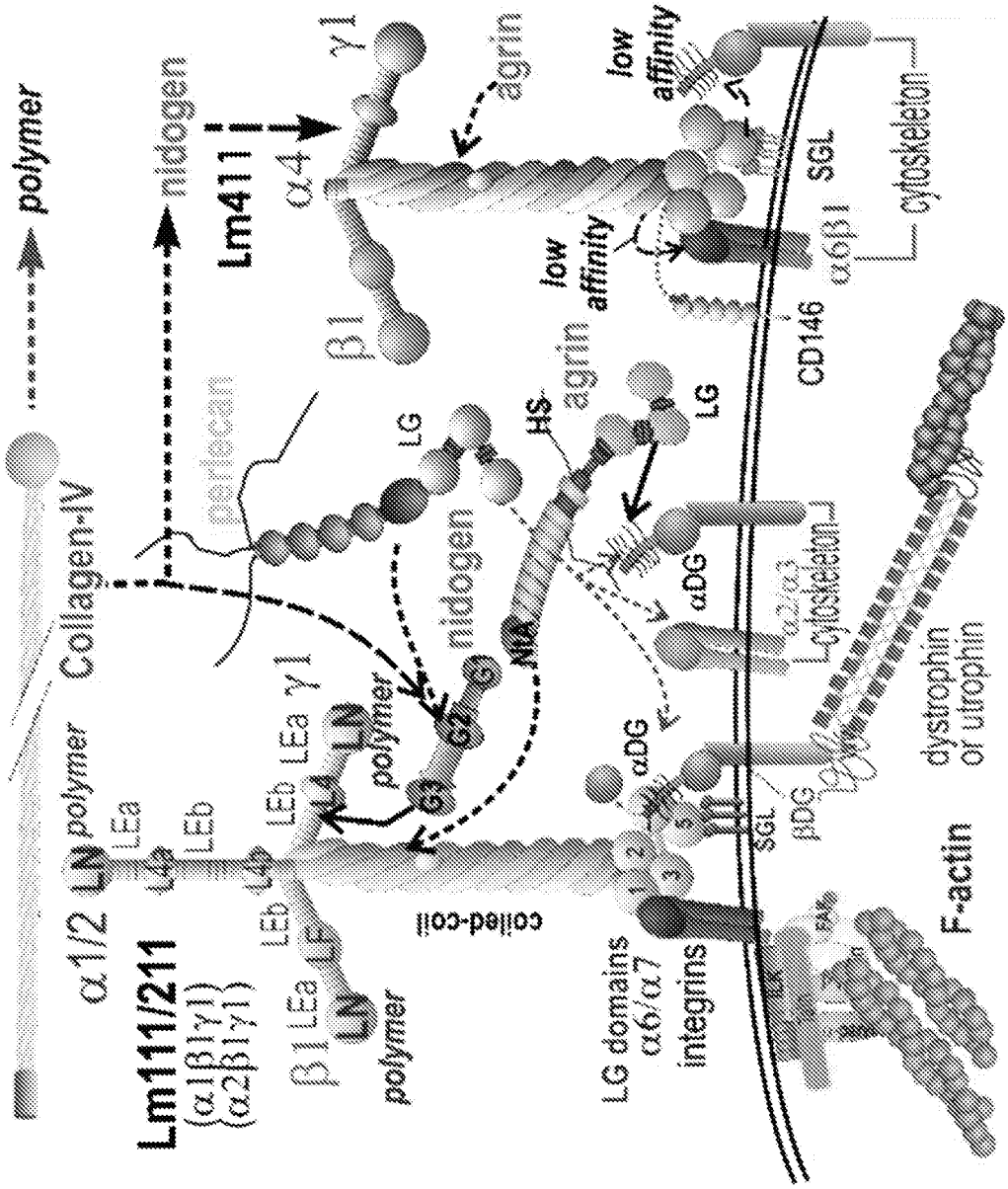

polymer
Collagen-IV
α1/2
LN
polymer
LEa
L4a
LEb
L4b
LEb
LEa
LF
β1 LEa
LN
polymer
Lm111/211
{α1β1γ1}
{α2β1γ1}
nidogen
perlecan
LEb
LEa γ1
LN
polymer
G3
G2
G1
LG
nidogen
coiled-coil
Lm411
α4
γ1
β1
agrin
low affinity
HS
agrin
low affinity
NtA
αDG
LG
CD146
α6β1
SGL
cytoskeleton
αDG
α2/α3
Cytoskeleton
SGL
βDG
dystrophin
or utrophin
LG domains
α6/α7
integrins
F-actin

FIG. 1

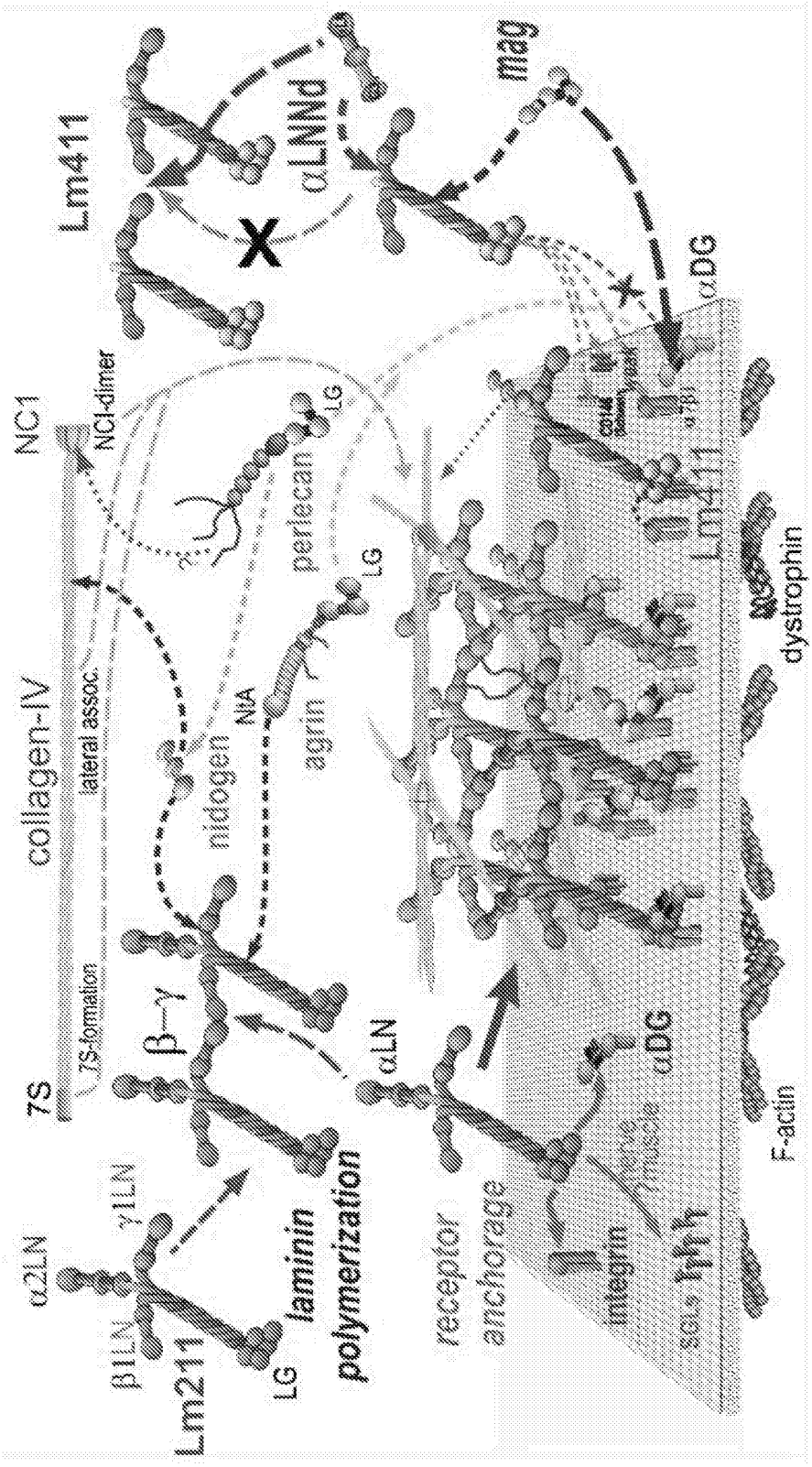

Lm411
αLNNd
mag
NC1
NC1-dimer
collagen-IV
lateral assoc.
7S
7S-formation
β–γ
nidogen
NA
perlecan
LG
agrin
LG
αLN
α2LN
γ1LN
β1LN
Lm211
LG
laminin
polymerization
receptor
anchorage
integrin
αDG
sarcolemma
F-actin
dystrophin
Lm411
αDG

FIG.2

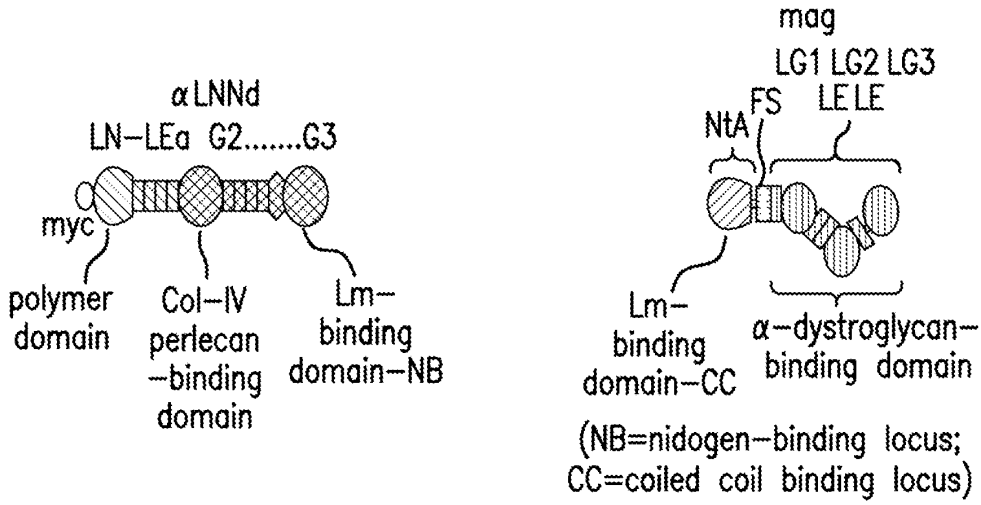

αLNNd
LN–LEa G2.....G3
myc
polymer domain
Col–IV perlecan –binding domain
Lm–binding domain–NB
mag
LG1 LG2 LG3
NtA
FS
LE LE
Lm–binding domain–CC
α–dystroglycan–binding domain
(NB=nidogen–binding locus; CC=coiled coil binding locus)

