full-length B-PLC. These activities include binding of the polypeptides to PIP2-enriched cell membranes, binding of IP3, sensing Ca^{2+} levels inside the cell, and catalytic activity (eg. enzymatic breakdown of PIP2 to IP3 and DAG to regulate intracellular signal transduction by elevating Ca^{2+} levels and increasing PKC-mediated phosphorylation, respectively). The above-mentioned signaling pathways can modulate neurotransmitter release and sensitivity of plasma membrane receptors to extracellular stimuli, i.e. intercellular communication, as well as determining cell fate. These activities may be assayed using standard routine assays. For example, a cell-based system which co-expresses B-PLC together with activating GPCRs (receptors to glutamate, acetylcholine, noradrenaline, dopamine, serotonin, various neuropeptides and chemotactic cytokines) and a reporter gene operationally linked to a promoter activated by PLC (such as ICAM reporter (Weyer U, et al. *Receptors Channels* 1 (1993), 193–200) can be used. Alternatively, instead of using a reporter gene, the kinetics of the B-PLC-dependent breakdown of PIP2 to IP3 and DAG can be determined by chromatographic analysis, e.g. by HPLC, or, when using radioactively labeled PIP2, by measuring radioactivity of particular cellular fractions. Alternatively, a reconstituted system consisting of PIP2-enriched lipid micelles and purified or recombinantly expressed B-PLC, GPCR and $G\alpha_q$ or $G\alpha_{11}$ subunits of G-proteins in combination with its various $P\gamma$ -subunits can be utilized to assess the enzymatic activity of B-PLC (Lee, S. B. and Rhee, S. G., *Curr. Opin. Cell Biol.* 7 (1995) 183–89).

In some embodiments the B-PLC polypeptides or fragments of the invention have a phospholipase activity. Assays for phospholipase activity are well known in the art, see,

e.g., Krug and Kent, 1981, *METHODS ENZYMOL* 72:347–51, and include phospholipase C-phosphatase coupled assays, classical radiochemical techniques (e.g., solution based radiolabeled mixed phospholipid micelle methods), bioluminescence assays, fluorescence quenching assays, and spectrophotometric techniques (e.g., Farooqui et al., 1984, *J Lipid Res* 25:1555–62), use of FlashPlates (Mullinax et al., “Monitoring Inositol-Specific Phospholipase C Activity Using a Phospholipid FlashPlate” NEN Life Science Products, Boston, Mass., and others known in the art. Each of the aforementioned articles is incorporated by reference herein in its entirety and for all purposes. In one embodiment, phospholipase activity is measured using the phospholipase C-phosphatase coupled assay described by Krug and Kent, supra. Suitable assays are also described in Krug and Kent, *Arch. Biochem. Biophys.* 231:400–410 (1984), which are incorporated herein by reference). Also, PLC activity can be determined by the hydrolysis of p-nitrophenylphosphorylcholine, Berka et al, 1982, *J. Bacteriol.* 152:239–245 and, which is incorporated herein by reference). All of the aforementioned references are incorporated herein by reference in their entirety and for all purposes.

Another activity of PLC proteins is IP_3 -binding activity. Thus, it is apparent that the B-PLC of the invention bind IP_3 . IP_3 binding can be detected using any standard assay. In one embodiment a fusion protein comprising an eptiope tag (e.g., glutathione S-transferase, GST) and the B-PLC coding region are expressed and purified (e.g., using a glutathione column). In a particular embodiment, the purified fusion proteins are incubated with radiolabeled IP_3 , (e.g., 3H —Ins (1,3,5) P_3) in 50 μ l of buffer for 30 min at room temperature. Then 10 μ l of bovine γ -globulin (30 mg/ml) and one ml of 20% polyethyleneglycol 6000 are added and the tubes incubated for 30 min on ice. After centrifugation at 100,000 \times g for 10 min, the precipitates are dissolved in 100 μ l of 0.1 N NaOH, and then the radioactivity was measured. In an embodiment, binding is detected when radioactivity is greater than background (e.g., in the absence of B-PLC protein, e.g. at least 2-fold greater).

In some embodiments, the B-PLC polypeptide of the invention is used as an immunogen (e.g., to produce anti-B-PLC antibodies). Typically, the immunogenic B-PLC fragments of the invention comprise at least about 6 contiguous residues of the B-PLC sequence, e.g., SEQ ID NO:2, more often at least about 8, about 15, or about 20, or about 25 contiguous residues. In some embodiments, the B-PLC polypeptide encoded by SEQ ID NO:9 is used as an immunogen to produce antibodies useful in the diagnostic assays of the invention.

The substantially pure, isolated or recombinant B-PLC polypeptides of the present invention can also be characterized by their ability to bind antibodies that are specifically immunoreactive with a polypeptide having the sequence shown in SEQ ID NO:2. Specific immunoreactivity is usually characterized by a specific binding affinity of an antibody for its ligand (e.g., B-PLC) of at least 10^7 , 10^8 , 10^9 , or 10^{10} M^{-1} .

For many applications, it will also be desirable to provide B-PLC polypeptides of the invention as labeled entities, i.e., covalently attached or linked to a detectable label or group, or cross-linkable group, to facilitate identification, detection and quantification of the polypeptide in a given circumstance. These detectable groups can comprise a detectable polypeptide group, e.g., an assayable enzyme or antibody epitope. Alternatively, the detectable group can be selected from a variety of other detectable groups or labels, such as

radiolabels (e.g., ^{125}I , ^{32}P , ^{35}S) or a chemiluminescent or fluorescent group. Similarly, the detectable group can be a substrate, cofactor, inhibitor or affinity ligand.

In addition, a B-PLC polypeptide can be modified by substituting one or more amino acid residues with a D-amino acid of the same type (e.g., D-lysine in place of L-lysine) to generate more stable peptides. Similarly, modification of the amino or carboxyl terminals can also be used to confer stabilizing properties upon the polypeptides of the invention, e.g., amidation of the carboxyl-terminus or acylation of the amino-terminus or pegylated derivatives.

B-PLC variants, including variants with conservative or nonconservative amino acid substitutions are useful as agonists and antagonists of B-PLC activity. For example, modification of key amino acid residues in the active site regions X and Y (e.g. histidine residues in positions 315 and 362 SEQ ID NO:2) of B-PLC as well as those in domains that determine the Ca^{2+} -dependence (EF-hand, C2-domain) are expected to render it enzymatically inactive. Such "dominant negative" B-PLC variants, i.e., B-PLC polypeptides which are capable of binding the substrate, but not turning it over, may be used as a competitive inhibitor of B-PLC, and can be used to down-regulate excessive B-PLC activity in conditions where it could be undesirable (Beekman A, et al. *Cancer Res.* 1998 (58) 910-3).

Elsewhere, mutations of amino acid residues involved in receiving the G-protein input from GPCRs, for example in the C2 domain, are used to alter responsiveness of B-PLC to a particular signaling pathway. Mutations of some nonessential amino acid residues in or near the active site regions X and Y can lead to B-PLC variants with elevated activity or to constitutively active B-PLC species. The latter can be used to compensate B-PLC deficiency in conditions where such inadequacies might occur. Variant B-PLCs can be constructed for in vivo expression in appropriate gene delivery vehicles such as adenoviral or similar vectors.

In various embodiment, the polypeptide of the invention are at least about 10, about 50, about 100, about 250, about 500 or about 1000 amino acid residues in length.

B. Production and Isolation of B-PLC Polypeptides

The B-PLC polypeptides of the present invention can be prepared using recombinant or synthetic methods, or can be isolated from natural cellular sources.

Suitable recombinant techniques for expressing B-PLC polypeptides from the B-PLC polynucleotides are disclosed infra. See also, Sambrook et al., 1989, *MOLECULAR CLONING: A LABORATORY MANUAL*, (2nd ed.) Vols. 1-3, Cold Spring Harbor Laboratory, and in Ausubel, supra. Synthetic methods for synthesizing polypeptides such as B-PLC polypeptides, variants, or fragments are described in Merrifield, 1963, *Amer. Chem. Soc.* 85:2149-2456, Atherton et al., 1989, *SOLID PHASE PEPTIDE SYNTHESIS: A PRACTICAL APPROACH*, IRL Press, and Merrifield, 1986, *Science* 232:341-347.

Isolation and purification of the B-PLC polypeptides of the present invention can be carried out by methods that are generally well known in the art. These methods include, but are not limited to, ion exchange, hydrophobic interaction, HPLC or affinity chromatography, to achieve the desired purity. In one embodiment, B-PLC polypeptides are purified using immunoaffinity chromatography. For example, antibodies raised against a B-PLC polypeptide or immunogenic fragment thereof (e.g., having a sequence or subsequence of SEQ ID NO:2) are coupled to a suitable solid support and contacted with a mixture of polypeptides containing the B-PLC polypeptide (e.g., a homogenate of brain tissue) under conditions conducive to the association of this

polypeptide with the antibody. Once the B-PLC polypeptide is bound to the immobilized antibody, the solid support is washed to remove unbound material and/or nonspecifically bound polypeptides. The desired polypeptide can then be eluted from the solid support in substantially pure form by, e.g., a change in pH or salt concentration of the buffer.

C. Peptide Analogs and Peptide Mimetics of B-PLC

Although primarily described in terms of "proteins" or "polypeptides," one of skill in the art will understand that structural analogs and derivatives of the above-described polypeptides, e.g., peptidomimetics, and the like can be used as substitutes for B-PLC, e.g., as B-PLC activity agonists, or, alternatively, as B-PLC activity antagonists. Peptidomimetics, or peptide mimetics, are peptide analogs commonly used in the pharmaceutical industry as non-peptide drugs with properties (e.g., a biological activity) analogous to those of the template peptide. (Fauchere, 1986, *Adv. Drug Res.* 15:29; Evans et al., 1987, *J. Med. Chem.* 30:1229). They are usually developed with the aid of computerized molecular modeling. Peptide mimetics that are structurally similar to therapeutically useful peptides can be used to produce an equivalent therapeutic effect. Peptide mimetics can have significant advantages over polypeptide embodiments, including, for example, more economical production and greater chemical stability.

IV. B-PLC Polynucleotides

In one aspect, the invention provides a polynucleotide having a sequence or subsequence of a mammalian (e.g., rat or human) B-PLC gene or RNA. The polynucleotides of the invention (e.g., RNA, DNA, PNA or chimeras), and may be single-stranded, double stranded, or a mixed hybrid. In one embodiment, the polynucleotide has a sequence of SEQ. ID NO:8 (FIG. 2) or NO:5 (FIG. 4) or subsequences thereof. The invention also provides polynucleotides with substantial sequence identity to the B-PLC polynucleotides disclosed herein. Thus, the invention provides naturally occurring alleles of mammalian (e.g., rat and human) B-PLC genes and variant polynucleotide sequences having one or more nucleotide deletions, insertions or substitutions relative to a B-PLC nucleic acid sequence disclosed herein.

As described infra, in some embodiments the polynucleotide of the invention encodes a polypeptide with substantial sequence similarity to SEQ. ID NO:2 (FIG. 1) or encodes a fragment of such a polypeptide (e.g., a fusion protein). Also contemplated are polynucleotides that, due to the degeneracy of the genetic code, are not substantially similar to SEQ ID NO:1, but encode the polypeptide of SEQ. ID NO:2 or a fragment thereof. In other embodiments, the invention provides B-PLC polynucleotides that do not necessarily encode B-PLC polypeptide but which are useful as e.g., probes, primers, antisense, triplex, or ribozyme reagents, and the like.

The invention also includes expression vectors, cell lines, and transgenic organisms comprising the B-PLC polynucleotides. In some embodiments, the vectors, cells, and organisms of the invention are capable of expressing the encoded B-PLC polypeptides.

Using the guidance of this disclosure, the B-PLC polynucleotides of the invention can be produced by recombinant means. See, e.g., Sambrook et al., (1989) *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Vols. 1-3, Cold Spring Harbor Laboratory; Berger and Kimmel, (1987) *Methods In Enzymology*, Vol. 152: Guide To Molecular Cloning Techniques, San Diego: Academic Press, Inc.; Ausubel et al., *Current Protocols In Molecular Biology*,

Greene Publishing and Wiley-Interscience, New York (1999). Alternatively, B-PLC polynucleotides or fragments can be chemically synthesized using routine methods well known in the art (see, e.g., Narang et al., 1979, *Meth. Enzymol.* 68:90; Brown et al., 1979, *Meth. Enzymol.* 68:109; Beaucage et al., 1981, *Tetra. Lett.*, 22:1859). In some embodiments, the B-PLC polynucleotides of the invention contain non-naturally occurring bases, e.g., deoxyinosine (see, Batzer et al., 1991, *Nucleic Acid Res.* 19:5081; Ohtsuka et al., 1985, *J. Biol. Chem.* 260:2605-2608; Rossolini et al., 1994, *Mol. Cell. Probes* 8:91-98) or modified backbone residues or linkages.

In various embodiments, polynucleotide of the invention is at least about 50, about 100, about 200, about 500, about 1000, about 2000 or about 3000 bases or basepairs in length. A. Polynucleotides Encoding B-PLC

In one aspect, the invention provides polynucleotides encoding B-PLC polypeptides such as an B-PLC polypeptide comprising the sequence of SEQ ID NO:2, a fragment thereof, a variant thereof (e.g., a conservative or allelic variant), or a B-PLC fusion polypeptide. In one embodiment, the polynucleotide of the invention comprises the sequence of SEQ ID NO:1 or a fragment thereof. In another embodiment, the polynucleotide encodes a naturally occurring B-PLC polypeptide or fragment, but has a sequence that differs from SEQ. ID NO:1 (e.g., as a result of the degeneracy of the genetic code).

The polynucleotides of invention are useful for expression of B-PLC polynucleotides (e.g., sense or antisense RNAs) and polypeptides. Methods for recombinant expression of polynucleotides and proteins are well known in the art. Typically, the B-PLC polynucleotides of the invention are used in expression vectors for the preparation of B-PLC polypeptides and polynucleotides. Expression vectors typically include transcriptional and/or translational control signals (e.g., the promoter, ribosome-binding site, and ATG initiation codon). In addition, the efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use. For example, the SV40 enhancer or CMV enhancer can be used to increase expression in mammalian host cells.

In one embodiment, DNA encoding an B-PLC polypeptide of the present invention is inserted into DNA constructs capable of introduction into and expression in an in vitro host cell, such as a bacterial (e.g., *E. coli*, *Bacillus subtilis*), yeast (e.g., *Saccharomyces*), insect (e.g., *Spodoptera frugiperda*), or mammalian cell culture systems. Examples of mammalian cell culture systems useful for expression and production of the polypeptides of the present invention include human embryonic kidney line (293; Graham et al., 1977, *J. Gen. Virol.* 36:59); CHO (ATCC CCL 61 and CRL 9618); human cervical carcinoma cells (HeLa, ATCC CCL 2); and others known in the art. The use of mammalian tissue cell culture to express polypeptides is discussed generally in Winnacker, FROM GENES TO CLONES (VCH Publishers, N.Y., N.Y., 1987) and Ausubel, supra.

In some embodiments, promoters from mammalian genes or from mammalian viruses are used, e.g., for expression in mammalian cell lines. Suitable promoters can be constitutive, cell type-specific, stage-specific, and/or modulatable or regulatable (e.g., by hormones such as glucocorticoids). Useful promoters include, but are not limited to, the metallothionein promoter, the constitutive adenovirus major late promoter, the dexamethasone-inducible MMTV promoter, the SV40 promoter, and promoter-enhancer combinations known in the art.

B-PLC polypeptides or fragments can also be expressed in transgenic animals (mouse, sheep, cow, etc.) and plants

(tobacco, arabidopsis, etc.) using appropriate expression vectors which integrate into the host cell chromosome.

B. Polynucleotide or Oligonucleotide Probes and Primers

In one embodiment, the invention provides oligonucleotide or polynucleotide probes and/or primers for detecting or amplifying B-PLC polynucleotides. In various embodiments, the polynucleotides (e.g., probes and primers) comprise at least 10 contiguous bases identical or exactly complementary to SEQ ID NO:1 or NO:3, usually at least 12 bases, typically at least 15 bases, generally at least 18 bases and often at least 25, at least 50, or at least 100 bases. When the B-PLC polynucleotides of the invention are used as probes or primers they are generally less than about 3000 bases in length; typically they contain between about 12 and about 100 contiguous nucleotides identical or exactly complementary to SEQ. ID NO:1 or NO:5, more often between about 12 and about 50 contiguous nucleotides, even more often between about 15 and about 25 contiguous nucleotides. In some embodiments of the invention, probes and primers having a sequence of SEQ ID NO:7, or a fragment thereof, are used in the methods (e.g., diagnostic, therapeutic methods, and screening methods) of the invention, in preparation pharmaceutical compositions, and the like.

In some embodiments, the probes and primers are modified, e.g., by adding restriction sites to the probes or primers. In other embodiments, primers or probes of the invention comprise additional sequences, such as linkers. In still some other embodiments, primers or probes of the invention are modified with detectable labels. For example, the primers and probes are chemically modified, e.g., derivatized, incorporating modified nucleotide bases, or containing a ligand capable of being bound by an anti-ligand (e.g., biotin).

The B-PLC primers of the invention can be used for a number of purposes, e.g., for amplifying an B-PLC polynucleotide in a biological sample for detection, or for cloning B-PLC genes from a variety of species. Using the guidance of the present disclosure, primers can be designed for amplification of the human B-PLC gene or regions encoding particular protein domains of the B-PLC gene. Exemplary primer pairs for amplifying domains are described in Table 1.

Domain to be amplified	Primer Pair
PH Domain	5' TATTAATTCAATGGTTGAG 3' (SEQ ID NO:10) 5' AAGTGTATGTTTTCCATAAG 3' (SEQ ID NO:11)
EF-hand	5' AGATAACATGAGGACTTG 3' (SEQ ID NO:12) 5' ACAAAGCTCATGAAAAACC 3' (SEQ ID NO:13)
PLC X-region	5' AGAACATAAGAAGGTCTGTC 3' (SEQ ID NO:14) 5' GTATTTCCCTTTCAGCAG 3' (SEQ ID NO:15)
PLC Y-region	5' GAGAACATGGAGCAACC 3' (SEQ ID NO:16) 5' CCTCATGATGGCTGCCGG 3' (SEQ ID NO:17)
C2-domain	5' GAGGGAGGAGGTCTCCTTC 3' (SEQ ID NO:18) 5' AATTGTGTACTGGCCCATG 3' (SEQ ID NO:19)

C. B-PLC Inhibitor Polynucleotides

The invention provides inhibitory polynucleotides such as antisense, triplex, and ribozyme reagents that target or hybridize to B-PLC polynucleotides. These polynucleotides may be used to treat disease states which are associated with elevated activity of B-PLC leading to rapid changes in intracellular Ca²⁺ levels and/or in PKC signaling. Acute neurodegenerative conditions such as ischemic stroke, head trauma or injury are prime candidates, as well as neuroinflammatory diseases with consequences to neurons.

1. Antisense Polynucleotides

In one aspect, the present invention provides antisense oligonucleotides and polynucleotides that can be used to inhibit expression of the B-PLC gene. Some therapeutic methods of the invention, described in additional detail infra, involve the administration of an oligonucleotide that functions to inhibit or stimulate B-PLC activity under in vivo physiological conditions, and is relatively stable under those conditions for a period of time sufficient for a therapeutic effect. Polynucleotides can be modified to impart such stability and to facilitate targeting delivery of the oligonucleotide to the desired tissue, organ, or cell.

The antisense polynucleotides of the invention comprise an antisense sequence of at least about 10 bases, typically at least 20, at least about 50, or at least about 100, and up to at least about 1000 to at least about 3000 contiguous nucleotides that specifically hybridize to a sequence from mRNA encoding B-PLC or mRNA transcribed from the B-PLC gene. More often, the antisense polynucleotide of the invention is from about 12 to about 50 nucleotides in length or from about 15 to about 25 nucleotides in length. In general, the antisense polynucleotide should be long enough to form a stable duplex but short enough, depending on the mode of delivery, to administer in vivo, if desired. The minimum length of a polynucleotide required for specific hybridization to a target sequence depends on several factors, such as G/C content, positioning of mismatched bases (if any), degree of uniqueness of the sequence as compared to the population of target polynucleotides, and chemical nature of the polynucleotide (e.g., methylphosphonate backbone, peptide nucleic acid, phosphorothioate), among other factors.

Generally, to assure specific hybridization, the antisense sequence is substantially complementary to the target B-PLC mRNA sequence. In certain embodiments, the antisense sequence is exactly complementary to the target sequence. The antisense polynucleotides may also include, however, nucleotide substitutions, additions, deletions, transitions, transpositions, or modifications, or other nucleic acid sequences or non-nucleic acid moieties so long as specific binding to the relevant target sequence corresponding to B-PLC RNA or its gene is retained as a functional property of the polynucleotide.

In one embodiment, the antisense sequence is complementary to relatively accessible sequences of the B-PLC mRNA (e.g., relatively devoid of secondary structure). This can be determined by analyzing predicted RNA secondary structures using, for example, the MFOLD program (Genetics Computer Group, Madison Wis.) and testing in vitro or in vivo as is known in the art. Examples of oligonucleotides that may be tested in cells for antisense suppression of B-PLC function are those capable of hybridizing to (i.e., substantially complementary to) SEQUENCE ID NO:1, for example, 5'-ATT GGG TTG CTC CAT-3' (SEQ ID NO:20) and 5'-TAG AAA GTA CCT ATG A-3' (SEQ ID NO:21). Another useful method for identifying effective antisense compositions uses combinatorial arrays of oligonucleotides (see, e.g., Milner et al., 1997, *Nature Biotechnology* 15:537).

The invention also provides an antisense polynucleotide that has sequences in addition to the antisense sequence (i.e., in addition to anti-B-PLC-sense sequence). In this case, the antisense sequence is contained within a polynucleotide of longer sequence. In another embodiment, the sequence of the polynucleotide consists essentially of, or is, the antisense sequence.

The antisense nucleic acids (DNA, RNA, modified, analogues, and the like) can be made using any suitable

method for producing a nucleic acid, such as the chemical synthesis and recombinant methods disclosed herein. In one embodiment, for example, antisense RNA molecules of the invention may be prepared by de novo chemical synthesis or by cloning. For example, an antisense RNA that hybridizes to B-PLC mRNA can be made by inserting (ligating) an B-PLC DNA sequence (e.g., SEQ. ID No; 1, or fragment thereof) in reverse orientation operably linked to a promoter in a vector (e.g., plasmid). Provided that the promoter and, preferably termination and polyadenylation signals, are properly positioned, the strand of the inserted sequence corresponding to the noncoding strand will be transcribed and act as an antisense oligonucleotide of the invention.

The antisense oligonucleotides of the invention can be used to inhibit B-PLC activity in cell-free extracts, cells, and animals, including mammals and humans. An example of a suitable antisense oligonucleotide is phosphorothioate antisense oligonucleotide having the sequence

5'-AGGATTCTCATTGGCGTATTTACTGGCTAGCA
CTTCATTG-3'(SEQ ID NO:22)

For general methods relating to antisense polynucleotides, see ANTISENSE RNA AND DNA, (1988), D.A. Melton, Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.). See also, Dagle et al., 1991, *Nucleic Acids Research*, 19:1805. For a review of antisense therapy, see, e.g., Uhlmann et al., *Chem. Reviews*, 90:543-584 (1990).

2. Triplex Oligo- and Polynucleotides

The present invention provides oligo- and polynucleotides (e.g., DNA, RNA, PNA or the like) that bind to double-stranded or duplex B-PLC nucleic acids (e.g., in a folded region of the B-PLC RNA or in the B-PLC gene), forming a triple helix-containing, or Atriplex=nucleic acid. Triple helix formation results in inhibition of B-PLC expression by, for example, preventing transcription of the B-PLC gene, thus reducing or eliminating B-PLC activity in a cell. Without intending to be bound by any particular mechanism, it is believed that triple helix pairing compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules to occur.

Triplex oligo- and polynucleotides of the invention are constructed using the base-pairing rules of triple helix formation (see, e.g., Cheng et al., 1988, *J. Biol. Chem.* 263: 15110; Ferrin and Camerini-Otero, 1991, *Science* 354:1494; Ramdas et al., 1989, *J. Biol. Chem.* 264:17395; Strobel et al., 1991, *Science* 254:1639; and Rigas et al., 1986, *Proc. Natl. Acad. Sci. U.S.A.* 83: 9591; each of which is incorporated herein by reference) and the B-PLC mRNA and/or gene sequence. Typically, the triplex-forming oligonucleotides of the invention comprise a specific sequence of from about 10 to at least about 25 nucleotides or longer complementary to a specific sequence in the B-PLC RNA or gene (i.e., large enough to form a stable triple helix, but small enough, depending on the mode of delivery, to administer in vivo, if desired). In this context, Acomplementary=means able to form a stable triple helix. In one embodiment, oligonucleotides are designed to bind specifically to the regulatory regions of the B-PLC gene (e.g., the B-PLC 5'-flanking sequence, promoters, and enhancers) or to the transcription initiation site, (e.g., between -10 and +10 from the transcription initiation site). For a review of recent therapeutic advances using triplex DNA, see Gee et al., in Huber and Carr, 1994, MOLECULAR AND IMMUNOLOGIC APPROACHES, Futura Publishing Co, Mt Kisco N.Y. and Rininsland et al., 1997, *Proc. Natl. Acad. Sci. USA* 94:5854, which are both incorporated herein by reference.