FIG.3A

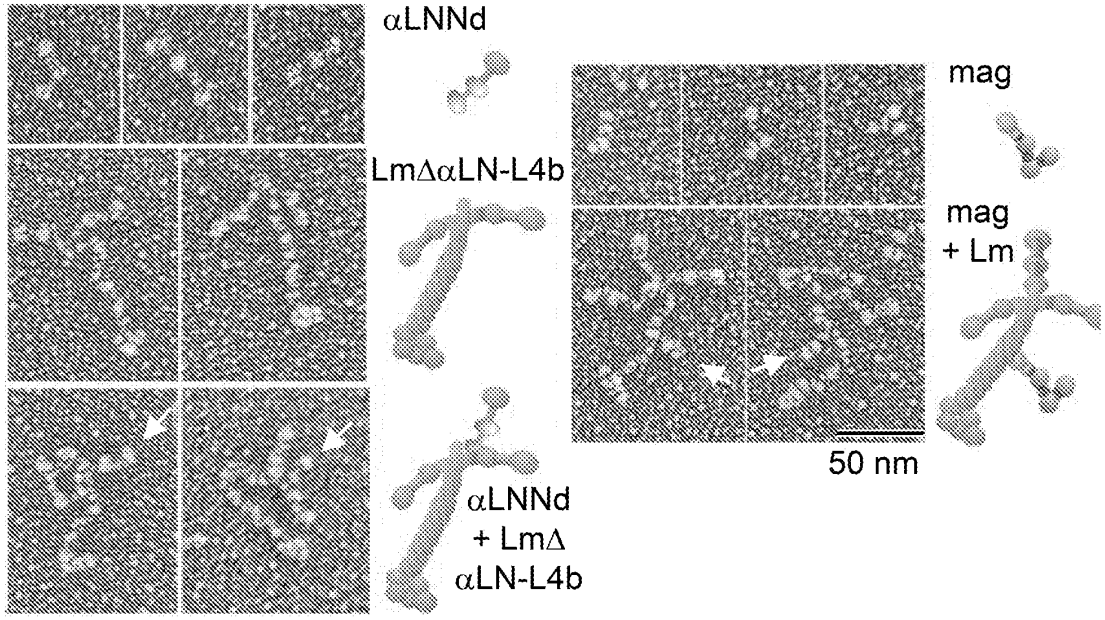

αLNNd
LmΔαLN-L4b
αLNNd + LmΔ αLN-L4b
mag
mag + Lm
50 nm

FIG.3B

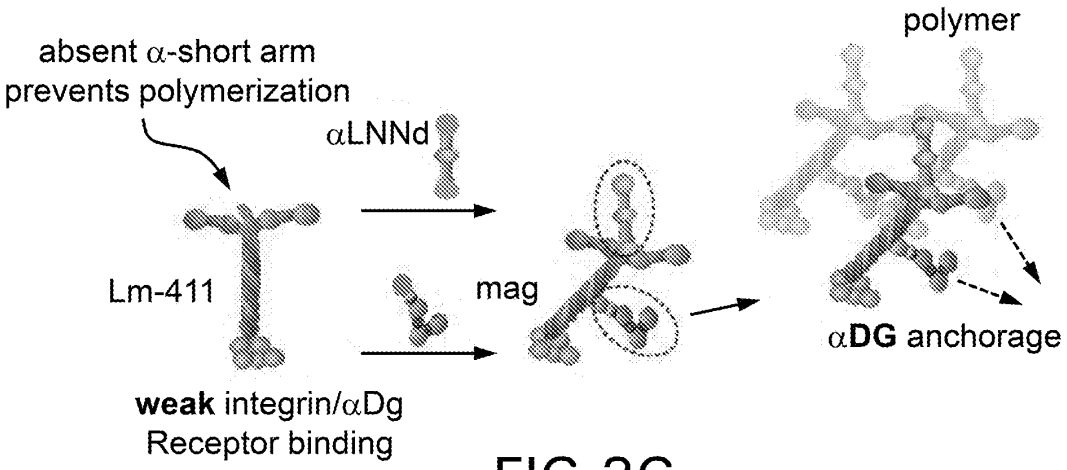

absent α-short arm
prevents polymerization
αLNNd
Lm-411
mag
polymer
αDG anchorage
weak integrin/αDg
Receptor binding

FIG.3C

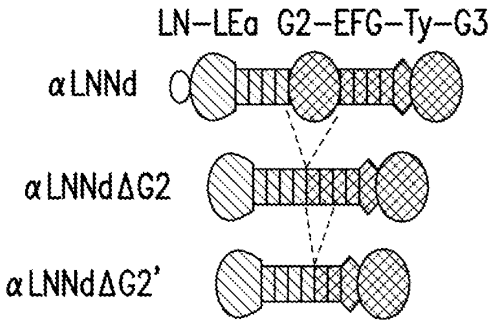

LN-LEa G2-EFG-Ty-G3
αLNNd
αLNNdΔG2
αLNNdΔG2'

FIG.3D

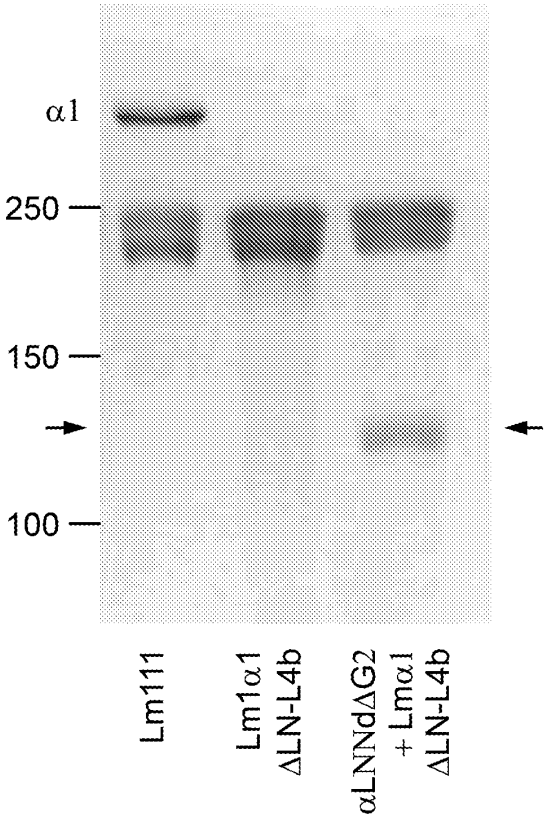


FIG.3E

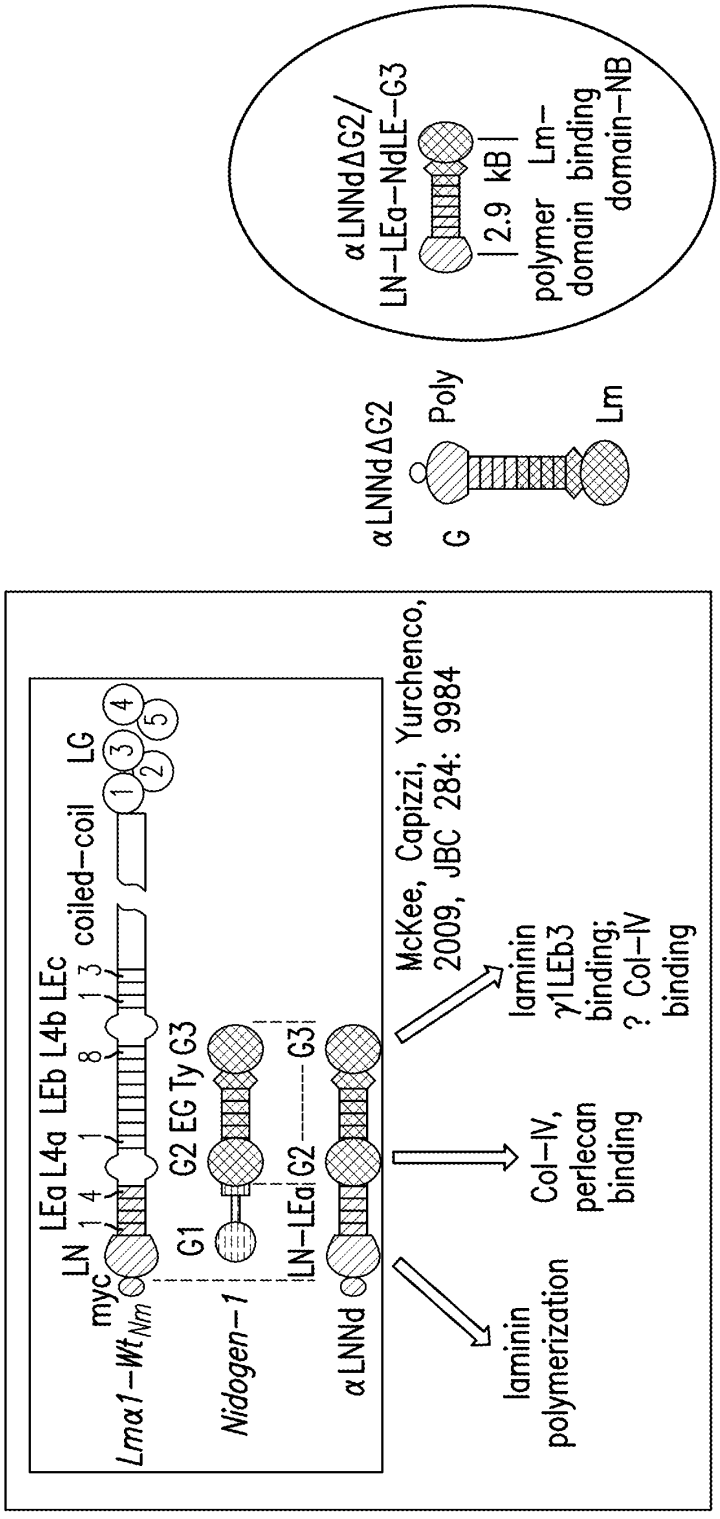

αLNNdΔG2/
LN–LEa–NdLE–G3
2.9 kB
polymer Lm–
domain binding
domain–NB
αLNNdΔG2
Poly
G
Lm
Lmα1–Wt$_{Nm}$
myc
LN
LEa L4a LEb L4b LEc
coiled–coil
LG
Nidogen–1
G1
G2 EG Ty G3
LN–LEa
G2
G3
αLNNd
McKee, Capizzi, Yurchenco,
2009, JBC 284: 9984
laminin
γ1LEb3
binding;
? Col–IV
binding
Col–IV,
perlecan
binding
laminin
polymerization