3. Ribozymes

The present invention also provides ribozymes useful for inhibition of B-PLC activity. The ribozymes of the invention bind and specifically cleave and inactivate B-PLC mRNA. Useful ribozymes can comprise 5'- and 3'-terminal sequences complementary to the B-PLC mRNA and can be engineered by one of skill on the basis of the B-PLC mRNA sequence disclosed herein (see PCT publication WO 93/23572, supra). Ribozymes of the invention include those having characteristics of group I intron ribozymes (Cech, 1995, *Biotechnology* 13:323) and others of hammerhead ribozymes (Edgington, 1992, *Biotechnology* 10:256).

Ribozymes of the invention include those having cleavage sites such as GUA, GUU and GUC. Other optimum cleavage sites for ribozyme-mediated inhibition of B-PLC activity in accordance with the present invention include those described in PCT publications WO 94/02595 and WO 93/23569, both incorporated herein by reference. Short RNA oligonucleotides between 15 and 20 ribonucleotides in length corresponding to the region of the target B-PLC gene containing the cleavage site can be evaluated for secondary structural features that may render the oligonucleotide more desirable. The suitability of cleavage sites may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays, or by testing for in vitro ribozyme activity in accordance with standard procedures known in the art.

As described by Hu et al., PCT publication WO 94/03596, incorporated herein by reference, antisense and ribozyme functions can be combined in a single oligonucleotide. Moreover, ribozymes can comprise one or more modified nucleotides or modified linkages between nucleotides, as described above in conjunction with the description of illustrative antisense oligonucleotides of the invention.

In one embodiment, the ribozymes of the invention are generated in vitro and introduced into a cell or patient. In another embodiment, gene therapy methods are used for expression of ribozymes in a target cell ex vivo or in vivo.

4. Administration of Oligonucleotides

In an embodiment, the therapeutic methods of the invention involve the administration of an oligonucleotide that functions to inhibit or stimulate B-PLC activity under in vivo physiological conditions, and is relatively stable under those conditions for a period of time sufficient for a therapeutic effect. As noted above, modified nucleic acids may be useful in imparting such stability, as well as for targeting delivery of the oligonucleotide to the desired tissue, organ, or cell.

Oligo- and poly-nucleotides can be delivered directly as a drug in a suitable pharmaceutical formulation, or indirectly by means of introducing a nucleic acid into a cell, including liposomes, immunoliposomes, ballistics, direct uptake into cells, and the like as described herein. For treatment of disease, the oligonucleotides of the invention will be administered to a patient in a therapeutically effective amount. A therapeutically effective amount is an amount sufficient to ameliorate the symptoms of the disease or modulate B-PLC activity in the target cell, e.g., as can be measured using a cell based assay, e.g., as described in §III(A), supra. Methods useful for delivery of oligonucleotides for therapeutic purposes are described in U.S. Pat. No. 5,272,065, incorporated herein by reference. Other details of administration of pharmaceutically active compounds are provided below. In another embodiment, oligo- and polynucleotides can be delivered using gene therapy and recombinant DNA expression plasmids of the invention. It will be recognized to those of skill that, to administer antibodies or therapeutic

oligonucleotides to the brain, it is sometime necessary administer via intracerebroventricular injections or other direct administration mode.

D. Allelic Variants and Homologs of B-PLC Polynucleotides

The invention also provides human allelic variants of the B-PLC polynucleotides of SEQ ID NO:1, and non-human homologs of B-PLC. The polynucleotide probes of the invention are used for isolating and expressing B-PLC from humans and non-human animals, using well known methods, e.g., Sambrook, supra, and Ausubel, supra. For example, a polynucleotide probe comprising all or some of the B-PLC cDNA sequence is labeled and used to screen a genomic or cDNA library by hybridization at moderate stringency (e.g., hybridization in 5×SSC/50% formamide at 42C for 16 h, and wash in 0.1×SSC/0.1% SDS at 50C for 30 min.). The cDNA library can be oligo-dT or random primed. The cDNA or genomic clones that hybridize with the probe are isolated and analyzed by restriction mapping, Southern hybridization, and DNA sequencing using methods that are well known in the art. Depending on the starting library used, a polynucleotide comprising human B-PLC gene, allelic cDNAs, or B-PLC homologs from non-human species can be isolated. B-PLC alleles and homologs can be assayed for various activities characteristic of B-PLC.

Another method for generating B-PLC variants having a desired activity is by directed evolution or "gene shuffling," as described, for example in Patten et al., 1997, *Curr. Opin. Biotech.* 8:724–733; PCT publications WO95/22625; WO97/20078; WO97/35957; WO97/35966; WO98/13487; WO98/13485; PCT 98/00852; PCT 97/24239, and U.S. Pat. No. 5,605,793.

E. Gene Therapy

Gene therapy refers to the introduction of an otherwise exogenous polynucleotide which produces a medically useful phenotypic effect upon the (typically) mammalian cell(s) into which it is transferred. In one aspect, the present invention provides gene therapy methods and compositions for treatment of B-PLC-associated conditions. In illustrative embodiments, gene therapy involves introducing into a cell a vector that expresses an B-PLC gene product (such as an B-PLC protein substantially similar to the B-PLC polypeptide having a sequence of SEQUENCE ID NO: 2 or 7, e.g., to increase B-PLC activity, or an inhibitory B-PLC polypeptide to reduce activity), expresses a nucleic acid having an B-PLC gene or mRNA sequence (such as an antisense RNA, e.g., to reduce B-PLC activity), expresses a polypeptide or polynucleotide that otherwise affects expression of B-PLC gene products (e.g., a ribozyme directed to B-PLC mRNA to reduce B-PLC activity), or replaces or disrupts an endogenous B-PLC sequence (e.g., gene replacement and Agene knockout, respectively). Numerous other embodiments will be evident to one of skill upon review of the disclosure herein.

Vectors useful in B-PLC gene therapy can be viral or nonviral, and include those described supra in relation to the B-PLC expression systems of the invention. It will be understood by those of skill in the art that gene therapy vectors may comprise promoters and other regulatory or processing sequences, such as are described in this disclosure. Usually the vector will comprise a promoter and, optionally, an enhancer (separate from any contained within the promoter sequences) that serve to drive transcription of an oligoribonucleotide, as well as other regulatory elements that provide for episomal maintenance or chromosomal integration and for high-level transcription, if desired. A plasmid useful for gene therapy can comprise other functional elements, such as selectable markers, identification

regions, and other sequences. The additional sequences can have roles in conferring stability both outside and within a cell, targeting delivery of B-PLC nucleotide sequences (sense or antisense) to a specified organ, tissue, or cell population, mediating entry into a cell, mediating entry into the nucleus of a cell and/or mediating integration within nuclear DNA. For example, aptamer-like DNA structures, or other protein binding moieties sites can be used to mediate binding of a vector to cell surface receptors or to serum proteins that bind to a receptor thereby increasing the efficiency of DNA transfer into the cell. Other DNA sites and structures can directly or indirectly bind to receptors in the nuclear membrane or to other proteins that go into the nucleus, thereby facilitating nuclear uptake of a vector. Other DNA sequences can directly or indirectly affect the efficiency of integration.

Suitable gene therapy vectors may, or may not, have an origin of replication. For example, it is useful to include an origin of replication in a vector for propagation of the vector prior to administration to a patient. However, the origin of replication can often be removed before administration if the vector is designed to integrate into host chromosomal DNA or bind to host mRNA or DNA.

As noted, the present invention also provides methods and reagents for gene replacement therapy (i.e., replacement by homologous recombination of an endogenous B-PLC gene with a recombinant gene). Vectors specifically designed for integration by homologous recombination may be used. Important factors for optimizing homologous recombination include the degree of sequence identity and length of homology to chromosomal sequences. The specific sequence mediating homologous recombination is also important, because integration occurs much more easily in transcriptionally active DNA. Methods and materials for constructing homologous targeting constructs are described by e.g., Mansour et al., 1988, *Nature* 336: 348; Bradley et al., 1992, *Bio/Technology* 10: 534. See also, U.S. Pat. Nos. 5,627,059; 5,487,992; 5,631,153; and 5,464,764. In one embodiment, gene replacement therapy involves altering or replacing all or a portion of the regulatory sequences controlling expression of the B-PLC gene that is to be regulated. For example, the B-PLC promoter sequences (e.g., such as are found in SEQUENCE ID NO: 6) may be disrupted (to decrease B-PLC expression or to abolish a transcriptional control site) or an exogenous promoter (e.g., to increase B-PLC expression) substituted.

The invention also provides methods and reagents for B-PLC Agene knockout (i.e., deletion or disruption by homologous recombination of an endogenous B-PLC gene using a recombinantly produced vector). In gene knockout, the targeted sequences can be regulatory sequences (e.g., the B-PLC promoter), or RNA or protein coding sequences. The use of homologous recombination to alter expression of endogenous genes is described in detail in U.S. Pat. No. 5,272,071 (and the U.S. Patents cited supra), WO 91/09955, WO 93/09222, WO 96/29411, WO 95/31560, and WO 91/12650. See also, Moynahan et al., 1996, *Hum. Mol. Genet.* 5:875.

Gene therapy vectors may be introduced into cells or tissues in vivo, in vitro or ex vivo. For ex vivo therapy, vectors may be introduced into cells, e.g., stem cells, taken from the patient and clonally propagated for autologous transplant back into the same patient (see, e.g., U.S. Pat. Nos. 5,399,493 and 5,437,994, the disclosures of which are herein incorporated by reference).

V. Antibodies

The present invention provides antibodies that are specifically immunoreactive with human B-PLC polypeptide.

Accordingly, the invention provides or makes use of antibodies that specifically recognize and bind polypeptides which have an amino acid sequence identical, or substantially identical, to the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:7 or an immunogenic fragment thereof.

The antibodies of the invention usually exhibit a specific binding affinity for B-PLC of at least about 10^7 , 10^8 , 10^9 , or 10^{10} M⁻¹.

The anti-B-PLC antibodies of the invention have a variety of uses, e.g., isolation of B-PLC polypeptides (e.g., by immunoaffinity chromatography), detection of B-PLC polypeptides, and for inhibition of B-PLC activity (e.g., in vivo or in vitro).

A. Production of Anti-B-PLC Antibodies

Anti-B-PLC antibodies of the present invention can be made by a variety of means well known to those of skill in the art, e.g., as described supra. As used herein, antibodies are broadly defined and specifically include fragments, chimeras and the like, that specifically binds an B-PLC polypeptide or epitope.

Methods for production of polyclonal or monoclonal antibodies are well known in the art. See, e.g., Coligan, *CURRENT PROTOCOLS IN IMMUNOLOGY*, Wiley/Greene, N.Y. (1991); Stites et al. (eds.) *BASIC AND CLINICAL IMMUNOLOGY* (7th ed.) Lange Medical Publications, Los Altos, Calif., and references cited therein ("Stites"); Goding, *MONOCLONAL ANTIBODIES: PRINCIPLES AND PRACTICE* (2d ed.) Academic Press, New York, N.Y. (1986); Kohler and Milstein, *Nature* 256:495-497 (1975) ("Kohler and Milstein"); and Harlow and Lane. These techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors. See, Huse et al., *Science* 246:1275-1281 (1989) ("Huse"); and Ward et al., *Nature* 341:544-546 (1989).

For production of polyclonal antibodies, an appropriate target immune system is selected, typically a mouse or rabbit, but also including goats, sheep, cows, chickens, guinea pigs, monkeys and rats. The immunoglobulins produced by the host can be precipitated, isolated and purified by routine methods, including affinity purification. Substantially monospecific antibody populations can be produced by chromatographic purification of polyclonal sera.

For monoclonal antibodies, appropriate animals will be selected and the desired immunization protocol followed. The antibodies of the invention may be of any isotype, e.g., IgM, IgD, IgG, IgA, and IgE, with IgG, IgA and IgM most preferred. Preferred monoclonal anti-B-PLC antibodies neutralize (i.e., inhibit or block) one or more biological activities of B-PLC. Such antibodies may be obtained by screening hybridoma supernatants for the desired inhibitory activity. Monoclonal antibodies with affinities of 10^8 liters/mole, preferably 10^9 to 10^{10} or stronger, can be produced by the methods described below. The production of non-human monoclonal antibodies, e.g., murine, lagomorpha, or equine, is well known and can be accomplished by, e.g., immunizing a host animal with a preparation containing B-PLC or fragments thereof. Antibody-producing cells obtained from the immunized animals are immortalized and screened, or screened first for the production of antibody which binds to the B-PLC polypeptide and then immortalized.

Some anti-B-PLC monoclonal antibodies of the present invention are humanized, human or chimeric, in order to reduce their potential antigenicity, without reducing their affinity for their target. Humanized antibodies have been

described in the art. See, e.g., Queen, et al., 1989, *Proc. Nat'l Acad. Sci. USA* 86:10029; U.S. Pat. Nos. 5,563,762; 5,693,761; 5,585,089 and 5,530,101. The human antibody sequences used for humanization can be the sequences of naturally occurring human antibodies or can be consensus sequences of several human antibodies. See Kettleborough et al., *Protein Engineering* 4:773 (1991); Kolbinger et al., *Protein Engineering* 6:971 (1993).

Humanized monoclonal antibodies against B-PLC can also be produced using transgenic animals having elements of a human immune system (see, e.g., U.S. Pat. Nos. 5,569,825; 5,545,806; 5,693,762; 5,693,761; and 5,7124,350).

Useful anti-B-PLC binding compositions can also be produced using phage display technology (see, e.g., Dower et al., WO 91/17271 and McCafferty et al., WO 92/01047). In these methods, libraries of phage are produced in which members display different antibodies on their outer surfaces. Antibodies are usually displayed as Fv or Fab fragments. Phage displaying antibodies with a desired specificity are selected by affinity enrichment to an B-PLC polypeptide.

Once expressed, the whole antibodies, their dimers, individual light and heavy chains, or other immunoglobulin forms of the present invention can be purified according to standard procedures of the art, including ammonium sulfate precipitation, affinity chromatography, gel electrophoresis and the like (see generally PROTEIN PURIFICATION: PRINCIPLES AND PRACTICE 3RD EDITION (Springer-Verlag, N.Y., 1994)).

An antibody (e.g. an anti-B-PLC antibody), is substantially pure when at least about 80%, more often at least about 90%, even more often at least about 95%, most often at least about 99% or more of the polypeptide molecules present in a preparation specifically bind the same antigen (e.g., B-PLC polypeptide). For pharmaceutical uses, anti-B-PLC immunoglobulins of at least about 90 to 95% homogeneity are preferred, and 98 to 99% or more homogeneity are most preferred.

B. Modification of B-PLC Antibodies

The antibodies of the present invention can be used with or without modification. Frequently, the antibodies will be labeled by joining, either covalently or non-covalently, a substance which provides for a detectable signal. Such labels include those that are well known in the art, e.g., radioactive, fluorescent, or bioactive (e.g., enzymatic) labels. As labeled binding entities, the antibodies of the invention may be particularly useful in diagnostic applications.

Also encompassed by the invention are hybrid antibodies that share the specificity of antibodies against a B-PLC polypeptide but are also capable of specific binding to a second moiety. In hybrid antibodies, one heavy and light chain pair is from one antibody and the other pair from an antibody raised against another epitope. This results in the property of multi-functional valency, i.e., ability to bind at least two different epitopes simultaneously. Such hybrids can be formed by fusion of hybridomas producing the respective component antibodies, or by recombinant techniques.

VI. Detection and Quantification of B-PLC Polynucleotides and Polypeptides

The present invention provides a number of methods for detection and quantification of B-PLC polypeptides and polynucleotides in biological samples. Altered levels of both B-PLC mRNA and protein can manifest a particular state of

disease such as ischemic stroke. The disclosed methods for quantification of B-PLC polynucleotides and polypeptides can be used for diagnostic purposes. Also, any mutations or single nucleotide polymorphisms in the B-PLC gene that may be associated with genetic predispositions to diseases with the B-PLC involvement, can be detected using the methods disclosed herein.

The biological samples can include, but are not limited to, a blood sample, serum, cells (including whole cells, cell fractions, cell extracts, and cultured cells or cell lines), tissues (including tissues obtained by biopsy), body fluids (e.g., urine, sputum, amniotic fluid), or from media (from cultured cells or cell lines), and the like. In one embodiment, the B-PLC polypeptides and polynucleotides are detected in tissue obtained from brain (e.g., human or nonhuman animal brain). In another embodiment, the B-PLC polypeptides and polynucleotides are detected in spleen, where low levels of B-PLC gene are expressed, but where elevated B-PLC levels can be indicative of an neuroinflammatory state of the body.

The methods of detecting or quantifying B-PLC polynucleotides include, but are not limited to, amplification-based assays with or without signal amplification, hybridization based assays, and combination amplification-hybridization assays. For detecting and quantifying B-PLC polypeptides, an exemplary method is an immunoassay that utilizes an antibody or other binding agents that specifically binds to an B-PLC polypeptide or epitope.

A. Assays for B-PLC Polynucleotides

1. Amplification-based Methods

The polymerase chain reaction (PCR), or its variations, is an exemplary amplification-based assay. Examples of techniques sufficient to direct persons of skill through in vitro amplification methods are found in PCR TECHNOLOGY: PRINCIPLES AND APPLICATIONS FOR DNA AMPLIFICATION, H. Erlich, Ed. Freeman Press, New York, N.Y. (1992); PCR PROTOCOLS: A GUIDE TO METHODS AND APPLICATIONS, eds. Innis, Gelfland, Snisky, and White, Academic Press, San Diego, Calif. (1990). Other suitable target amplification methods include the ligase chain reaction (LCR; e.g., Wu and Wallace, 1989, *Genomics* 4:560); strand displacement amplification (SDA; e.g., Walker et al., 1992, *Proc. Natl. Acad. Sci. U.S.A.* 89:392-396); the nucleic acid sequence based amplification (NASBA, Cangene, Mississauga, Ontario; e.g., Compton, 1991, *Nature* 350:91), and the like.

One useful variant of PCR is PCR ELISA (e.g., Boehringer Mannheim Cat. No. 1 636 111) in which digoxigenin-dUTP is incorporated into the PCR product. The PCR reaction mixture is denatured and hybridized with a biotin-labeled oligonucleotide designed to anneal to an internal sequence of the PCR product. The hybridization products are immobilized on streptavidin coated plates and detected using anti-digoxigenin antibodies.

2. Hybridization-based Methods

A variety of methods for specific DNA and RNA measurement using polynucleotide hybridization techniques are known to those of skill in the art (see Sambrook, supra). Hybridization based assays refer to assays in which a polynucleotide probe is hybridized to a target polynucleotide. Usually the polynucleotide hybridization probes of the invention are entirely or substantially identical to a contiguous sequence of the B-PLC nucleic acid sequence. Preferably, polynucleotide probes are at least about 10 bases, often at least about 20 bases, and sometimes at least about 200 bases or more in length. Methods of selecting polynucleotide probe sequences for use in polynucleotide hybridization are discussed in Sambrook, supra.

Polynucleotide hybridization formats are known to those skilled in the art. In some formats, at least one of the target and probe is immobilized. The immobilized polynucleotide may be DNA, RNA, or another oligo- or poly-nucleotide, and may comprise natural or non-naturally occurring nucleotides, nucleotide analogs, or backbones. Such assays may be in any of several formats including: Southern, Northern, dot and slot blots, high-density polynucleotide or oligonucleotide arrays (e.g., GeneChips™ Affymetrix), dip sticks, pins, chips, or beads. All of these techniques are well known in the art and are the basis of many commercially available diagnostic kits. Hybridization techniques are generally described in Hames et al., ed., NUCLEIC ACID HYBRIDIZATION, A PRACTICAL APPROACH IRL Press, (1985); Gall and Pardue *Proc. Natl. Acad. Sci., U.S.A.*, 63: 378–383 (1969); and John et al., *Nature*, 223: 582–587 (1969).

In one embodiment, in situ hybridization is used to detect B-PLC sequences in a sample. In situ hybridization assays are well known and are generally described in Angerer et al., *METHODS ENZYMOL.*, 152: 649–660 (1987) and Ausubel, supra.

B. B-PLC Polypeptide Assays

In one embodiment, the B-PLC polynucleotide is detected in a sample using an anti-B-PLC antibody of the invention. A number of well established immunological binding assays are suitable for detecting and quantifying B-PLC of the present invention. See, e.g., U.S. Pat. Nos. 4,366,241; 4,376,110; 4,517,288; and 4,837,168, and also *METHODS IN CELL BIOLOGY VOLUME 37: ANTIBODIES IN CELL BIOLOGY*, Asai, ed. Academic Press, Inc. New York (1993); *BASIC AND CLINICAL IMMUNOLOGY* 7th Edition, Stites & Terr, eds. (1991); Harlow, supra [e.g., Chapter 14], and Ausubel, supra, [e.g., Chapter 11], each of which is incorporated by reference in its entirety and for all purposes.

Immunoassays for detecting B-PLC may be competitive or noncompetitive. Usually the B-PLC gene product being assayed is detected directly or indirectly using a detectable label. The particular label or detectable group used in the assay is usually not a critical aspect of the invention, so long as it does not significantly interfere with the specific binding of the antibody or antibodies used in the assay. The label may be covalently attached to the capture agent (e.g., an anti-B-PLC antibody), or may be attached to a third moiety, such as another antibody, that specifically binds to the B-PLC polypeptide at a different epitope than recognized by the capture agent.

1. Non-Competitive Immunoassay

Noncompetitive immunoassays are assays in which the amount of captured analyte (here, the B-PLC polypeptide) is directly measured. One such assay is a two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on the captured analyte. See, e.g., Maddox et al., 1983, *J. Exp. Med.*, 158:1211 for background information. In such an assay, the amount of B-PLC in the sample is directly measured. For example, using a so-called “sandwich” assay, the capture agent (here, the anti-B-PLC antibodies) can be bound directly to a solid substrate where they are immobilized. These immobilized antibodies then capture polypeptide present in the test sample. B-PLC thus immobilized is then bound by a labeling agent, such as a second B-PLC antibody bearing a label. Alternatively, the second B-PLC antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second can be

modified with a detectable moiety, such as biotin, to which a third labeled molecule can specifically bind, such as enzyme-labeled streptavidin.

2. Competitive Immunoassay

In competitive assays, the amount of B-PLC polypeptide present in the sample is measured indirectly by measuring the amount of an added (exogenous) B-PLC displaced (or competed away) from a capture agent (e.g., anti-B-PLC antibody) by the analyte present in the sample (e.g., B-PLC polypeptide). In one competitive assay, a known amount of B-PLC is added to the sample and the sample is then contacted with a capture agent (e.g., an anti-B-PLC antibody) that specifically binds to B-PLC. The amount of B-PLC bound to the antibody is inversely proportional to the concentration of B-PLC present in the sample.

Preferably, the antibody is immobilized on a solid substrate. The amount of B-PLC bound to the antibody may be determined either by measuring the amount of B-PLC present in an B-PLC/antibody complex, or alternatively by measuring the amount of remaining uncomplexed B-PLC. The amount of B-PLC may be detected by providing a labeled B-PLC molecule.

For example, using the hapten inhibition assay, the analyte (in this case B-PLC) is immobilized on a solid substrate. A known amount of anti-B-PLC antibody is added to the sample, and the sample is then contacted with the immobilized B-PLC. In this case, the amount of anti-B-PLC antibody bound to the immobilized B-PLC is inversely proportional to the amount of B-PLC present in the sample. Again the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

3. Other Assays

In addition to the competitive and non-competitive B-PLC polypeptide immunoassays, the present invention also provides other assays for detection and quantification of B-PLC polypeptides. For example, Western blot (immunoblot) analysis can be used to detect and quantify the presence of B-PLC in the sample. The technique generally comprises separating sample polypeptides by gel electrophoresis on the basis of molecular weight, transferring the separated polypeptides to a suitable solid support (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind B-PLC. The anti-B-PLC antibodies specifically bind to B-PLC on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (e.g., labeled sheep anti-mouse antibodies) that specifically bind to the anti-B-PLC.

Furthermore, assays such as liposome immunoassays (LIA) are also encompassed by the present invention. LIA utilizes liposomes that is designed to bind specific molecules (e.g., antibodies) and to release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (see, Monroe et al., *Amer. Clin. Prod. Rev.* 5:34–41(1986)).

VII. Association of B-PLC Expression and Ischemia

As is apparent from the examples, infra, the reagents disclosed herein find uses in the diagnostic, therapeutic and industrial arts. As shown in the examples, B-PLC expression is induced is induced after damaging ischemia. It will be appreciated that, using detection methods such as those disclosed herein, expression of B-PLC is useful as a diag-

nostic marker for stroke and other neurological stresses. After ischemia, necrotic and apoptotic cell death occurs that can lead to the release of intracellular proteins (such as B-PLC) or polynucleotides into circulation. Thus, in one embodiment, a test sample (e.g., blood, serum, cerebral-spinal fluid, tissue) from a patient or animal is incubated with an anti-B-PLC antibody of the invention, and the presence or amount of B-PLC is detected.

The amount of B-PLC gene product that is diagnostic of a disease or condition is typically, at least about two, often at least five, frequently at least about ten or about 50 times higher than the levels in cells from tissues (e.g. blood) in a healthy animal or human, and can be easily determined by comparing the expression of the gene in healthy and diseased animals. In some cases, it will be desirable to establish normal or baseline values (or ranges) for gene product expression levels. Normal levels of expression or normal expression products can be determined for any particular population, subpopulation, or group of organisms according to standard methods well known to those of skill in the art and employing the methods and reagents of the invention. Generally, baseline (normal) levels of protein or mRNA are determined by quantitating the amount of protein and/or mRNA in biological samples (e.g., fluids, cells or tissues) obtained from normal (healthy) subjects, e.g., a human subject. For example, normal or control values of protein or mRNA can be determined by quantitating the amount of protein/RNA in a biological sample from the same patient (at different times or stages of progression of a condition) or, from a different individual (e.g., a healthy individual or control animal). In an embodiment, baseline levels are defined from persons of the same or a different age and standard statistical methods used to determination of baseline levels of expression in a healthy population. By comparing the levels of a B-PLC gene product, mutant or variant in the sample with the amount in a healthy cell or tissue of the same type, a different amount of the gene product in the sample as compared to the healthy cell or tissue is prognostic or diagnostic of neurological condition (e.g., a hypoxic-ischemic brain insult such as stroke).