FIG.4

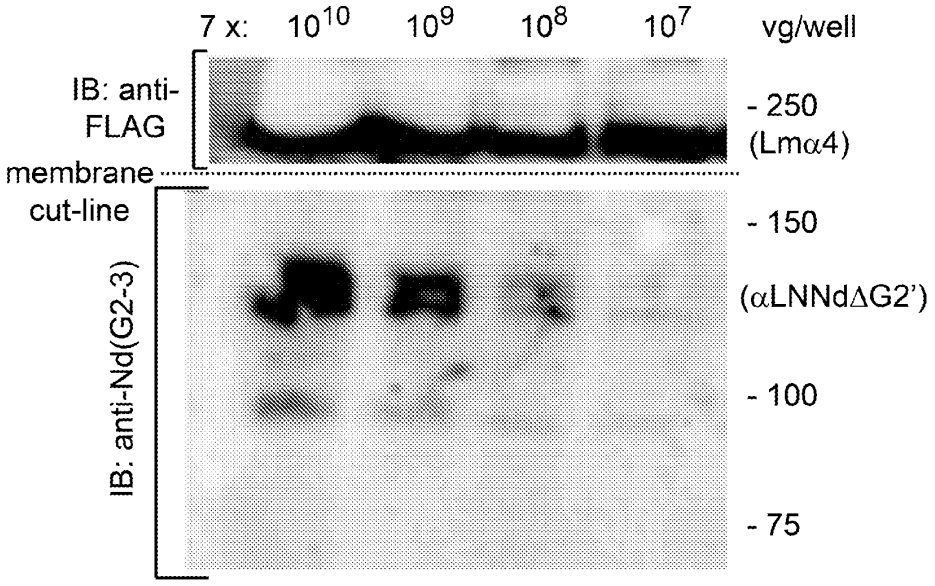

7 x: 10^{10} 10^{9} 10^{8} 10^{7} vg/well
IB: anti-FLAG
membrane cut-line
IB: anti-Nd(G2-3)
- 250
(Lmα4)
- 150
(αLNNdΔG2')
- 100
- 75

FIG.5A

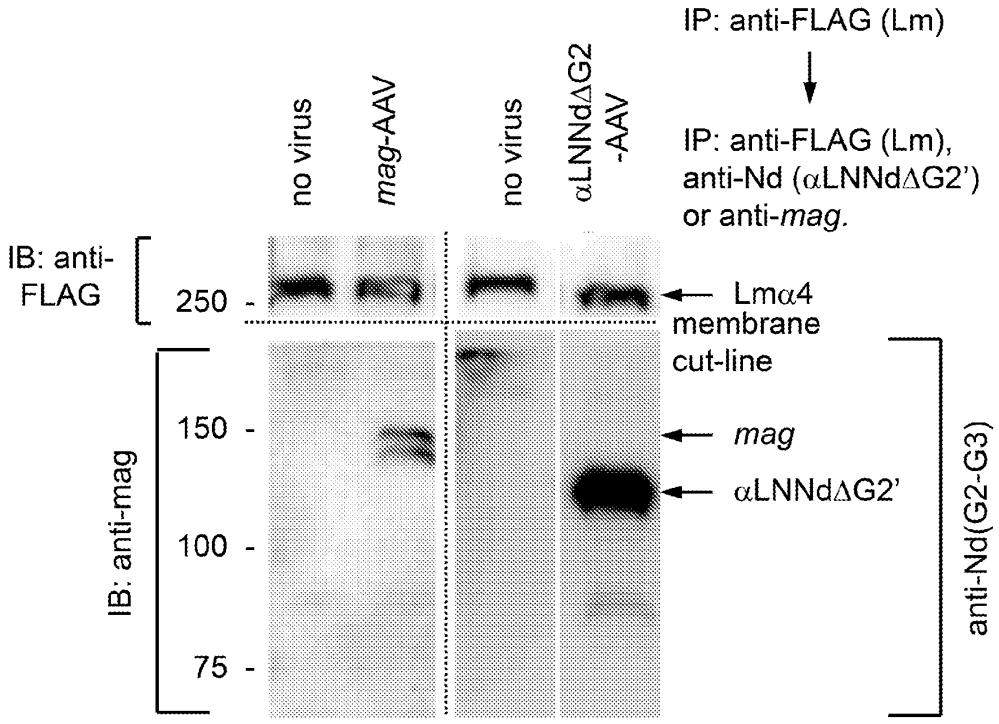

IP: anti-FLAG (Lm)
IP: anti-FLAG (Lm), anti-Nd (αLNNdΔG2') or anti-mag.
no virus
mag-AAV
no virus
αLNNdΔG2 -AAV
IB: anti-FLAG
250 -
Lmα4
membrane cut-line
IB: anti-mag
150 -
100 -
75 -
mag
αLNNdΔG2'
anti-Nd(G2-G3)

FIG.5B

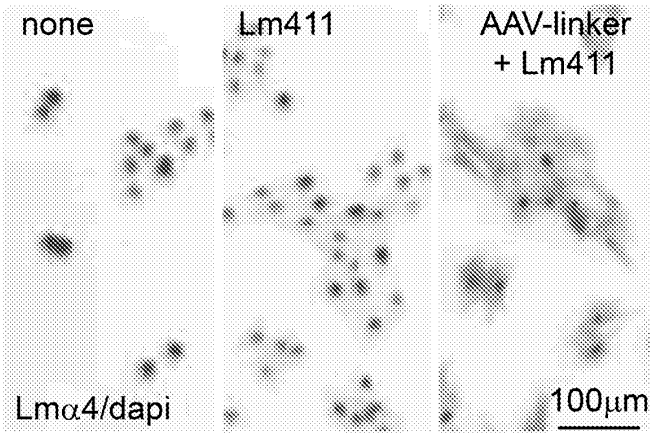

none
Lm411
AAV-linker
+ Lm411
Lmα4/dapi
100μm

FIG.5C

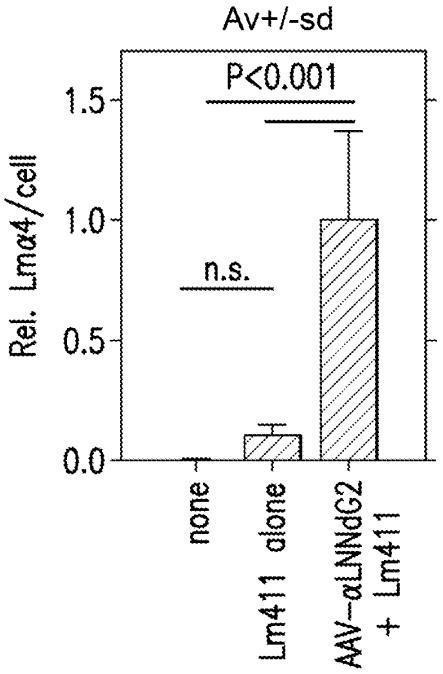

Av+/-sd
P<0.001
n.s.
Rel. Lmα4/cell
1.5
1.0
0.5
0.0
none
Lm411 alone
AAV-αLNNdG2
+ Lm411