In carrying out the diagnostic and prognostic methods of the invention, it will sometimes be useful to refer to "diagnostic" and "prognostic values." As used herein, "diagnostic value" refers to a value that is determined for the gene product detected in a sample which, when compared to a normal (or "baseline") range of the gene product is indicative of the presence of a disease. "Prognostic value" refers to an amount of the gene product detected in a given cell, tissue, or other biological sample (e.g., blood). The amount (including a zero amount) of the gene product detected in a sample is compared to the prognostic value for the cell such that the relative comparison of the values indicates the presence of disease or the likely outcome of the disease progression. In one embodiment, for example, to assess stroke prognosis, data are collected to obtain a statistically significant correlation of gene product levels with different stroke stages, classes or grades. A predetermined range of expression levels is established for the same cell or tissue sample obtained from subjects having known clinical outcomes. A sufficient number of measurements is made to produce a statistically significant value (or range of values) to which a comparison will be made. The predetermined range of expression levels or activity for a given cell or tissue sample can then be used to determine a value or range for the level of gene product that would correlate to favorable (or less unfavorable) prognosis. The level of gene product from a biological sample (e.g., a patient sample) can

then be determined and compared to the low and high ranges and used to predict a clinical outcome. As noted, the effect of therapeutic treatments (e.g., for stroke) can also be monitored by detecting the expression of B-PLC genes or gene products, or their appearance in tissues (e.g., blood) in a patient receiving a treatment for a neurological condition. The restricted tissue expression of B-PLC described *infra* (FIG. 6) is advantageous in diagnostic and prognostic application, by providing a high degree of specificity and low background.

In one aspect, the invention provides methods for treating a condition characterized by increased B-PLC expression in a mammal, by modulating the activity or expression of B-PLC in a cell or tissue in the mammal. As described herein, the PLC/IP₃ regulatory network affects intracellular Ca²⁺ concentration. Elevated Ca²⁺ levels have been correlated with apoptotic and necrotic cell death. Thus, in one aspect, B-PLC expression or activity is inhibited to prevent neuronal loss after stroke. The disease states expected to benefit from their treatment with B-PLC agonists or antagonists include those which are associated with rapid changes in intracellular Ca²⁺ levels and/or in PKC signaling. Examples of conditions that will benefit using the reagents of the invention include acute neurodegenerative conditions such as ischemic stroke, head trauma or injury, as well as neuroinflammatory diseases with consequences to neurons. In a related aspect, the invention provides a method of identifying an agent for treatment or prevention of a hypoxic-ischemic brain insult, by determining whether a compound or treatment is a modulator of activity or expression of a B-PLC.

As described elsewhere herein, the invention also provides assay methods which are capable of screening compounds that modulate the activity, expression, and distribution of the B-PLC genes and proteins disclosed herein.

A variety of assays can be used to evaluate the modulators of B-PLC expression or activity. In one embodiment, the ability of an agent to modulate (e.g., inhibit) binding between a B-PLC polypeptide and IP₃ is determined. In one embodiment, the ability of an agent to modulate (e.g., inhibit) phospholipase catalytic activity is determined.

One suitable assay is a cell-based assay. Cells which are stably or transiently transfected with a vector or expression cassette having a nucleic acid sequence encoding a B-PLC protein (e.g., having the sequence of SEQ ID NO:2 or 7, or a variant thereof) are used. In a related embodiment, cells that naturally express B-PLC (e.g., non-recombinant cells) are used, either primary cultures from brain or established cell lines. The cells are maintained under conditions appropriate for expression of the B-PLC polypeptide and are contacted with a putative agent. The lipase activity, IP₃-binding activity, or the expression of B-PLC gene products is determined in the presence and absence of the agent.

Optionally, a cellular fraction, such as a membrane fraction, containing the receptor can be used in lieu of whole cells. Alternatively, a property such as a signaling activity, cellular response function and the like is measured in the presence and absence of a test compound, e.g., using recombinant cells expressing a protein of the invention.

In another embodiment, the recombinant B-PLC protein of the invention is expressed, and optionally, purified, and the effect of agents on the biological activity of the protein is assessed. In one embodiment, the protein or fragment is expressed as a fusion protein (e.g., with an epitope tag domain) to facilitate purification and to provide other advantages.

Several methods of automating assays have been developed in recent years so as to permit screening of tens of thousands of compounds in a short period. See, e.g., Fodor et al., 1991, *Science* 251: 767-73.

Assays for catalytic activity can be carried out using routine methods known in the art, e.g., see references listed supra. Similarly, assays for binding between B-PLC and IP3 can be carried out using routine methods known in the art, e.g. as described herein.

Thus, in an embodiment, the invention provides a method of identifying an agent that modulates of B-PLC activity by contacting a cell or composition comprising a B-PLC protein and detecting a difference in protein activity in the presence of the agent compared to the absence of the agent. In an embodiment, the B-PLC polypeptide is encoded by a polynucleotide with the sequence of SEQ. ID. NO:1, or a polynucleotide that hybridizes under stringent conditions to SEQ. ID. NO:1. In an embodiment the polypeptide has the sequence of SEQ ID NO:2 or a conservatively substituted variant thereof. In one embodiment, the difference in protein activity is a difference in binding of IP₃.

In a related embodiment, the invention provides a method of identifying an agent that modulates of B-PLC expression comprising contacting a cell that expresses the B-PLC protein of SEQ ID NO:2 or NO:7 or a naturally occurring allele thereof, and detecting a change in B-PLC expression in the presence of the agent compared to the absence of the agent. In an embodiment, the cell is a cell in a non-human animal.

VIII. Pharmaceutical Compositions

The present invention further provides therapeutic compositions comprising agonists, antagonists, or targets of B-PLC and methods of treating physiologic or pathologic conditions mediated by B-PLC, in particular neurological conditions such as ischemic stroke.

B-PLC polypeptides, fragments thereof, sense and anti-sense polypeptides, anti-B-PLC antibodies or binding fragments thereof, and antagonists or agonists of B-PLC activity, can be directly administered under sterile conditions to the host to be treated. However, while it is possible for the active ingredient to be administered alone, it is often preferable to present it as a pharmaceutical formulation. Formulations typically comprise at least one active ingredient together with one or more acceptable carriers thereof. Each carrier should be both pharmaceutically and physiologically acceptable in the sense of being compatible with the other ingredients and not injurious to the patient. For example, the bioactive agent can be complexed with carrier proteins such as ovalbumin or serum albumin prior to their administration in order to enhance stability or pharmacological properties such as half-life. Furthermore, therapeutic formulations of this invention can be combined with or used in association with other chemotherapeutic or chemopreventive agents.

Therapeutic formulation containing known PLC inhibitors such as U73122, manoalide (Bennett CF, et al. Mol

Pharmacol. 1987 (32) 587-93) or derivatives thereof may be used to attenuate excessive B-PLC activity in conditions described supra.

Therapeutic formulations can be prepared by any methods well known in the art of pharmacy. See, e.g., Gilman et al (eds.) (1990) Goodman and Gilman's: The Pharmacological Bases of Therapeutics (8th ed.) Pergamon Press; and (1990) Remington's Pharmaceutical Sciences (17th ed.) Mack Publishing Co., Easton, Pa.; Avis et al (eds.) (1993) Pharmaceutical Dosage Forms: Parenteral Medications Dekker, N.Y.; Lieberman et al. (eds.) (1990) Pharmaceutical Dosage Forms: Tablets Dekker, N.Y.; and Lieberman et al (eds.) (1990) Pharmaceutical Dosage Forms: Disperse Systems Dekker, N.Y.

The therapeutic formulations can conveniently be presented in unit dosage form and administered in a suitable therapeutic dose. A suitable therapeutic dose can be determined by any of the well known methods such as clinical studies on mammalian species to determine maximum tolerable dose and on normal human subjects to determine safe dosage.

The therapeutic formulations can be delivered by any effective means which could be used for treatment. These means include but are not limited to oral, rectal, nasal, pulmonary administration, or parenteral (including subcutaneous, intramuscular, intravenous and intradermal) infusion into the bloodstream.

IX. Kits

Reagents useful for the therapeutic and diagnostic (detection) methods of the invention are conveniently provided in kit form. Thus, the present invention encompasses kits that contain polypeptides, antibodies, and polynucleotides of the present invention.

In one embodiment, the kit comprises one or more of the following in a container: (1) B-PLC polynucleotides (e.g., oligonucleotide primers or probes corresponding to the B-PLC cDNA sequence and capable of amplifying the target polynucleotides); (2) anti-B-PLC antibodies; (3) B-PLC polypeptides or fragments, optionally coated on a solid surface (such as a slide, multiple well plate, or test tube) (4) a B-PLC polynucleotide (e.g., for use as positive controls in assays), (5) and tubes. Instructions for carrying out the detection methods of the invention, and calibration curves can also be included.

X. EST Sequences

The ESTs (and corresponding clones) listed below have sequence similarity to a human or rodent B-PLC of the invention. In some embodiments the polynucleotide or polypeptides fragments are contemplated to be other than one or more of the molecules listed in Table 2 or translation products thereof. However, inclusion in Table 2 should not be construed as an indication that any sequence or polynucleotide is prior art.

TABLE 2

-
- 1) gb|AW408450.1|AW408450 UI-HF-BK0-abm-c-02-0-UL.r1 NIH_MGC_36
Homo sapiens cDNA clone IMAGE:3056642 5' Length = 455
 2) gb|AA277075.1|AA277075 vc06e01.r1 *Mus musculus* cDNA clone
 IMAGE:765720 5'; Length = 517
 3) gb|AA772973.1|AA772973 af33h09.s1 *Homo sapiens* cDNA clone
 IMAGE:1033505 3'; Length = 471

TABLE 2-continued

4)	gb AW493796.1 AW493796 UI-M-BH3-aug-c-08-0-UI.s1 NIH_BMAP_M_S4 <i>Mus musculus</i> cDNA clone UI-M-BH3-aug-c-08-0-UI 3' Length = 436
5)	gb AW500653.1 AW500653 UI-HF-BN0-akk-h-02-0-UI.r1 NIH_MGC_50 <i>Homo sapiens</i> cDNA clone IMAGE:3077595 5' Length = 434
6)	gb BE655266.1 BE655266 UI-M-BG1-aij-g-02-0-UI.r1 NIH_BMAP_MSC_N <i>Mus musculus</i> cDNA clone UI-M-BG1-aij-g-02-0-UI 5' Length = 390
7)	gb AA690679.1 AA690679 vu53h08.r1 <i>Mus musculus</i> cDNA clone IMAGE:1195167 5; Length = 484
8)	emb AL024179.1 AL024179 k8311b43 <i>Mus musculus</i> cDNA clone 528- 6E13 5' Length = 366
9)	gb AW478640.1 AW478640 21359 MARC 1BOV <i>Bos taurus</i> cDNA 5' Length = 345
10)	gb T78839.1 T78839 yc96g09.r1 <i>Homo sapiens</i> cDNA clone IMAGE:23861 5' Length = 553
11)	gb AW428387.1 AW428387 66309 MARC 4BOV <i>Bos taurus</i> cDNA 5' Length = 312
12)	gb AW466123.1 AW466123 BP230021B20H7 <i>Bos taurus</i> cDNA clone BP230021B20H7 5' Length = 549

XI. EXAMPLES

The following examples are provided to further illustrate the present invention. They are not included to limit the invention in any way.

Example 1

Isolation of Rat B-PLC Polynucleotide

The B-PLC cDNA was identified among the sequences comprising the library of genes upregulated during ischemic preconditioning in the rat hippocampal tissue. Rats of the same strain, age and sex were divided into two experimental groups: a.) animals in the first group underwent surgery including a single 3 minute bilateral occlusion of the carotid arteries ("experimental group") and b.) animals in the second group were sham operated ("control group"). The animals were sacrificed 4 hours after the operation and the CA1 and CA3 regions of their hippocampi were dissected. Poly-A+RNA prepared from the collected tissues was converted in double-stranded cDNA (dscDNA). Subtractive hybridization was carried out using the dscDNA from preconditioned animals with an excess of dscDNA prepared from the sham operated animals. Differentially expressed gene fragments were cloned into a plasmid vector, and the resulting library was transformed in *E. coli* cells.

Inserts of recombinant clones were amplified by the polymerase chain reaction (PCR). The PCR products (fragments of 200–2,000 bp in size) were sequenced using an oligonucleotide complementary to common vector sequences. The resulting sequence information was compared to public databases using the BLAST (blastn and tblastx) algorithm and determined to have similarity to phospholipase-encoding sequences.

Nucleotide sequences of genes upregulated in the rat hippocampus upon ischemic preconditioning were analyzed by the BLAST software to identify the relationship of the isolated genes to those available in the GENBANK.

Example 2

Isolation of Human B-PLC Polynucleotide

A partial rat cDNA clone encoding a novel PLC, SEQ ID NO:3 (see FIG. 3), was obtained as described in Example 1. The rat clone was used to screen human hippocampal and fetal brain cDNA libraries in the lambda phage vector to isolate the full-length human PLC cDNA. A radioactively

20 labeled DNA fragment corresponding to SEQ ID NO:3 was hybridized under low stringency (hybridization in 5×SSC/50% formamide at 42C for 16 h, and wash in 0.1×SSC/0.1% SDS at 50C for 30 min.) to human cDNA libraries immobilized to membrane filters. Positive, hybridizing human
25 cDNA clones were isolated and sequenced. At least 20 different hybridizing clones were isolated from both libraries. Lambda DNA from all clones was isolated and mapped by restriction digests. The longest overlapping clones were used to deduce the nucleotide sequence encoding the B-PLC
30 protein.

Example 3

Tissue-Specific Expression of human B-PLC mRNA

35 The expression pattern of B-PLC was determined by Northern blotting. mRNA was isolated using standard methods (Sambrook et al., supra) from the following rat organs: brain, heart, lung, liver, kidney, spleen, thymus, testis, adrenal glands. mRNAs were separated by gel electrophoresis and blotted to nylon membrane filter (Sambrook). The membranes were prehybridized in 7% SDS, 0.5 M NaHPO₄, 1 mM EDTA at 65° C. for 15 minutes. Using fresh prehybridization solution, the membranes were hybridized with the labeled probe for 18 hours. The hybridized membranes were briefly rinsed in 5% SDS, 40 mM NaHPO₄, 1 mM EDTA and then washed for 45 minutes at 65° C. with fresh solution. This wash solution was replaced with 1% SDS, 40 mM NaHPO₄, 1 mM EDTA and washed twice for 45 minutes at 65° C. with fresh solution. After washing, the membranes were sandwiched between plastic wrap and exposed overnight to Kodak X-OMAT AR film with a Dupont Lightening Plus intensifying screen at –70° C.

45 The results are shown in FIG. 6. Numbers in boxes indicate sizes of RNA size standards. The size of the predominant B-PLC mRNA is 5 kb. An additional transcript of about 3.5 kb can be detected in brain mRNA, and may indicate the presence of a splice variant of B-PLC in that
50 tissue.

Example 4

In Situ Hybridization of B-PLC Probe to Rat Brain

65 The distribution of the B-PLC mRNA in the rat brain was determined by in situ hybridization. Thin brain slices were cut from control rat brains and from brains of rats that had

received 3 min global ischemic pulse (ischemic preconditioning), 10 min global ischemia (damaging ischemia) or ischemic preconditioning 48 h prior to damaging ischemia. An antisense oligo complementary to the rat B-PLC mRNA (having the sequence 5'-AGGATTCTCATTGGCGTATTACTGGCTAGCACT TCATTG-3') (SEQ ID NO: 22) was radioactively labeled with ³⁵S and allowed to hybridize to the brain slices according to a standard protocol (Wisden, W. & Morris, B. J. in *In Situ Hybridization Protocols for the Brain* (ed. Wisden, W. & Morris, B. J.), Academia, London, 1994, 9-30). Signal from the specifically bound oligonucleotides was detected after several weeks exposure to Kodak BIOMAX film at -70° C. The expression of B-PLC could be observed in all major brain areas such as cerebral cortex and hippocampus

(see FIG. 7). Furthermore, a significant upregulation of the B-PLC mRNA was detectable in cortex and hippocampus in rat brain slices that had received global ischemia for 10 min.

All references cited herein are incorporated herein by reference in their entirety and for all purposes to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference in its entirety for all purposes.

Many modifications and variations of this invention can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. The specific embodiments described herein are offered by way of example only, and the invention is to be limited only by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 22