FIG.5D

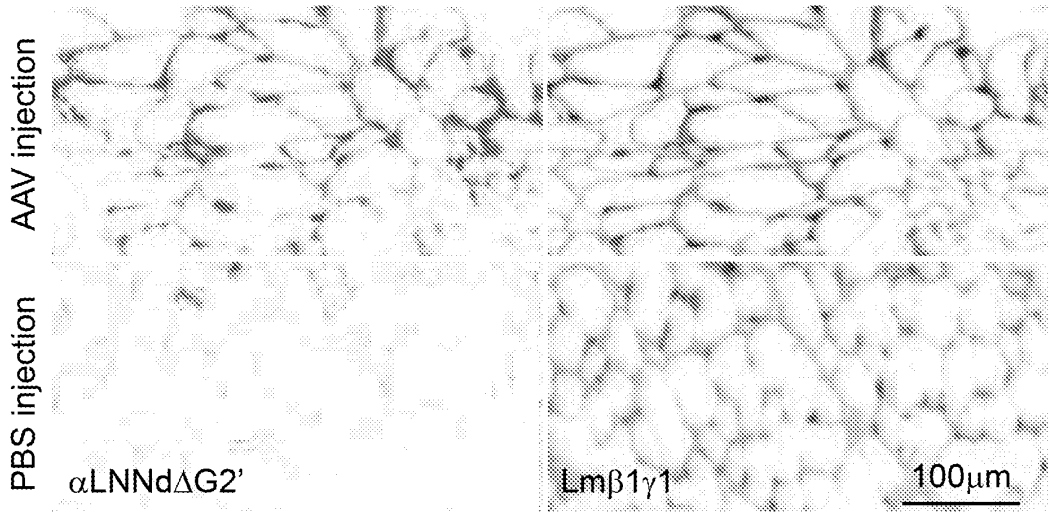


FIG.5E

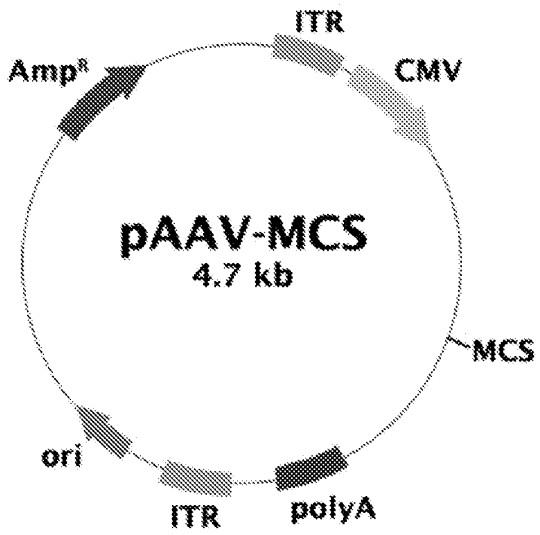


FIG.6

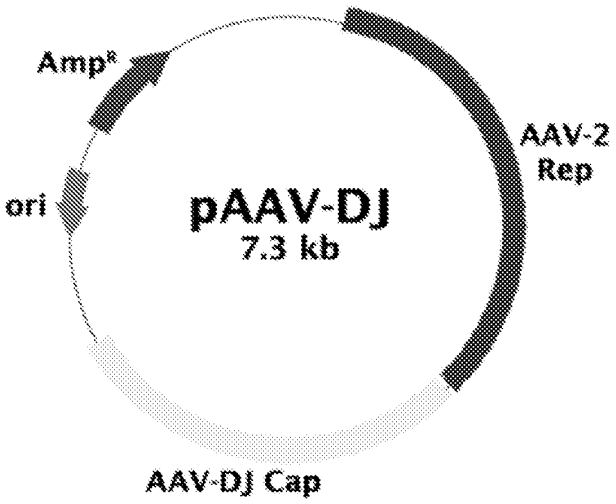


FIG.7

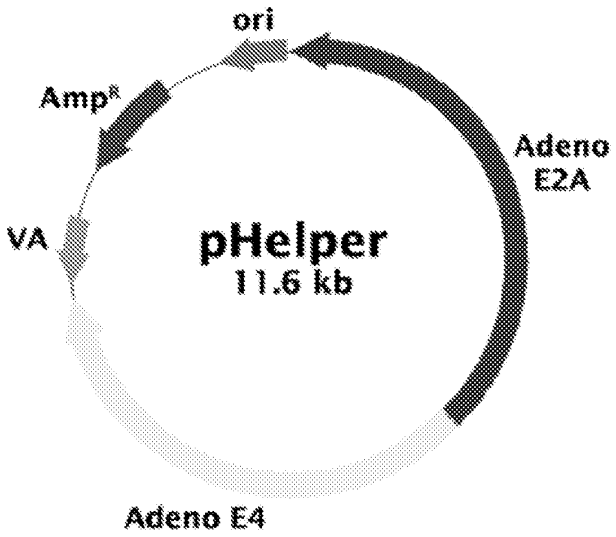


FIG.8

Score	Expect	Method	Identities	Positives	Gaps
1855 bits(4806)	0.0	Compositional matrix adjust.	875/1002(87%)	935/1002(93%)	0/1002(0%)

```
Query  1    MRAWIFFLLCLAGRALARQRGLFPAILNLASNAHISTNATCGEKGPEMFCKLVEHVPGRP  60
            MRAWIFFLLCLAGRALA+QRGLFPAILNLA+NAHIS NATCGEKGPEMFCKLVEHVPGRP
Sbjct  1    MRAWIFFLLCLAGRALAQQRGLFPAILNLATNAHISANATCGEKGPEMFCKLVEHVPGRP  60

Query  61   VRNPQCRICDGNSANPRERHPISHAIDGTNNWWQSPSIQNGREYHWVTITLDLRQVFQVA  120
            VR+ QCR+CDGNS NPRERHPISHAIDGTNNWWQSPSIQNGREYHWVT+TLDLRQVFQVA
Sbjct  61   VRHAQCRVCDGNSTNPRERHPISHAIDGTNNWWQSPSIQNGREYHWVTVTLDLRQVFQVA  120

Query  121  YVIIKAANAPRPGNWILERSLDGTTFSPWQYYAVSDSECLSRYNITPRRGPPTYRADDEV  180
            Y+IIKAANAPRPGNWILERS+DG  F PWQYYAVSD+ECL+RY ITPRRGPPTYRAD+EV
Sbjct  121  YIIIKAANAPRPGNWILERSVDGVKFKPWQYYAVSDTECLTRYKITPRRGPPTYRADNEV  180

Query  181  ICTSYYSRLVPLEHGEIHTSLINGRPSADDLSPKLLEFTSARYIRLRLQRIRTLNADLMT  240
            ICTSYYS+LVPLEHGEIHTSLINGRPSADD SP+LLEFTSARYIRLRLQRIRTLNADLMT
Sbjct  181  ICTSYYSKLVPLEHGEIHTSLINGRPSADDPSPQLLEFTSARYIRLRLQRIRTLNADLMT  240

Query  241  LSHREPKELDPIVTRRYYYSIKDISVGGMCICYGHASSCPWDETTKKLQCQCEHNTCGES  300
            LSHR+ ++LDPIVTRRYYYSIKDISVGGMCICYGHASSCPWDE  K+LQCQCEHNTCGES
Sbjct  241  LSHRDLRDLDPIVTRRYYYSIKDISVGGMCICYGHASSCPWDEEAKQLQCQCEHNTCGES  300

Query  301  CNRCCPGYHQQPWRPGTVSSGNTCEACNCHNKAKDCYYDESVAKQKKSLNTAGQFRGGGV  360
            C+RCCPGYHQQPWRPGT+SSGN CE CNCHNKAKDCYYD SVAK+++SLNTAGQ+ GGGV
Sbjct  301  CDRCCPGYHQQPWRPGTISSGNECEECNCHNKAKDCYYDSSVAKERRSLNTAGQYSGGGV  360

Query  361  CINCLQNTMGINCETCIDGYYRPHKVSPYEDEPCRPCNCDPVGSLSSVCIKDDLHSDLHN  420
            C+NC QNT GINCETCID YYRPHKVSPY+D PCRPCNCDPVGSLSSVCIKDD H+DL N
Sbjct  361  CVNCSQNTTGINCETCIDQYYRPHKVSPYDDHPCRPCNCDPVGSLSSVCIKDDRHADLAN  420

Query  421  GKQPGQCPCKEGYTGEKCDRCQLGYKDYPTCVSCGCNPVGSASDEPCTGPCVCKENVEGK  480
            GK PGQCPC++GY G+KCDRCQ GY+ +P C+ C C  VGS +++PC  PC+CK+NVEGK
Sbjct  421  GKWPGQCPCRKGYAGDKCDRCQFGYRGFPNCIPCDCRTVGSLNEDPCIEPCLCKKNVEGK  480

Query  481  ACDRCKPGFYNLKEKNPRGCSECFCFGVSDVCPINYCETGLHNCDIPQRAQCIYTGGSSY  540
```

FIG.9

```
                CDRCKPGFYNLKE+NP GCSECFCFGVS VCPINYCETGLHNCDIPQRAQCIY GGSSY
Sbjct  481      NCDRCKPGFYNLKERNPEGCSECFCFGVSGVCPINYCETGLHNCDIPQRAQCIYMGGSSY  540

Query  541      TCSCLPGFSGDGQACQDVDECQPSRCHPDAFCYNTPGSFTCQCKPGYQGDGFRCVPGEVE  600
                TCSCLPGFSGDG+AC+DVDECQ SRCHPDAFCYNTPGSFTCQCKPGYQGDGFRC+PGEV
Sbjct  541      TCSCLPGFSGDGRACRDVDECQHSRCHPDAFCYNTPGSFTCQCKPGYQGDGFRCMPGEVS  600

Query  601      KTRCQHEREHILGAAGATDPQRPIPPGLFVPECDAHGHYAPTQCHGSTGYCWCVDRDGRE  660
                KTRCQ EREHILGAAG  D QRP   G+FVP+CD +GHY PTQCH STGYCWCVDRDGRE
Sbjct  601      KTRCQLEREHILGAAGGADAQRPTLQGMFVPQCDEYGHYVPTQCHHSTGYCWCVDRDGRE  660

Query  661      VEGTRTRPGMTPPCLSTVAPPIHQGPAVPTAVIPLPPGTHLLFAQTGKIERLPLEGNTMR  720
                +EG+RT PGM PPCLSTVAPPIHQGP VPTAVIPLPPGTHLLFAQTGKIERLPLE NTM+
Sbjct  661      LEGSRTPPGMRPPCLSTVAPPIHQGPVVPTAVIPLPPGTHLLFAQTGKIERLPLERNTMK  720

Query  721      KTEAKAFLHVPAKVIIGLAFDCVDKMVYWTDITEPSIGRASLHGGEPTTIIRQDLGSPEG  780
                KTE KAFLH+PAKVIIGLAFDCVDK+VYWTDI+EPSIGRASLHGGEPTTIIRQDLGSPEG
Sbjct  721      KTERKAFLHIPAKVIIGLAFDCVDKVVYWTDISEPSIGRASLHGGEPTTIIRQDLGSPEG  780

Query  781      IAVDHLGRNIFWTDSNLDRIEVAKLDGTQRRVLFETDLVNPRGIVTDSVRGNLYWTDWNR  840
                IA+DHLGR IFWTDS LDRIEVAK+DGTQRRVLF+T LVNPRGIVTD VRGNLYWTDWNR
Sbjct  781      IALDHLGRTIFWTDSQLDRIEVAKMDGTQRRVLFDTGLVNPRGIVTDPVRGNLYWTDWNR  840

Query  841      DNPKIETSYMDGTNRRILVQDDLGLPNGLTFDAFSSQLCWVDAGTNRAECLNPSQPSRRK  900
                DNPKIETS+MDGTNRRIL QD+LGLPNGLTFDAFSSQLCWVDAGT+RAECLNP+QP RRK
Sbjct  841      DNPKIETSHMDGTNRRILAQDNLGLPNGLTFDAFSSQLCWVDAGTHRAECLNPAQPGRRK  900

Query  901      ALEGLQYPFAVTSYGKNLYFTDWKMNSVVALDLAISKETDAFQPHKQTRLYGITTALSQC  960
                 LEGLQYPFAVTSYGKNLY+TDWK NSV+A+DLAISKE D F PHKQTRLYGIT ALSQC
Sbjct  901      VLEGLQYPFAVTSYGKNLYYTDWKTNSVIAMDLAISKEMDTFHPHKQTRLYGITIALSQC  960

Query  961      PQGHNYCSVNNGGCTHLCLATPGSRTCRCPDNTLGVDCIEQK                    1002
                PQGHNYCSVNNGGCTHLCL TPGSRTCRCPDNTLGVDCIE+K
Sbjct  961      PQGHNYCSVNNGGCTHLCLPTPGSRTCRCPDNTLGVDCIERK                    1002
```