<210> SEQ ID NO 1

<211> LENGTH: 3006

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

```

atgccaacag agaagaagat cagcagtgca agtgattgta ttaattcaat ggttgagggt      60
tcagaactca aaaaggttcg ctccaactct agaatttato ataggtactt tctactggat      120
gctgacatgc agagcctaag gtgggagcca tctaagaagg attctgagaa agccaagatt      180
gacattaat ccatcaagga agtgagaacg ggaaaaaaca cagacatatt ccgcagcaat      240
ggcatttctg accagatato tgaagattgt gcgttttccg tcatatatgg agagaattat      300
gagtcactgg atttggttgc cactctcgca gatggtgcaa acatctgggt tacaggactg      360
cggtacctaa ttcttatagg aaaacatata cttgatatgt tagaaagtag ccaagataac      420
atgaggactt cttgggttcc acaaatgttt agtgaaattg atgtagataa ccttggacat      480
ataactctgt gtaatgctgt gcaatgtatc agaaacctca atcctggttt aaaaacgagc      540
aaaattgagc ttaagttcaa agaattgcat aaatcaaagg acaaagctgg taccgaggtc      600
acaaaggaag aattttattga ggtttttcat gagctttgta ctgacctga aattttattc      660
cttttagttc agttttcaag caataaagaa ttcccttgata ccaaggacct tatgatgttt      720
cttgaggcag aacagggtgt ggcacatata aatgaggaaa taagccttga aattattcac      780
aaatatgaac catccaaaga gggtcaggaa aagggtctgc tctccataga cgggttcaact      840
aattacctta tgcacctga ctgttatata ttcgatccag aacataagaa ggtotgtcag      900
gatatgaagc aaactctgtc tcattacttt ataaactcat ctcataatac aacttaata      960
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<210> SEQ ID NO 2
<211> LENGTH: 1001
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
    
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<400> SEQUENCE: 2

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Tyr His Arg Tyr Phe Leu Leu Asp Ala Asp Met Gln Ser Leu Arg Trp
    35             40             45
Glu Pro Ser Lys Lys Asp Ser Glu Lys Ala Lys Ile Asp Ile Lys Ser
    50             55             60
Ile Lys Glu Val Arg Thr Gly Lys Asn Thr Asp Ile Phe Arg Ser Asn
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Gly Ile Ser Asp Gln Ile Ser Glu Asp Cys Ala Phe Ser Val Ile Tyr
    
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Ala	Asn	Ile	Trp	Val	Thr	Gly	Leu	Arg	Tyr	Leu	Ile	Ser	Tyr	Gly	Lys				
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His	Thr	Leu	Asp	Met	Leu	Glu	Ser	Ser	Gln	Asp	Asn	Met	Arg	Thr	Ser				
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Trp	Val	Ser	Gln	Met	Phe	Ser	Glu	Ile	Asp	Val	Asp	Asn	Leu	Gly	His				
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Ile	Thr	Leu	Cys	Asn	Ala	Val	Gln	Cys	Ile	Arg	Asn	Leu	Asn	Pro	Gly				
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Leu	Lys	Thr	Ser	Lys	Ile	Glu	Leu	Lys	Phe	Lys	Glu	Leu	His	Lys	Ser				
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Lys	Asp	Lys	Ala	Gly	Thr	Glu	Val	Thr	Lys	Glu	Glu	Phe	Ile	Glu	Val				
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Phe	His	Glu	Leu	Cys	Thr	Arg	Pro	Glu	Ile	Tyr	Phe	Leu	Leu	Val	Gln				
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Phe	Ser	Ser	Asn	Lys	Glu	Phe	Leu	Asp	Thr	Lys	Asp	Leu	Met	Met	Phe				
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Leu	Glu	Ala	Glu	Gln	Gly	Val	Ala	His	Ile	Asn	Glu	Glu	Ile	Ser	Leu				
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Glu	Ile	Ile	His	Lys	Tyr	Glu	Pro	Ser	Lys	Glu	Gly	Gln	Glu	Lys	Gly				
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Trp	Leu	Ser	Ile	Asp	Gly	Phe	Thr	Asn	Tyr	Leu	Met	Ser	Pro	Asp	Cys				
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Tyr	Ile	Phe	Asp	Pro	Glu	His	Lys	Lys	Val	Cys	Gln	Asp	Met	Lys	Gln				
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Pro	Leu	Ser	His	Tyr	Phe	Ile	Asn	Ser	Ser	His	Asn	Thr	Tyr	Leu	Ile				
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Glu	Asp	Gln	Phe	Arg	Gly	Pro	Ser	Asp	Ile	Thr	Gly	Tyr	Ile	Arg	Ala				
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Leu	Lys	Met	Gly	Cys	Arg	Ser	Val	Glu	Leu	Asp	Val	Trp	Asp	Gly	Pro				
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Asp	Asn	Glu	Pro	Val	Ile	Tyr	Thr	Gly	His	Thr	Met	Thr	Ser	Gln	Ile				
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Val	Phe	Arg	Ser	Val	Ile	Asp	Ile	Ile	Asn	Lys	Tyr	Ala	Phe	Phe	Ala				
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Ser	Glu	Tyr	Pro	Leu	Ile	Leu	Cys	Leu	Glu	Asn	His	Cys	Ser	Ile	Lys				
	385				390					395					400				
Gln	Gln	Lys	Val	Met	Val	Gln	His	Met	Lys	Lys	Leu	Leu	Gly	Asp	Lys				
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Leu	Tyr	Thr	Thr	Ser	Pro	Asn	Val	Glu	Glu	Ser	Tyr	Leu	Pro	Ser	Pro				
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Asp	Val	Leu	Lys	Gly	Lys	Ile	Leu	Ile	Lys	Ala	Lys	Lys	Leu	Ser	Ser				
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Asn	Cys	Ser	Gly	Val	Glu	Gly	Asp	Val	Thr	Asp	Glu	Asp	Glu	Gly	Ala				
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Glu	Met	Ser	Gln	Arg	Met	Gly	Lys	Glu	Asn	Met	Glu	Gln	Pro	Asn	Asn				
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Val	Pro	Val	Lys	Arg	Phe	Gln	Leu	Cys	Lys	Glu	Leu	Ser	Glu	Leu	Val				
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Ser	Ile	Cys	Lys	Ser	Val	Gln	Phe	Lys	Glu	Phe	Gln	Val	Ser	Phe	Gln				
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Val Gln Lys Tyr Trp Glu Val Cys Ser Phe Asn Glu Val Leu Ala Ser
 515 520 525
 Lys Tyr Ala Asn Glu Asn Pro Gly Asp Phe Val Asn Tyr Asn Lys Arg
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 Phe Leu Ala Arg Val Phe Pro Ser Pro Met Arg Ile Asp Ser Ser Asn
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 Met Asn Pro Gln Asp Phe Trp Lys Cys Gly Cys Gln Ile Val Ala Met
 565 570 575
 Asn Phe Gln Thr Pro Gly Leu Met Met Asp Leu Asn Ile Gly Trp Phe
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 Arg Gln Asn Gly Asn Cys Gly Tyr Val Leu Arg Pro Ala Ile Met Arg
 595 600 605
 Glu Glu Val Ser Phe Phe Ser Ala Asn Thr Lys Asp Ser Val Pro Gly
 610 615 620
 Val Ser Pro Gln Leu Leu His Ile Lys Ile Ile Ser Gly Gln Asn Phe
 625 630 635 640
 Pro Lys Pro Lys Gly Ser Gly Ala Lys Gly Asp Val Val Asp Pro Tyr
 645 650 655
 Val Tyr Val Glu Ile His Gly Ile Pro Ala Asp Cys Ala Glu Gln Arg
 660 665 670
 Thr Lys Thr Val His Gln Asn Gly Asp Ala Pro Ile Phe Asp Glu Ser
 675 680 685
 Phe Glu Phe Gln Ile Asn Leu Pro Glu Leu Ala Met Val Arg Phe Val
 690 695 700
 Val Leu Asp Asp Asp Tyr Ile Gly Asp Glu Phe Met Gly Gln Tyr Thr
 705 710 715 720
 Ile Pro Phe Glu Cys Leu Gln Thr Gly Tyr Arg His Val Pro Leu Gln
 725 730 735
 Ser Leu Thr Gly Glu Val Leu Ala His Ala Ser Leu Phe Val His Val
 740 745 750
 Ala Ile Thr Asn Arg Arg Val Gly Gly Lys Pro His Lys Arg Gly Leu
 755 760 765
 Ser Val Arg Lys Gly Lys Lys Ser Arg Glu Tyr Ala Ser Leu Arg Thr
 770 775 780
 Leu Trp Ile Lys Thr Val Asp Glu Val Phe Lys Asn Ala Gln Pro Pro
 785 790 795 800
 Ile Arg Asp Ala Thr Asp Leu Arg Glu Asn Met Gln Asn Ala Val Val
 805 810 815
 Ser Phe Lys Glu Leu Cys Gly Leu Ser Ser Val Ala Asn Leu Met Gln
 820 825 830
 Cys Met Leu Ala Val Ser Pro Arg Phe Leu Gly Pro Asp Asn Thr Pro
 835 840 845
 Leu Val Val Leu Asn Leu Ser Glu Gln Tyr Pro Thr Met Glu Leu Gln
 850 855 860
 Gly Ile Val Ser Glu Val Leu Lys Lys Ile Val Thr Thr Tyr Asp Met
 865 870 875 880
 Met Ile Gln Ser Leu Lys Ala Leu Ile Glu Asn Ala Asp Ala Val Tyr
 885 890 895
 Glu Lys Ile Val His Cys Gln Lys Ala Ala Met Glu Phe His Glu His
 900 905 910
 Leu His Ser Ile Gly Thr Lys Glu Gly Leu Lys Glu Arg Lys Leu Gln
 915 920 925

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Lys Ala Val Glu Ser Phe Thr Trp Asn Ile Thr Ile Leu Lys Gly Gln
 930 935 940

Ala Asp Leu Leu Lys Tyr Ala Lys Asn Glu Thr Leu Glu Asn Leu Lys
 945 950 955 960

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

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

Glu Lys Ala Asn Asp Glu Thr Gly Glu
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<210> SEQ ID NO 3
 <211> LENGTH: 598
 <212> TYPE: DNA
 <213> ORGANISM: Rattus sp.

<400> SEQUENCE: 3

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 tgggaagtgt gttcattcaa tgaagtgcta gccagtaaat acgccaatga gaatcctggg 240
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 aactgtggct atgttcttcg accagccatc atgaggggaag aagtctcctt cttcagtgcc 480
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<210> SEQ ID NO 4
 <211> LENGTH: 161
 <212> TYPE: PRT
 <213> ORGANISM: Rattus sp.

<400> SEQUENCE: 4

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Phe Gln Val Gln Lys Tyr Trp Glu Val Cys Ser Phe Asn Glu Val Leu
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Ala Ser Lys Tyr Ala Asn Glu Asn Pro Gly Asp Phe Val Asn Tyr Asn
 35 40 45

Lys Arg Phe Leu Ala Arg Val Phe Pro Ser Pro Met Arg Ile Asp Ser
 50 55 60

Ser Asn Met Asn Pro Gln Asp Phe Trp Lys Cys Gly Cys Gln Ile Val
 65 70 75 80

Ala Met Asn Phe Gln Thr Pro Gly Leu Met Met Asp Leu Asn Ile Gly
 85 90 95

Trp Phe Arg Gln Asn Gly Asn Cys Gly Tyr Val Leu Arg Pro Ala Ile
 100 105 110

Met Arg Glu Glu Val Ser Phe Phe Ser Ala Asn Thr Asp Lys Ser Val
 115 120 125

Pro Gly Val Ser Pro Gln Leu Leu His Ile Lys Ile Ile Ser Gly Gln
 130 135 140

Asn Phe Pro Lys Pro Lys Gly Ser Gly Ala Lys Gly Asp Val Val Asp

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<210> SEQ ID NO 5			
<211> LENGTH: 2958			
<212> TYPE: DNA			
<213> ORGANISM: Rattus sp.			
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tgcaagcgac	tgcatcaact	caatggtgga	gggctctgaa ctcaagaagg ttcgttcaaa 180
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<210> SEQ ID NO 6
<211> LENGTH: 4147
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Clone
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acgggtacc gccatgtccc cctgcagtcc ttaactggag aggtccttgc acatgcttct	2700
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tattaaaact gtgaatgtat gtagcaatcc tgcgtgtgaa ggcaataaaa ctctttaaca 3660
ggcaattata ttgctggcca aaatagtcta tatttgata caaagacatt ctaactcagt 3720
tccagtatga agaaagatta ttactctag ctccactgag aaacattttc ctaagtgaaa 3780
acaattttct aagatggaaa tggattggat tgtcaaatta ttatttattg gagaaaaaaa 3840
cctgatctac acatttttac ttatatgggg ttgccagagt ctctgggttc tagatgattt 3900
tggtgccatg cttgctgagc cataattact aaagagaatg taagtggacg ggttcctgga 3960
atccccgggg tccctggaga gccatcgagg agaatgtgca attggactga agctccctgg 4020
ctgaagatac atgcccagtc agcacatggg tagagatgat gtaaaagcag ccaactctgga 4080
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<210> SEQ ID NO 7
<211> LENGTH: 1154
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Clone
        KIAA1092 (Genbank ID AB029015)
    
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<400> SEQUENCE: 7

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Arg Gly Phe Val Gln Ala Gly Arg Gly Ala Pro Met Ala Glu Cys Gly
          20           25           30
Arg Gly Gly Ala Ala Gly Gly Ala Leu Pro Thr Ser Pro Gly Pro Ala
          35           40           45
Leu Gly Ala Lys Gly Ala Leu Lys Ala Gly Val Gly Glu Gly Gly Gly
          50           55           60
Gly Gly Gly Arg Leu Gly His Gly Arg Ala Arg Tyr Asp Ser Gly Gly
          65           70           75           80
Val Ser Asn Gly Asp Cys Ser Leu Gly Val Ser Gly Asp Glu Ala Arg
          85           90           95
Ala Ser Pro Thr Arg Gly Pro Arg Gly Val Ala Leu Ala Pro Thr Pro
          100          105          110
Ser Ala Val Val Cys Thr Leu Pro Arg Glu Ser Lys Pro Gly Gly Leu
          115          120          125
Pro Arg Arg Ser Ser Ile Ile Lys Asp Gly Thr Lys Gln Lys Arg Glu
          130          135          140
Arg Lys Lys Thr Val Ser Phe Ser Ser Met Pro Thr Glu Lys Lys Ile
          145          150          155          160
Ser Ser Ala Ser Asp Cys Ile Asn Ser Met Val Glu Gly Ser Glu Leu
          165          170          175
Lys Lys Val Arg Ser Asn Ser Arg Ile Tyr His Arg Tyr Phe Leu Leu
          180          185          190
Asp Ala Asp Met Gln Ser Leu Arg Trp Glu Pro Ser Lys Lys Asp Ser
          195          200          205
Glu Lys Ala Lys Ile Asp Ile Lys Ser Ile Lys Glu Val Arg Thr Gly
          210          215          220
    
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Lys Asn Thr Asp Ile Phe Arg Ser Asn Gly Ile Ser Asp Gln Ile Ser
 225 230 235 240
 Glu Asp Cys Ala Phe Ser Val Ile Tyr Gly Glu Asn Tyr Glu Ser Leu
 245 250 255
 Asp Leu Val Ala Asn Ser Ala Asp Val Ala Asn Ile Trp Val Thr Gly
 260 265 270
 Leu Arg Tyr Leu Ile Ser Tyr Gly Lys His Thr Leu Asp Met Leu Glu
 275 280 285
 Ser Ser Gln Asp Asn Met Arg Thr Ser Trp Val Ser Gln Met Phe Ser
 290 295 300
 Glu Ile Asp Val Asp Asn Leu Gly His Ile Thr Leu Cys Asn Ala Val
 305 310 315 320
 Gln Cys Ile Arg Asn Leu Asn Pro Gly Leu Lys Thr Ser Lys Ile Glu
 325 330 335
 Leu Lys Phe Lys Glu Leu His Lys Ser Lys Asp Lys Ala Gly Thr Glu
 340 345 350
 Val Thr Lys Glu Glu Phe Ile Glu Val Phe His Glu Leu Cys Thr Arg
 355 360 365
 Pro Glu Ile Tyr Phe Leu Leu Val Gln Phe Ser Ser Asn Lys Glu Phe
 370 375 380
 Leu Asp Thr Lys Asp Leu Met Met Phe Leu Glu Ala Glu Gln Gly Val
 385 390 395 400
 Ala His Ile Asn Glu Glu Ile Ser Leu Glu Ile Ile His Lys Tyr Glu
 405 410 415
 Pro Ser Lys Glu Gly Gln Glu Lys Gly Trp Leu Ser Ile Asp Gly Phe
 420 425 430
 Thr Asn Tyr Leu Met Ser Pro Asp Cys Tyr Ile Phe Asp Pro Glu His
 435 440 445
 Lys Lys Val Cys Gln Asp Met Lys Gln Pro Leu Ser His Tyr Phe Ile
 450 455 460
 Asn Ser Ser His Asn Thr Tyr Leu Ile Glu Asp Gln Phe Arg Gly Pro
 465 470 475 480
 Ser Asp Ile Thr Gly Tyr Ile Arg Ala Leu Lys Met Gly Cys Arg Ser
 485 490 495
 Val Glu Leu Asp Val Trp Asp Gly Pro Asp Asn Glu Pro Val Ile Tyr
 500 505 510
 Thr Gly His Thr Met Thr Ser Gln Ile Val Phe Arg Ser Val Ile Asp
 515 520 525
 Ile Ile Asn Lys Tyr Ala Phe Phe Ala Ser Glu Tyr Pro Leu Ile Leu
 530 535 540
 Cys Leu Glu Asn His Cys Ser Ile Lys Gln Gln Lys Val Met Val Gln
 545 550 555 560
 His Met Lys Lys Leu Leu Gly Asp Lys Leu Tyr Thr Thr Ser Pro Asn
 565 570 575
 Val Glu Glu Ser Tyr Leu Pro Ser Pro Asp Val Leu Lys Gly Lys Ile
 580 585 590
 Leu Ile Lys Ala Lys Lys Leu Ser Ser Asn Cys Ser Gly Val Glu Gly
 595 600 605
 Asp Val Thr Asp Glu Asp Glu Gly Ala Glu Met Ser Gln Arg Met Gly
 610 615 620
 Lys Glu Asn Met Glu Gln Pro Asn Asn Val Pro Val Lys Arg Phe Gln
 625 630 635 640
 Leu Cys Lys Glu Leu Ser Glu Leu Val Ser Ile Cys Lys Ser Val Gln

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645					650					655					
Phe	Lys	Glu	Phe	Gln	Val	Ser	Phe	Gln	Val	Gln	Lys	Tyr	Trp	Glu	Val
			660					665					670		
Cys	Ser	Phe	Asn	Glu	Val	Leu	Ala	Ser	Lys	Tyr	Ala	Asn	Glu	Asn	Pro
		675					680					685			
Gly	Asp	Phe	Val	Asn	Tyr	Asn	Lys	Arg	Phe	Leu	Ala	Arg	Val	Phe	Pro
	690					695					700				
Ser	Pro	Met	Arg	Ile	Asp	Ser	Ser	Asn	Met	Asn	Pro	Gln	Asp	Phe	Trp
705				710						715					720
Lys	Cys	Gly	Cys	Gln	Ile	Val	Ala	Met	Asn	Phe	Gln	Thr	Pro	Gly	Leu
			725						730					735	
Met	Met	Asp	Leu	Asn	Ile	Gly	Trp	Phe	Arg	Gln	Asn	Gly	Asn	Cys	Gly
			740					745					750		
Tyr	Val	Leu	Arg	Pro	Ala	Ile	Met	Arg	Glu	Glu	Val	Ser	Phe	Phe	Ser
		755					760					765			
Ala	Asn	Thr	Lys	Asp	Ser	Val	Pro	Gly	Val	Ser	Pro	Gln	Leu	Leu	His
		770				775					780				
Ile	Lys	Ile	Ile	Ser	Gly	Gln	Asn	Phe	Pro	Lys	Pro	Lys	Gly	Ser	Gly
785				790						795					800
Ala	Lys	Gly	Asp	Val	Val	Asp	Pro	Tyr	Val	Tyr	Val	Glu	Ile	His	Gly
			805						810					815	
Ile	Pro	Ala	Asp	Cys	Ala	Glu	Gln	Arg	Thr	Lys	Thr	Val	His	Gln	Asn
			820					825						830	
Gly	Asp	Ala	Pro	Ile	Phe	Asp	Glu	Ser	Phe	Glu	Phe	Gln	Ile	Asn	Leu
		835					840					845			
Pro	Glu	Leu	Ala	Met	Val	Arg	Phe	Val	Val	Leu	Asp	Asp	Asp	Tyr	Ile
	850					855					860				
Gly	Asp	Glu	Phe	Ile	Gly	Gln	Tyr	Thr	Ile	Pro	Phe	Glu	Cys	Leu	Gln
865					870					875					880
Thr	Gly	Tyr	Arg	His	Val	Pro	Leu	Gln	Ser	Leu	Thr	Gly	Glu	Val	Leu
				885					890					895	
Ala	His	Ala	Ser	Leu	Phe	Val	His	Val	Ala	Ile	Thr	Asn	Arg	Arg	Gly
			900					905						910	
Gly	Gly	Lys	Pro	His	Lys	Arg	Gly	Leu	Ser	Val	Arg	Lys	Gly	Lys	Lys
		915					920					925			
Ser	Arg	Glu	Tyr	Ala	Ser	Leu	Arg	Thr	Leu	Trp	Ile	Lys	Thr	Val	Asp
	930					935					940				
Glu	Val	Phe	Lys	Asn	Ala	Gln	Pro	Pro	Ile	Arg	Asp	Ala	Thr	Asp	Leu
945					950					955					960
Arg	Glu	Asn	Met	Gln	Asn	Ala	Val	Val	Ser	Phe	Lys	Glu	Leu	Cys	Gly
			965						970					975	
Leu	Ser	Ser	Val	Ala	Asn	Leu	Met	Gln	Cys	Met	Leu	Ala	Val	Ser	Pro
			980					985					990		
Arg	Phe	Leu	Gly	Pro	Asp	Asn	Thr	Pro	Leu	Val	Val	Leu	Asn	Leu	Ser
		995					1000					1005			
Glu	Gln	Tyr	Pro	Thr	Met	Glu	Leu	Gln	Gly	Ile	Val	Pro	Glu	Val	Leu
	1010					1015					1020				
Lys	Lys	Ile	Val	Thr	Thr	Tyr	Asp	Met	Met	Ile	Gln	Ser	Leu	Lys	Ala
1025					1030					1035					1040
Leu	Ile	Glu	Asn	Ala	Asp	Ala	Val	Tyr	Glu	Lys	Ile	Val	His	Cys	Gln
			1045					1050						1055	
Lys	Ala	Ala	Met	Glu	Phe	His	Glu	His	Leu	His	Ser	Ile	Gly	Thr	Lys
			1060					1065					1070		

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Glu Gly Leu Lys Glu Arg Lys Leu Gln Lys Ala Val Glu Ser Phe Thr
 1075 1080 1085
 Trp Asn Ile Thr Ile Leu Lys Gly Gln Ala Asp Leu Leu Lys Tyr Ala
 1090 1095 1100
 Lys Asn Glu Thr Leu Glu Asn Leu Lys Gln Ile His Phe Ala Ala Val
 1105 1110 1115 1120
 Ser Cys Gly Leu Asn Lys Pro Gly Thr Glu Asn Ala Asp Val Gln Lys
 1125 1130 1135
 Pro Arg Arg Ser Leu Glu Val Ile Pro Glu Lys Ala Asn Asp Glu Thr
 1140 1145 1150

Gly Glu

<210> SEQ ID NO 8
 <211> LENGTH: 3238
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

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 tagaatttat cataggtact ttctactgga tgctgacatg cagagcctaa ggtgggagcc 180
 atctaagaag gattctgaga aagccaagat tgacattaaa tccatcaag aagtgagaac 240
 gggaaaaaac acagacatat tccgcagcaa tggcatttct gaccagatat ctgaagattg 300
 tgcgttttcc gtcatatatg gagagaatta tgagtcactg gatttggttg ccaactctcg 360
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 acttgatatg ttagaaagta gccaaagata catgaggact tcttggtttt cacaatggtt 480
 tagtgaatt gatgtagata accttgaca tataactctg tgtaatgctg tgcaatgtat 540
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 taaatcaaag gacaagctg gtaccgaggt cacaagga gaatttattg aggtttttca 660
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 attccttgat accaaggacc ttatgatgtt tcttgaggca gaacagggtg tggcacatat 780
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 attcgatcca gaacataaga aggtctgtca ggatagaa caacctctgt ctctactact 960
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 agaactgtct gaactgtgca gcatctgcaa atcagttcag ttcaaagaat ttcaggtgtc 1560
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<210> SEQ ID NO 9
<211> LENGTH: 916
<212> TYPE: PRT
<213> ORGANISM: Rattus sp.

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<400> SEQUENCE: 9

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Met Val Glu Gly Ser Glu Leu Lys Lys Val Arg Ser Asn Ser Arg Ile
                20             25            30
Tyr His Arg Tyr Phe Leu Leu Asp Ala Asp Met Gln Ser Leu Arg Trp
                35             40            45
Glu Pro Ser Lys Lys Asp Ser Glu Lys Ala Lys Ile Asp Ile Lys Ser
 50             55            60
Ile Lys Glu Val Arg Thr Gly Lys Asn Thr Asp Ile Phe Pro Gln Gln
 65             70            75            80
Trp Ala Phe Leu Ser Lys Tyr Leu Lys Asp Cys Ala Phe Ser Val Ile

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85					90					95					
Tyr	Gly	Glu	Asn	Met	Ser	His	Ser	Asp	Leu	Val	Ala	Asn	Ser	Ala	Asp
			100					105					110		
Val	Ala	Asn	Ile	Trp	Val	Thr	Gly	Leu	Arg	Tyr	Leu	Ile	Ser	Tyr	Gly
		115					120					125			
Lys	His	Thr	Leu	Asp	Met	Leu	Glu	Ser	Ser	Gln	Asp	Asn	Met	Arg	Thr
	130					135					140				
Cys	Trp	Val	Ser	Gln	Met	Phe	Ser	Glu	Ile	Asp	Val	Asp	Asp	Leu	Gly
145					150					155					160
His	Ile	Thr	Leu	Cys	Asn	Ala	Val	Gln	Cys	Ile	Arg	Asn	Leu	Asn	Pro
			165						170					175	
Gly	Leu	Lys	Thr	Ser	Lys	Ile	Glu	Leu	Lys	Phe	Lys	Glu	Leu	His	Lys
		180						185						190	
Ser	Lys	Asp	Lys	Thr	Gly	Thr	Glu	Ile	Thr	Lys	Glu	Glu	Phe	Val	Glu
		195					200					205			
Val	Phe	His	Glu	Leu	Cys	Thr	Arg	Pro	Glu	Ile	Tyr	Phe	Leu	Leu	Val
	210					215					220				
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Phe	Leu	Asp	Thr	Lys	Asp	Leu	Met	Met
225					230					235					240
Phe	Leu	Glu	Ala	Glu	Gln	Gly	Val	Ala	His	Ile	Asn	Glu	Glu	Ile	Ser
			245						250					255	
Leu	Glu	Ile	Ile	His	Lys	Tyr	Glu	Pro	Ser	Lys	Glu	Gly	Gln	Glu	Lys
			260					265						270	
Gly	Trp	Leu	Ser	Ile	Asp	Gly	Phe	Thr	Asn	Tyr	Leu	Met	Ser	Pro	Asp
		275					280						285		
Cys	Tyr	Ile	Phe	Asp	Pro	Glu	His	Lys	Lys	Val	Cys	Gln	Asp	Met	Lys
	290					295					300				
Gln	Pro	Leu	Ser	His	Tyr	Phe	Ile	Asn	Ser	Ser	His	Asn	Thr	Tyr	Leu
305					310					315					320
Ile	Glu	Asp	Gln	Phe	Pro	Gly	Pro	Ser	Asp	Ile	Thr	Gly	Tyr	Ile	Arg
			325						330					335	
Ala	Leu	Lys	Met	Gly	Cys	Arg	Ser	Val	Glu	Leu	Asp	Val	Trp	Asp	Gly
			340					345					350		
Pro	Asp	Asn	Glu	Pro	Val	Ile	Tyr	Thr	Gly	His	Thr	Met	Thr	Ser	Gln
		355					360					365			
Ile	Val	Phe	Arg	Ser	Val	Ile	Asp	Ile	Ile	Asn	Lys	Tyr	Ala	Phe	Phe
	370					375					380				
Ala	Ser	Glu	Tyr	Pro	Leu	Ile	Leu	Cys	Leu	Glu	Asn	His	Cys	Ser	Ile
385					390					395					400
Lys	Gln	Gln	Lys	Val	Met	Val	Gln	His	Met	Lys	Lys	Ile	Leu	Gly	Asp
			405						410					415	
Lys	Leu	Tyr	Thr	Thr	Ser	Pro	Asn	Met	Glu	Glu	Ser	Tyr	Leu	Pro	Ser
			420					425						430	
Pro	Asp	Val	Leu	Lys	Gly	Lys	Ile	Leu	Ile	Lys	Ala	Lys	Lys	Leu	Ser
		435					440						445		
Ser	Asn	Cys	Ser	Gly	Val	Glu	Gly	Asp	Val	Thr	Asp	Glu	Asp	Glu	Gly
	450					455					460				
Ala	Glu	Met	Ser	Gln	Arg	Met	Gly	Lys	Glu	Asn	Val	Glu	Gln	Pro	Asn
465					470					475					480
His	Val	Pro	Val	Lys	Arg	Phe	Gln	Leu	Cys	Lys	Asp	Leu	Ser	Glu	Leu
				485					490					495	
Val	Ser	Ile	Cys	Lys	Ser	Val	Gln	Phe	Lys	Glu	Phe	Gln	Val	Ser	Phe
			500					505						510	

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Gln Val Gln Lys Tyr Trp Glu Val Cys Ser Phe Asn Glu Val Leu Ala
 515 520 525
 Ser Lys Tyr Ala Asn Glu Asn Pro Gly Asp Phe Val Asn Tyr Asn Lys
 530 535 540
 Arg Phe Leu Ala Arg Val Phe Pro Ser Pro Met Arg Ile Asp Ser Ser
 545 550 555 560
 Asn Met Asn Pro Gln Asp Phe Trp Lys Cys Gly Cys Gln Ile Val Ala
 565 570 575
 Met Asn Phe Gln Thr Pro Gly Leu Met Met Asp Leu Asn Ile Gly Trp
 580 585 590
 Phe Arg Gln Asn Gly Asn Trp Ala Leu Val Leu Arg Pro Ala Ile Met
 595 600 605
 Arg Glu Glu Val Ser Phe Phe Ser Ala Asn Thr Lys Asp Ser Val Pro
 610 615 620
 Gly Val Ser Pro Gln Leu Leu His Ile Lys Ile Ile Ser Gly Gln Asn
 625 630 635 640
 Phe Pro Lys Pro Lys Gly Ser Gly Ala Lys Gly Asp Val Val Asp Pro
 645 650 655
 Tyr Val Tyr Val Glu Ile His Gly Ile Pro Ala Asp Cys Ala Glu Gln
 660 665 670
 Arg Thr Lys Thr Val Asn Gln Asn Gly Asp Ala Pro Met Phe Asp Glu
 675 680 685
 Ser Phe Glu Phe Gln Ile Asn Leu Pro Glu Leu Ala Met Val Arg Phe
 690 695 700
 Val Val Leu Asp Asp Asp Tyr Ile Gly Asp Glu Phe Ile Gly Gln Tyr
 705 710 715 720
 Thr Ile Pro Phe Glu Cys Leu Gln Thr Gly Tyr Arg His Val Pro Leu
 725 730 735
 Gln Ser Leu Thr Gly Glu Val Leu Ala His Ala Ser Leu Phe Val His
 740 745 750
 Val Ala Ile Thr Asn Arg Arg Gly Gly Gly Lys Pro His Lys Arg Gly
 755 760 765
 Leu Ser Val Arg Lys Gly Lys Lys Ser Arg Glu Tyr Ala Ser Leu Arg
 770 775 780
 Thr Leu Trp Ile Lys Thr Val Asp Glu Val Phe Lys Asn Ala Gln Pro
 785 790 795 800
 Pro Ile Arg Asp Ala Thr Asp Leu Arg Glu Asn Met Gln Asn Ala Val
 805 810 815
 Val Ser Phe Lys Glu Leu Cys Gly Leu Ser Ser Val Ala Asn Leu Met
 820 825 830
 Gln Cys Met Leu Ala Val Ser Pro Arg Phe Leu Gly Pro Asp Asn Thr
 835 840 845
 Pro Leu Val Val Leu Asn Leu Ser Glu Pro Tyr Pro Thr Met Glu Leu
 850 855 860
 Gln Ala Ile Val Pro Glu Val Leu Lys Lys Ile Val Thr Thr Tyr Asp
 865 870 875 880
 Met Met Ile Gln Ser Leu Lys Ala Arg Leu Lys Met Gln Met Leu Cys
 885 890 895
 Met Lys Arg Leu Cys Thr Val Arg Arg Gln Pro Trp Asn Phe Met Asn
 900 905 910
 Thr Cys Thr Ala
 915

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<210> SEQ ID NO 10
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
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 <220> FEATURE:
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<400> SEQUENCE: 22

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40

What is claimed is:

1. A method for the diagnosis of a neurological condition in an animal, comprising
 - (a) obtaining a biological sample from the animal; and
 - (b) detecting an increased level of B-PLC comprising the polypeptide of SEQ ID NO:7 in the sample compared to the level in a healthy animal, wherein said increased level is diagnostic of a neurological condition in the animal.
2. The method of claim 1, wherein the biological sample is blood.
3. The method of claim 1, wherein the increased level of B-PLC is detected using an immunoassay.
4. The method of claim 1, wherein the neurological condition is hypoxic-ischemic brain insult or a neuroinflammatory disease.

5. The method of claim 4, wherein the neurological condition is hypoxic-ischemic brain insult which is a stroke.

6. A method for the diagnosis of a neurological condition in an animal, comprising
 - (a) obtaining a biological sample from the animal; and
 - (b) detecting an increased level of B-PLC in the sample compared to the level in a healthy animal by using an antibody that specifically binds the polypeptide of SEQ ID NO:7, wherein said increased level is diagnostic of a neurological condition in the animal.

* * * * *