FIG.9 continued

```
1     ATGAGGGCCT GGATCTTCTT TCTCCTTTGC CTGGCCGGGA GGGCTCTGGC ACGGCAGAGA GGCCTGTTTC CTGCCATTCT CAATCTTGCC AGCAATGCTC ACATCAGCAC
        M  R  A  W  I  F  F  L  L  C  L  A  G  G  R  A  L  A  R  Q  R  G  L  F  F  P  A  I  L  N  L  A  S  N  A  H  I  S  T
111   CAATGCCACC TGTGGCGAGA AGGGGCCGGA GATGTTCTGC AAACTTGTGG AGCATGTGCC AGGTCGGCCC GTCCGAAACC CACAGTGCCG GATCTGTGAT GGCAACAGCG
        N  A  T  C  G  E  K  G  P  E  M  F  C  K  L  V  E  H  V  P  G  R  P  V  R  N  P  Q  C  R  I  C  D  G  N  S  A
221   CAAACCCCAG AGAACGCCAT CCAATATCAC ATGCCATAGA TGGCACCAAT AACTGGTGGC AAAGTCCCAG CATTCAGAAT GGGAGAGAAT ATCACTGGGT CACAATCACT
        N  P  R  E  R  H  P  I  S  H  A  I  D  G  T  N  N  W  W  Q  S  P  S  I  Q  N  G  R  E  Y  H  W  V  T  I  T
331   CTGGACTTAA GACAGGTCTT TCAAGTTGCA TATGTCATCA TTAAAGCTGC CAATGCCCCT CGACCTGGAA ACTGGATTTT GGAGCGTTCT CTGGATGGCA CCACGTTCAG
        L  D  L  R  Q  V  F  Q  V  A  Y  V  I  I  K  A  A  N  A  P  R  P  G  N  W  I  L  E  R  S  L  D  G  T  T  F  S
441   CCCCTGGCAG TATTATGCAG TCAGCGACTC AGAGTGTTTG TCTCGTTACA ATATAACTCC AAGACGAGGG CCACCCACCT ACAGGCCTGA TGATGAAGTG ATCTGCACCT
        P  W  Q  Y  Y  A  V  S  D  S  E  C  L  S  R  Y  N  I  T  P  R  R  G  P  P  T  Y  R  A  D  D  E  V  I  C  T  S
551   CCTATTATTC CAGATTGGTG CCACTTGAGC ATGGAGAGAT TCATACATCA CTCATCAATG GCAGACCAAG CGCTGACGAT CTTTCACCCA AGTTGTTGGA ATTCACTTCT
        Y  Y  S  R  L  V  P  L  E  H  G  E  I  H  T  S  L  I  N  G  R  P  S  A  D  D  L  S  P  K  L  L  E  F  T  S
661   GCACGATATA TTCGCCTTCG CTTGCAACGC ATTAGAACGC TCAATGCAGA TCTCATGACC CTTAGCCACC GGGAACCTAA AGAACTGGAT CCTATTGTTA CCAGACGCTA
        A  R  Y  I  R  L  R  L  Q  R  I  R  T  L  N  A  D  L  M  T  L  S  H  R  E  P  K  E  L  D  P  I  V  T  R  R  Y
771   TTATTATTCA ATAAAGGACA TTTCTGTTGG AGGCATGTGT ATCTGCTATG GCCATGCTAG TAGCTGCCCA TGGGATGAAA CTACAAAGAA ACTGCAGTGT CAATGTGAGC
        Y  Y  S  I  K  D  I  S  V  G  G  M  C  I  C  Y  G  H  A  S  S  C  P  W  D  E  T  T  K  K  L  Q  C  Q  C  E  H
881   ATAATACTTG CGGGGAGAGC TGTAACAGGT GCTGTCCTGG GTACCATCAG CAGCCCTGGA GGCCGGGAAC CGTGTCCTCC GGCAATACAT GTGAACCATG TAATTGTCAC
        N  T  C  G  E  S  C  N  R  C  C  P  G  Y  H  Q  Q  P  W  R  P  G  T  V  S  S  G  N  T  C  E  A  C  N  C  H
991   AATAAAGCCA AAGACTGTTA CTATGATGAA AGTGTTGCAA AGCAGAAGAA AAGTTTGAAT ACTGCTGGAC AGTTCAGAGG AGGAGGGGTT TGCATAAATT GCTTGCAGAA
        N  K  A  K  D  C  Y  Y  D  E  S  V  A  K  Q  K  K  S  L  N  T  A  G  Q  F  R  G  G  G  V  C  I  N  C  L  Q  N
1101  CACCATGGGA ATCAACTGTG AAACCTGTAT TGATGGATAT TATAGACCAC ACAAAGTGTC TCCTTATGAG GATGAGCCTT GCCGCCCCTG TAATTGTGAC CCTGTGGGGT
        T  M  G  I  N  C  E  T  C  I  D  G  Y  Y  R  P  H  K  V  S  P  Y  E  D  E  P  C  R  P  C  N  C  D  P  V  G  S
1211  CCCTCAGTTC TGTCTGTATT AAGGATGACC TCCATTCTGA CTTACACAAT GGGAAGCAGC CAGGTCAGTG CCCATGTAAG GAAGGTTATA CAGGAGAAAA ATGTGATCGC
        L  S  S  V  C  I  K  D  D  L  H  S  D  L  H  N  G  K  Q  P  G  Q  C  P  C  K  E  G  Y  T  G  E  K  C  D  R
1321  TGCCAACTTG GCTATAAGGA TTACCCGACC TGTGTCTCCT GTGGGTGCAA CCCAGTGGGC AGTGCCAGTG ATGAGCCCTG CACAGGCCCC TGTGTTTGTA AGGAAAACGT
        C  Q  L  G  Y  K  D  Y  P  T  C  V  S  C  G  C  N  P  V  G  S  A  S  D  E  P  C  T  G  P  C  V  C  K  E  N  V
1431  TGAGGGGAAG GCCTGTGATC GCTGCAAGCC AGGATTCTAT AACTTGAAGG AAAAAAACCC CCGGGGCTGC TCCGAGTGCT TCTGCTTTGG CGTTTCTGAT GTCTGCCCCA
        E  G  K  A  C  D  R  C  K  P  G  F  Y  N  L  K  E  K  N  P  R  G  C  S  E  C  F  C  F  G  V  S  D  V  C  P  I
```

FIG.10

```
1541  TCAACTACTG TGAAACTGGC CTTCATAACT GCGACATACC CCAGCGGGCC CAGTGTATCT ACACAGGAGG CTCCTCCTAC ACCTGTTCCT GCTTGCCAGG CTTTTCTGGG
        N  Y  C  E  T  G  L  H  N  C  D  I  P  Q  R  A  Q  C  I  Y  T  G  G  S  S  Y  T  C  S  C  L  P  G  F  S  G
1651  GATGGCCAAG CCTGCCAAGA TGTAGATGAA TGCCAGCCAA GCCGATGTCA CCCTGACGCC TTCTGCTACA ACACTCCAGG CTCTTTCACG TGCCAGTGCA AACCTGGTTA
        D  G  Q  A  C  Q  D  V  D  E  C  Q  P  S  R  C  H  P  D  A  F  C  Y  N  T  P  G  S  F  T  C  Q  C  K  P  G  Y
1761  TCAGGGAGAC GGCTTCCGTT GCGTGCCCGG AGAGGTGGAG AAAACCCGGT GCCAGCACGA GCGAGAACAC ATTCTCGGGG CAGCGGGGGC GACAGACCCA CAGCGACCCA
        Q  G  D  G  F  R  C  V  P  G  E  V  E  K  T  R  C  Q  H  E  R  E  H  I  L  G  A  A  G  A  T  D  P  Q  R  P  I
1871  TTCCTCCGGG GCTGTTCGTT CCTGAGTGCG ATGCGCACGG GCACTACCCG CCCACCCAGT GCCACGGCAG CACCGGCTAC TGCTGGTGCG TGGATCGCGA CGGCGGCGAG
        P  P  G  L  F  V  P  E  C  D  A  H  G  H  Y  A  P  T  Q  C  H  G  S  T  G  Y  C  W  C  V  D  R  D  G  R  E
1981  GTGGAGGGCA CCAGGACCAG GCCCGGGATG ACGCCCCCGT GTCTGAGTAC AGTGGCTCCC CCGATTCACC AAGGACCTGC GGTGCCTACC GCCGTGATCC CCTTGCCTCC
        V  E  G  T  R  T  R  P  G  M  T  P  P  C  L  S  T  V  A  P  P  I  H  Q  G  P  A  V  P  T  A  V  I  P  L  P  P
2091  TGGCACCCAT TTACTCTTTG CCCAGACTGG GAAGATTGAG CGCCTGCCCC TGGAGGGAAA TACCATGAGG AAGACAGAAG CAAAGCGCTT CCTTCATGTC CCGGCTAAAG
        G  T  H  L  L  F  A  Q  T  G  K  I  E  R  L  P  L  E  G  N  T  M  R  K  T  E  A  K  A  F  L  H  V  P  A  K  V
2201  TCATCATTGG ACTGGCCTTT GACTGCGTGG ACAAGATGGT TTACTGGACG GACATCACTG AGCCTTCCAT TGGGAGAGCT AGTCTACATG GTGGAGAGCC AACCACCATC
        I  I  G  L  A  F  D  C  V  D  K  M  V  Y  W  T  D  I  T  E  P  S  I  G  R  A  S  L  H  G  G  E  P  T  T  I
2311  ATTAGACAAG ATCTTGGAAG TCCAGAAGGT ATCGCTGTTG ATCACCTTGG CCGCAACATC TTCTGGACAG ACTCTAACCT GGATCGAATA GAAGTGGCGA AGCTGGACGG
        I  R  Q  D  L  G  S  P  E  G  I  A  V  D  H  L  G  R  N  I  F  W  T  D  S  N  L  D  R  I  E  V  A  K  L  D  G
2421  CACGCAGCGC CGGGTGCTCT TTGAGACTGA CTTGGTGAAT CCCAGAGGCA TTGTAACGGA TTCCGTGAGA GGGAACCTTT ACTGGACAGA CTGGAACAGA GATAACCCCA
        T  Q  R  R  V  L  F  E  T  D  L  V  N  P  R  G  I  V  T  D  S  V  R  G  N  L  Y  W  T  D  W  N  R  D  N  P  K
2531  AGATTGAAAC TTCCTACATG GACGGCACGA ACCGCAGGAT CCTTGTGCAG GATGACCTGG GCTTGCCCAA TGCACTGACC TTCGATGCGT TCTCATCTCA GCTCTGCTGG
        I  E  T  S  Y  M  D  G  T  N  R  R  I  L  V  Q  D  D  L  G  L  P  N  G  L  T  F  D  A  F  S  S  Q  L  C  W
2641  GTGGATGCAG GCACCAATCG GGCGCAATGC CTGAACCCCA GTCAGCCCAG CAGACGCAAG GCTCTCGAAG GGCTCCAGTA TCCTTTTGCT GTGACGAGCT ACGGGAAGAA
        V  D  A  G  T  N  R  A  E  C  L  N  P  S  Q  P  S  R  R  K  A  L  E  G  L  Q  Y  P  F  A  V  T  S  Y  G  K  N
2751  TCTGTATTTC ACAGACTGGA AGATGAATTC CGTGGTTGCT CTCGATCTTG CAATTTCCAA GGAGACGGAT GCTTTCCAAC CCCACAAGCA GACCCGGCTG TATGGCATCA
        L  Y  F  T  D  W  K  M  N  S  V  V  A  L  D  L  A  I  S  K  E  T  D  A  F  Q  P  H  K  Q  T  R  L  Y  G  I  T
2861  CCACGGCCCT GTCTCAGTGT CCGCAAGGCC ATAACTACTG CTCAGTGAAC AATGGCGGCT GCACCCACCT ATGCTTGGCC ACCCCAGGGA GCAGGACCTG CCGTTGCCCT
        T  A  L  S  Q  C  P  Q  G  H  N  Y  C  S  V  N  N  G  G  C  T  H  L  C  L  A  T  P  G  S  R  T  C  R  C  P
2971  GACAACACCT TGGGAGTTGA CTGTATCGAA CAGAAATGA
        D  N  T  L  G  V  D  C  I  E  Q  K  .
```

FIG.10 continued

```
1     ATGAGGGCCT GGATCTTCTT TCTCCTTTGC CTGGCCCGGA GGGCTCTGGC ACGGCAGAGA GGCCTGTTTC CTGCCATTCT CAATCTTGCC AGCAATGCTC ACATCAGCAC
      M  R  A  W  I  F  F  L  L  C  L  A  G  G  R  A  L  A  R  Q  R  G  L  F  P  A  I  L  N  L  A  S  N  A  H  I  S  T
111   CAATGCCACC TGTGGCGAGA AGGGGCCGGA GATGTTCTGC AAACTTGTGG AGCATGTGCC AGGTCGGCCC GTCCGAAACC CACAGTGCCG GATCTGTGAT GGCAACAGCG
      N  A  T  C  G  E  K  G  P  E  M  F  C  K  L  V  E  H  V  P  G  R  P  V  R  N  P  Q  C  R  I  C  D  G  N  S  A
221   CAAACCCCAG AGAACGCCAT CCAATATCAC ATGCCATAGA TGGCACCAAT AACTGGTGGC AAAGTCCCAG CATTCAGAAT GGGAGAGAAT ATCACTGGGT CACAATCACT
      N  P  R  E  R  H  P  I  S  H  A  I  D  G  T  N  N  W  W  Q  S  P  S  I  Q  N  G  R  E  Y  H  W  V  T  I  T
331   CTGGACTTAA GACAGGTCTT TCAAGTTGCA TATGTCATCA TTAAAGCTGC CAATGCCCCT CGACCTGGAA ACTGGATTTT GGAGCGTTCT CTGGATGGCA CCACGTTCAG
      L  D  L  R  Q  V  F  Q  V  A  Y  Y  V  I  I  K  A  A  N  A  P  R  P  G  N  W  I  L  E  R  S  L  D  G  T  T  F  S
441   CCCCTGGCAG TATTATGCAG TCAGCGACTC AGAGTGTTTG TCTCGTTACA ATATAACTCC AAGACCAGGG CCACCCACCT ACAGGGCTGA TGATGAAGTG ATCTGCACCT
      P  W  Q  Y  Y  A  V  S  D  S  E  C  L  S  R  Y  N  I  T  P  R  R  G  P  P  T  Y  R  A  D  D  E  V  I  C  T  S
551   CCTATTATTC CAGATTGGTG CCACTTGAGC ATGGAGAGAT TCATACATCA CTCATCAATG GCAGACCAAG CGCTGACGAT CTTTCACCCA AGTTGTTGGA ATTCACTTCT
      Y  Y  S  R  L  V  P  L  E  H  G  E  I  H  T  S  L  I  N  G  R  P  S  A  D  D  L  S  P  K  L  L  E  F  T  S
661   GCACGATATA TTCGCCTTCG CTTGCAACGC ATTAGAACCG TCAATGCAGA TCTCATGACC CTTAGCCACC GGGAACCTAA AGAACTGGAT CCTATTGTTA CCAGACGCTA
      A  R  Y  I  R  L  R  L  Q  R  I  R  T  L  N  A  D  L  M  T  L  S  H  R  E  P  K  E  L  D  P  I  V  T  R  R  Y
771   TTATTATTCA ATAAAGGACA TTTCTGTTGG AGGCATGTGT ATCTGCTATG GCCATGCTAG TAGCTGCCCA TGGGATGAAA CTACAAAGAA ACTGCAGTGT CAATGTGAGC
      Y  Y  S  I  K  D  I  S  V  G  G  M  C  I  C  Y  G  H  A  S  S  C  P  W  D  E  T  T  K  K  L  Q  C  Q  C  E  H
881   ATAATACTTG CGGGGAGAGC TGTAACAGGT GCTGTCCTGG GTACCATCAG CAGCCCTGGA GGCCGGGAAC CGTGTCCTCC GGCAATACAT GTGAAGCATG TAATTGTCAC
      N  T  C  G  E  S  C  N  R  C  C  P  G  Y  H  Q  Q  P  W  R  P  G  T  V  S  S  G  N  T  C  E  A  C  N  C  H
991   AATAAAGCCA AAGACTGTTA CTATGATGAA AGTGTTGCAA AGCAGAAGAA AAGTTTGAAT ACTGCTGGAC AGTTCAGAGG AGGAGGGGTT TGCATAAATT GCTTGCAGAA
      N  K  A  K  D  C  Y  Y  D  E  S  V  A  K  Q  K  K  S  L  N  T  A  G  Q  F  R  G  G  G  V  C  I  N  C  L  Q  N
1101  CACCATGGGA ATCAACTGTG AAACCTGTAT TGATGGATAT TATAGACCAC ACAAAGTGTC TCCTTATGAG GATGAGCCTT GCCGCCCCTG TAATTGTGAC CCTGTGGGGT
      T  M  G  I  N  C  E  T  C  I  D  G  Y  Y  R  P  H  K  V  S  P  Y  E  D  E  P  C  R  P  C  N  C  D  P  V  G  S
1211  CCCTCAGTTC TGTCTGTATT AAGGATGACC TCCATTCTGA CTTACACAAT GGGAAGCAGC CAGGTCAGTG CCCATGTAAG GAAGGTTATA CAGGAGAAAA ATGTGATCGC
      L  S  S  V  C  I  K  D  D  L  H  S  D  L  H  N  G  K  Q  P  G  Q  C  P  C  K  E  G  Y  T  G  E  K  C  D  R
1321  TGCCAACTTG GCTATAAGGA TTACCCGACC TGTGTCTCCT GTGGGTGCAA CCCAGTGGGC AGTGCCAGTG ATGAGCCCTG CACAGGGCCC TGTGTTTGTA AGGAAAACGT
      C  Q  L  G  Y  Y  K  D  Y  Y  P  T  C  V  S  C  G  C  N  P  V  G  S  A  S  D  E  P  C  T  G  P  C  V  C  K  E  N  V
```

FIG.11

```
1431  TGAGGGGAAG GCCTGTGATC GCTGCAAGCC AGGATTCTAT AACTTGAAGG AAAAAAACCC CCGGGCCTGC TCCGAGTGCT TCTGCTTTGG CGTTTCTGAT GTCTGCCCCA
          E  G  K  A  C  D  R  C  K  P  G  F  Y  N  L  K  E  K  N  P  R  G  C  S  E  C  F  C  F  G  V  S  D  V  C  P  I
1541  TCAACTACTG TGAAACTGGC CTTCATAACT GCGACATACC CCAGCGGGCC CAGTGTATCT ACACAGGAGG CTCCTCCTAC ACCTGTTCCT GCTTGCCAGG CTTTTCTGGG
            N  Y  C  E  T  G  L  H  N  C  D  I  P  Q  R  A  Q  C  I  Y  T  G  G  S  S  Y  T  C  S  C  L  P  G  F  S  G
1651  GATGGCCAAG CCTGCCAAGA TGTAGATGAA TGCCAGCCAA GCCGATGTCA CCCTGACGCC TTCTGCTACA ACACTCCAGG CTCTTTCACG TGCCAGTGCA AACCTGGTTA
          D  G  Q  A  C  Q  D  V  D  E  C  Q  P  S  R  C  H  P  D  A  F  C  Y  N  T  P  G  S  F  T  C  Q  C  K  P  G  Y
1761  TCAGGGAGAC GGCTTCCGTT GCGTGCCCGG AGAGGTGGAG AAAACCCGGT GCCAGCACGA GCGAGAACAC ATTCTCGGGG CAGCGGGGGC GACAGACCCA CAGCGACCCA
            Q  G  D  G  F  R  C  V  P  G  E  V  E  K  T  R  C  Q  H  E  R  E  H  I  L  G  A  A  G  A  T  D  P  Q  R  P  I
1871  TTCCTCCGGG GCTGTTCGTT CCTGAGTGCG ATGCGCACGG GCACTACGCG CCCACCCAGT GCCACGGCAG CACCGGCTAC TGCTGGTGCG TGGATCGCGA CGGCCGCGAG
            P  P  G  L  F  V  P  E  C  D  A  H  G  H  Y  A  P  T  Q  C  H  G  S  T  G  Y  C  W  C  V  D  R  D  G  R  E
1981  GTGGAGGGCA CCAGGACCAG GCCCGGGATG ACGCCCCCGT GTCTGAGTAC AGTGGCTCCC CCGATTCACC AAGGACCTGC GGTGCCTACC GCCGTGATCC CCTTGCCTCC
          V  E  G  T  R  T  R  P  G  M  T  P  P  C  L  S  T  V  A  P  P  I  H  Q  G  P  A  V  P  T  A  V  I  P  L  P  P
2091  TGGGACCCAT TTACTCTTTG CCCAGACTGG GAAGATTGAG CGCCTGCCCC TGGAGGGAAA TACCATGAGG AAGACAGAAG CAAGGCGTT CCTTCATGTC CCGGCTAAAG
            G  T  H  L  L  F  A  Q  T  G  K  I  E  R  L  P  L  E  G  N  T  M  R  K  T  E  A  K  A  F  L  H  V  P  A  K  V
2201  TCATCATTGG ACTGGCCTTT GACTGCGTGG ACAAGATGGT TTACTGGACG GACATCACTG AGCCTTCCAT TGGGAGAGCT AGTCTACATG GTGGAGAGCC AACCACCATC
            I  I  G  L  A  F  D  C  V  D  K  M  V  Y  W  T  D  I  T  E  P  S  I  G  R  A  S  L  H  G  G  E  P  T  T  I
2311  ATTAGACAAG ATCTTGGAAG TCCAGAAGGT ATCGCTGTTG ATCACCTTGG CCGCAACATC TTCTGGACAG ACTCTAACCT GGATCGAATA GAAGTGGCGA AGCTGGACGG
          I  R  Q  D  L  G  S  P  E  G  I  A  V  D  H  L  G  R  N  I  F  W  T  D  S  N  L  D  R  I  E  V  A  K  L  D  G
2421  CACGCAGCGC CGGGTGCTCT TTGAGACTGA CTTGGTGAAT CCCAGAGGCA TTGTAACGGA TTCCGTGAGA GGGAACCTTT ACTGGACAGA CTGGAACAGA GATAACCCCA
            T  Q  R  R  V  L  F  E  T  D  L  V  N  P  R  G  I  V  T  D  S  V  R  G  N  L  Y  W  T  D  W  N  R  D  N  P  K
2531  AGATTGAAAC TTCCTACATG GACGGCACGA ACCGGAGGAT CCTTGTGCAG GATGACCTGG GCTTGCCCAA TGGACTGACC TTCGATGCGT TCTCATCTCA GCTCTGCTGG
          I  E  T  S  Y  M  D  G  T  N  R  R  I  L  V  Q  D  D  L  G  L  P  N  G  L  T  F  D  A  F  S  S  Q  L  C  W
2641  GTGGATGCAG GCACCAATCG GGCGGAATGC CTGAACCCCA GTCAGCCCAG CAGACGCAAG GCTCTGGAAG GGCTCCAGTA TCCTTTTGCT GTGACGAGCT ACGGGAAGAA
            V  D  A  G  T  N  R  A  E  C  L  N  P  S  Q  P  S  R  R  K  A  L  E  G  L  Q  Y  P  F  A  V  T  S  Y  G  K  N
2751  TCTGTATTTC ACAGACTGGA AGATGAATTC CGTGGTTGCT CTCGATCTTG CAATTTCCAA GGAGACGGAT GCTTTCCAAC CCCACAAGCA GACCCGGCTG TATGGCATCA
          L  Y  F  T  D  W  K  M  N  S  V  V  A  L  D  L  A  I  S  K  E  T  D  A  F  Q  P  H  K  Q  T  R  L  Y  G  I  T
2861  CCACGGCCCT GTCTCAGTGT CCGCAAGGCC ATAACTACTG CTCAGTGAAC AATGGCGGCT GCACCCACCT ATGCTTGGCC ACCCCAGGGA GCAGGACCTG CCGTTGCCCT
            T  A  L  S  Q  C  P  Q  G  H  N  Y  C  S  V  N  N  G  G  C  T  H  L  C  L  A  T  P  G  S  R  T  C  R  C  P
2971  GACAACACCT TGGGAGTTGA CTGTATCGAA CAGAAATGA
      D  N  T  L  G  V  D  C  I  E  Q  K  .
```

FIG.11 continued

ATGAGGGCCTGGATCTTCTTTCTCCTTTGCCTGGCCGGGGAGGGCTCTGGCACAGCAGAGAGGCTTGTTCCCTG
CCATTCTCAACCTGGCCACCAATGCCCACATCAGCGCCAATGCTACCTGTGGAGAGAAGGGGCCTGAGATGTT
CTGCAAACTCGTGGAGCACGTGCCGGGCCGGCCTGTTCGACACGCCCAATGCCGGGTCTGTGACGGTAACAG
TACGAATCCTAGAGAGCGCCATCCGATATCACACGCAATCGATGGCACCAACAACTGGTGGCAGAGCCCCAG
TATTCAGAATGGGAGAGAGTATCACTGGGTCACTGTCACCCTGGACTTACGGCAGGTCTTTCAAGTTGCATAC
ATCATCATTAAAGCTGCCAATGCCCCTCGGCCTGGAAACTGGATTTTGGAGCGCTCCGTGGATGGCGTCAAGT
TCAAACCCTGGCAGTACTATGCCGTCAGCGATACAGAGTGTTTGACCCGCTACAAAATAACTCCACGGCGGGG
ACCTCCCACTTACAGAGCAGACAACGAAGTCATCTGCACCTCGTATTATTCAAAGCTGGTGCCACTTGAACATG
GAGAGATTCACACATCACTCATCAATGGCAGACCCAGCGCTGACGACCCCTCACCCCAGTTGCTGGAATTCAC
CTCAGCACGGTACATTCGCCTTCGTCTTCAGCGCATCAGAACACTCAACGCAGACCTCATGACCCTTAGCCATC
GGGACCTCAGAGACCTTGACCCCATTGTCACAAGACGTTATTACTATTCGATAAAAGACATTTCCGTTGGAGG
CATGTGCATTTGCTACGGCCATGCCAGCAGCTGCCCGTGGGATGAAGAAGCAAAGCAACTACAGTGTCAGTG
TGAACACAATACGTGTGGCGAGAGCTGCGACAGGTGCTGTCCTGGCTACCATCAGCAGCCCTGGAGGCCCGG
AACCATTTCCTCCGGCAACGAGTGTGAGGAATGCAACTGTCACAACAAAGCCAAAGATTGTTACTATGACAGC
AGTGTTGCAAAGGAGAGGAGAAGCCTGAACACTGCCGGGCAGTACAGTGGAGGAGGGGTTTGTGTCAACTG
CTCGCAGAATACCACAGGGATCAACTGTGAAACCTGTATCGACCAGTATTACAGACCTCACAAGGTATCTCCTT
ATGATGACCACCCTTGCCGTCCCTGTAACTGTGACCCTGTGGGGTCTCTGAGTTCTGTCTGTATCAAGGATGAC
CGCCATGCCGATTTAGCCAATGGAAAGTGGCCAGGTCAGTGTCCATGTAGGAAAGGTTATGCTGGAGATAAA
TGTGACCGCTGCCAGTTTGGCTACCGGGGTTTCCCAAATTGCATCCCCTGTGACTGCAGGACTGTCGGCAGCC
TGAATGAGGATCCATGCATAGAGCCGTGTCTTTGTAAGAAAAATGTTGAGGGTAAGAACTGTGATCGCTGCA
AGCCAGGATTCTACAACTTGAAGGAACGAAACCCCGAGGGCTGCTCCGAGTGCTTCTGCTTCGGTGTCTCTGG
TGTCTGTCCCATCAACTACTGTGAAACTGGTCTCCACAACTGTGATATCCCCCAGCGAGCCCAGTGCATCTATA
TGGGTGGTTCCTCCTACACCTGCTCCTGTCTGCCTGGCTTCTCTGGGGATGGCAGAGCCTGCCGAGACGTGGA
TGAATGCCAGCACAGCCGATGTCACCCCGATGCCTTCTGCTACAACACACCAGGCTCTTTCACATGTCAGTGCA
AGCCTGGCTATCAGGGGGATGGCTTCCGATGCATGCCCGGAGAGGTGAGCAAAACCCGGTGTCAACTGGAA
CGAGAGCACATCCTTGGAGCAGCCGGCGGGGCAGATGCACAGCGGCCCACCCTGCAGGGGATGTTTGTGCCT
CAGTGTGATGAATATGGACACTATGTACCCACCCAGTGTCACCACAGCACTGGCTACTGCTGGTGTGTGGACC
GAGATGGTCGGGAGCTGGAGGGTAGCCGTACCCCACCTGGGATGAGGCCCCCGTGTCTGAGTACAGTGGCT
CCTCCTATTCACCAGGGACCAGTAGTACCTACAGCTGTCATCCCCCTGCCTCCAGGGACACACTTACTCTTTGCT
CAGACTGGAAAGATTGAACGCCTGCCCCTGGAAAGAAACACCATGAAGAAGACAGAACGCAAGGCCTTTCTC
CATATCCCTGCAAAAGTCATCATTGGACTGGCCTTTGACTGCGTGGACAAGGTGGTTTACTGGACAGACATCA
GCGAGCCTTCCATTGGGAGAGCCAGCCTCCACGGTGGAGAGCCAACCACCATCATTCGACAAGATCTTGGAA
GCCCTGAAGGCATTGCCCTTGACCATCTTGGTCGAACCATCTTCTGGACGGACTCTCAGTTGGATCGAATAGA
AGTTGCAAAGATGGATGGCACCCAGCGCCGAGTGCTGTTTGACACGGGTTTGGTGAATCCCAGAGGCATTGT
GACAGACCCCGTAAGAGGGAACCTTTATTGGACAGATTGGAACAGAGATAATCCCAAAATTGAGACTTCTCAC
ATGGATGGCACCAACCGGAGGATTCTCGCACAGGACAACCTGGGCTTGCCCAATGGTCTGACCTTTGATGCAT
TCTCATCTCAGCTTTGCTGGGTGGATGCAGGCACCCATAGGGCAGAATGCCTGAACCCAGCTCAGCCTGGCAG
ACGCAAAGTTCTCGAAGGGCTCCAGTATCCTTTCGCTGTGACTAGCTATGGGAAGAATTTGTACTACACAGAC
TGGAAGACGAATTCAGTGATTGCCATGGACCTTGCTATATCCAAAGAGATGGATACCTTCCACCCACACAAGC
AGACCCGGCTATATGGCATCACCATCGCCCTGTCCCAGTGTCCCCAAGGCCACAATTACTGCTCAGTGAATAAT
GGTGGATGTACCCACCTCTGCTTGCCCACTCCAGGGAGCAGGACCTGCCGATGTCCTGACAACACCCTGGGAG
TTGACTGCATTGAACGGAAATGA

FIG.12

MRAWIFFLLCLAGRALAQQRGLFPAILNLATNAHISANATCGEKGPEMFCKLVEHVPGRPVRHAQCRVCDGNSTN
PRERHPISHAIDGTNNWWQSPSIQNGREYHWVTVTLDLRQVFQVAYIIIKAANAPRPGNWILERSVDGVKFKPW
QYYAVSDTECLTRYKITPRRGPPTYRADNEVICTSYYSKLVPLEHGEIHTSLINGRPSADDPSPQLLEFTSARYIRLRLQ
RIRTLNADLMTLSHRDLRDLDPIVTRRYYYSIKDISVGGMCICYGHASSCPWDEEAKQLQCQCEHNTCGESCDRCC
PGYHQQPWRPGTISSGNECEECNCHNKAKDCYYDSSVAKERRSLNTAGQYSGGGVCVNCSQNTTGINCETCIDQ
YYRPHKVSPYDDHPCRPCNCDPVGSLSSVCIKDDRHADLANGKWPGQCPCRKGYAGDKCDRCQFGYRGFPNCIP
CDCRTVGSLNEDPCIEPCLCKKNVEGKNCDRCKPGFYNLKERNPEGCSECFCFGVSGVCPINYCETGLHNCDIPQRA
QCIYMGGSSYTCSCLPGFSGDGRACRDVDECQHSRCHPDAFCYNTPGSFTCQCKPGYQGDGFRCMPGEVSKTRC
QLEREHILGAAGGADAQRPTLQGMFVPQCDEYGHYVPTQCHHSTGYCWCVDRDGRELEGSRTPPGMRPPCLST
VAPPIHQGPVVPTAVIPLPPGTHLLFAQTGKIERLPLERNTMKKTERKAFLHIPAKVIIGLAFDCVDKVVYWTDISEPS
IGRASLHGGEPTTIIRQDLGSPEGIALDHLGRTIFWTDSQLDRIEVAKMDGTQRRVLFDTGLVNPRGIVTDPVRGNL
YWTDWNRDNPKIETSHMDGTNRRILAQDNLGLPNGLTFDAFSSQLCWVDAGTHRAECLNPAQPGRRKVLEGLQ
YPFAVTSYGKNLYYTDWKTNSVIAMDLAISKEMDTFHPHKQTRLYGITIALSQCPQGHNYCSVNNGGCTHLCLPTP
GSRTCRCPDNTLGVDCIERK

FIG.13

ATGAGGGCCTGGATCTTCTTTCTCCTTTGCCTGGCCGGGAGGGCTCTGGCACGGCAGAGAGGCCTGTTTCCTG
CCATTCTCAATCTTGCCAGCAATGCTCACATCAGCACCAATGCCACCTGTGGCGAGAAGGGGCCGGAGATGTT
CTGCAAACTTGTGGAGCATGTGCCAGGTCGGCCCGTCCGAAACCCACAGTGCCGGATCTGTGATGGCAACAG
CGCAAACCCCAGAGAACGCCATCCAATATCACATGCCATAGATGGCACCAATAACTGGTGGCAAAGTCCCAGC
ATTCAGAATGGGAGAGAATATCACTGGGTCACAATCACTCTGGACTTAAGACAGGTCTTTCAAGTTGCATATG
TCATCATTAAAGCTGCCAATGCCCCTCGACCTGGAAACTGGATTTTGGAGCGTTCTCTGGATGGCACCACGTTC
AGCCCCTGGCAGTATTATGCAGTCAGCGACTCAGAGTGTTTGTCTCGTTACAATATAACTCCAAGACGAGGGC
CACCCACCTACAGGGCTGATGATGAAGTGATCTGCACCTCCTATTATTCCAGATTGGTGCCACTTGAGCATGG
AGAGATTCATACATCACTCATCAATGGCAGACCAAGCGCTGACGATCTTTCACCCAAGTTGTTGGAATTCACTT
CTGCACGATATATTCGCCTTCGCTTGCAACGCATTAGAACGCTCAATGCAGATCTCATGACCCTTAGCCACCGG
GAACCTAAAGAACTGGATCCTATTGTTACCAGACGCTATTATTATTCAATAAAGGACATTTCTGTTGGAGGCAT
GTGTATCTGCTATGGCCATGCTAGTAGCTGCCCATGGGATGAAACTACAAAGAAACTGCAGTGTCAATGTGAG
CATAATACTTGCGGGGAGAGCTGTAACAGGTGCTGTCCTGGGTACCATCAGCAGCCCTGGAGGCCGGGAACC
GTGTCCTCCGGCAATACATGTGAAGCATGTAATTGTCACAATAAAGCCAAAGACTGTTACTATGATGAAAGTG
TTGCAAAGCAGAAGAAAAGTTTGAATACTGCTGGACAGTTCAGAGGAGGAGGGGTTTGCATAAATTGCTTGC
AGAACACCATGGGAATCAACTGTGAAACCTGTATTGATGGATATTATAGACCACACAAAGTGTCTCCTTATGA
GGATGAGCCTTGCCGCCCCTGTAATTGTGACCCTGTGGGGTCCCTCAGTTCTGTCTGTATTAAGGATGACCTCC
ATTCTGACTTACACAATGGGAAGCAGCCAGGTCAGTGCCCATGTAAGGAAGGTTATACAGGAGAAAAATGTG
ATCGCTGCCAACTTGGCTATAAGGATTACCCGACCTGTGTCTCCTGTGGGTGCAACCCAGTGGGCAGTGCCAG
TGATGAGCCCTGCACAGGGCCCTGTGTTTGTAAGGAAAACGTTGAGGGGAAGGCCTGTGATCGCTGCAAGCC
AGGATTCTATAACTTGAAGGAAAAAAACCCCCGGGGCTGCTCCGAGTGCTTCTGCTTTGGCGTTTCTGATGTC
TGCCCCATCAACTACTGTGAAACTGGCCTTCATAACTGCGACATACCCCAGCGGGCCCAGTGTATCTACACAG
GAGGCTCCTCCTACACCTGTTCCTGCTTGCCAGGCTTTTCTGGGGATGGCCAAGCCTGCCAAGATGTAGATGA
ATGCCAGCCAAGCCGATGTCACCCTGACGCCTTCTGCTACAACACTCCAGGCTCTTTCACGTGCCAGTGCAAAC
CTGGTTATCAGGGAGACGGCTTCCGTTGCGTGCCCGGAGAGGTGGAGAAAACCCGGTGCCAGCACGAGCGA
GAACACATTCTCGGGGCAGCGGGGGCGACAGACCCACAGCGACCCATTCCTCCGGGGCTGTTCGTTCCTGAG
TGCGATGCGCACGGGCACTACGCGCCCACCCAGTGCCACGGCAGCACCGGCTACTGCTGGTGCGTGGATCGC
GACGGCCGCGAGGTGGAGGGCACCAGGACCAGGCCCGGGATGACGCCCCCGTGTCTGAGTACAGTGGCTCC
CCCGATTCACCAAGGACCTGCGGTGCCTACCGCCGTGATCCCCTTGCCTCCTGGGACCCATTTACTCTTTGCCC
AGACTGGGAAGATTGAGCGCCTGCCCCTGGAGGGAAATACCATGAGGAAGACAGAAGCAAAGGCGTTCCTT
CATGTCCCGGCTAAAGTCATCATTGGACTGGCCTTTGACTGCGTGGACAAGATGGTTTACTGGACGGACATCA
CTGAGCCTTCCATTGGGAGAGCTAGTCTACATGGTGGAGAGCCAACCACCATCATTAGACAAGATCTTGGAAG
TCCAGAAGGTATCGCTGTTGATCACCTTGGCCGCAACATCTTCTGGACAGACTCTAACCTGGATCGAATAGAA
GTGGCGAAGCTGGACGGCACGCAGCGCCGGGTGCTCTTTGAGACTGACTTGGTGAATCCCAGAGGCATTGTA
ACGGATTCCGTGAGAGGGAACCTTTACTGGACAGACTGGAACAGAGATAACCCCAAGATTGAAACTTCCTAC
ATGGACGGCACGAACCGGAGGATCCTTGTGCAGGATGACCTGGGCTTGCCCAATGGACTGACCTTCGATGCG
TTCTCATCTCAGCTCTGCTGGGTGGATGCAGGCACCAATCGGGCGGAATGCCTGAACCCCAGTCAGCCCAGCA
GACGCAAGGCTCTCGAAGGGCTCCAGTATCCTTTTGCTGTGACGAGCTACGGGAAGAATCTGTATTTCACAGA
CTGGAAGATGAATTCCGTGGTTGCTCTCGATCTTGCAATTTCCAAGGAGACGGATGCTTTCCAACCCCACAAG
CAGACCCGGCTGTATGGCATCACCACGGCCCTGTCTCAGTGTCCGCAAGGCCATAACTACTGCTCAGTGAACA
ATGGCGGCTGCACCCACCTATGCTTGGCCACCCCAGGGAGCAGGACCTGCCGTTGCCCTGACAACACCTTGGG
AGTTGACTGTATCGAACAGAAATGA

FIG.14

MRAWIFFLLCLAGRALARQRGLFPAILNLASNAHISTNATCGEKGPEMFCKLVEHVPGRPVRNPQCRICDGNSANP
RERHPISHAIDGTNNWWQSPSIQNGREYHWVTITLDLRQVFQVAYVIIKAANAPRPGNWILERSLDGTTFSPWQY
YAVSDSECLSRYNITPRRGPPTYRADDEVICTSYYSRLVPLEHGEIHTSLINGRPSADDLSPKLLEFTSARYIRLRLQRIR
TLNADLMTLSHREPKELDPIVTRRYYYSIKDISVGGMCICYGHASSCPWDETTKKLQCQCEHNTCGESCNRCCPGY
HQQPWRPGTVSSGNTCEACNCHNKAKDCYYDESVAKQKKSLNTAGQFRGGGVCINCLQNTMGINCETCIDGYY
RPHKVSPYEDEPCRPCNCDPVGSLSSVCIKDDLHSDLHNGKQPGQCPCKEGYTGEKCDRCQLGYKDYPTCVSCGC
NPVGSASDEPCTGPCVCKENVEGKACDRCKPGFYNLKEKNPRGCSECFCFGVSDVCPINYCETGLHNCDIPQRAQC
IYTGGSSYTCSCLPGFSGDGQACQDVDECQPSRCHPDAFCYNTPGSFTCQCKPGYQGDGFRCVPGEVEKTRCQHE
REHILGAAGATDPQRPIPPGLFVPECDAHGHYAPTQCHGSTGYCWCVDRDGREVEGTRTRPGMTPPCLSTVAPPI
HQGPAVPTAVIPLPPGTHLLFAQTGKIERLPLEGNTMRKTEAKAFLHVPAKVIIGLAFDCVDKMVYWTDITEPSIGR
ASLHGGEPTTIIRQDLGSPEGIAVDHLGRNIFWTDSNLDRIEVAKLDGTQRRVLFETDLVNPRGIVTDSVRGNLYWT
DWNRDNPKIETSYMDGTNRRILVQDDLGLPNGLTFDAFSSQLCWVDAGTNRAECLNPSQPSRRKALEGLQYPFA
VTSYGKNLYFTDWKMNSVVALDLAISKETDAFQPHKQTRLYGITTALSQCPQGHNYCSVNNGGCTHLCLATPGSR
TCRCPDNTLGVDCIEQK.

FIG.15