

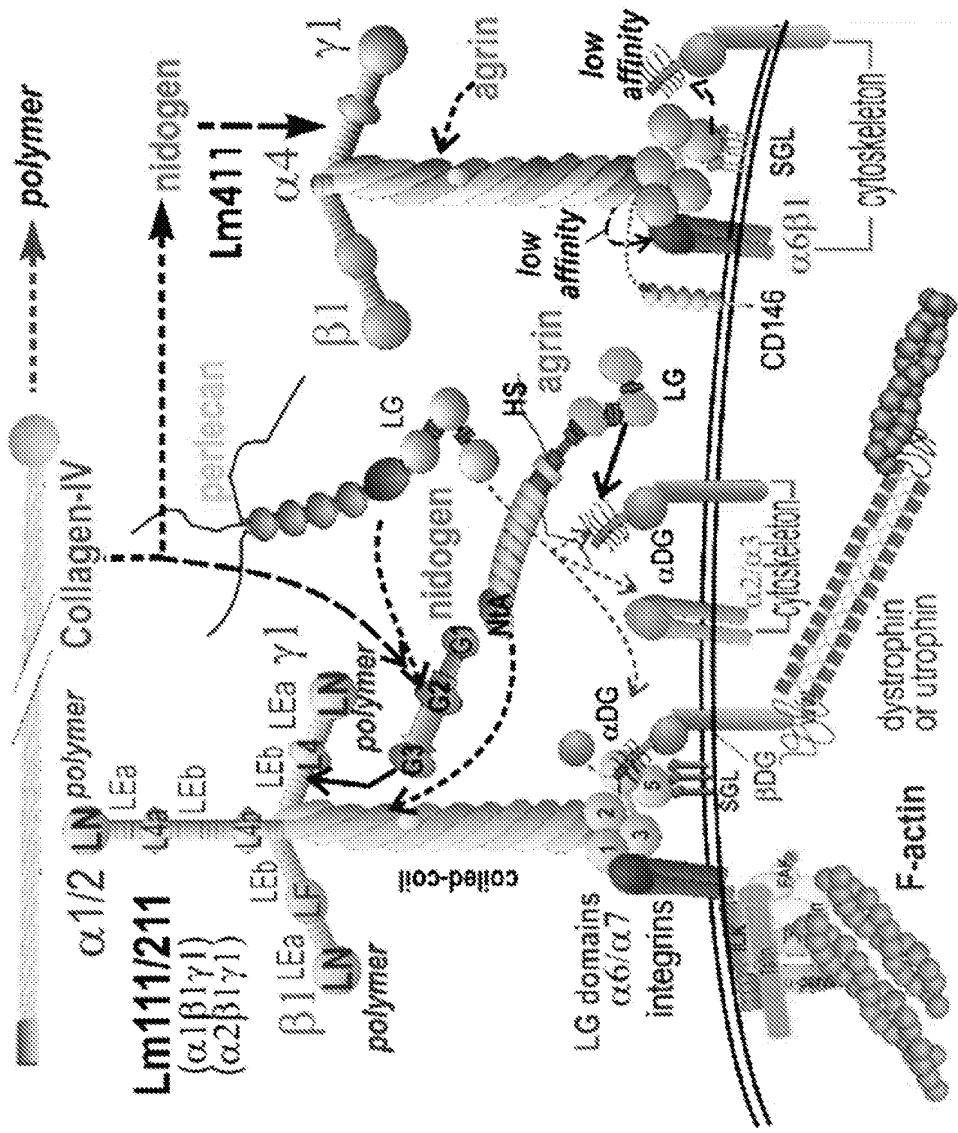


FIG.1

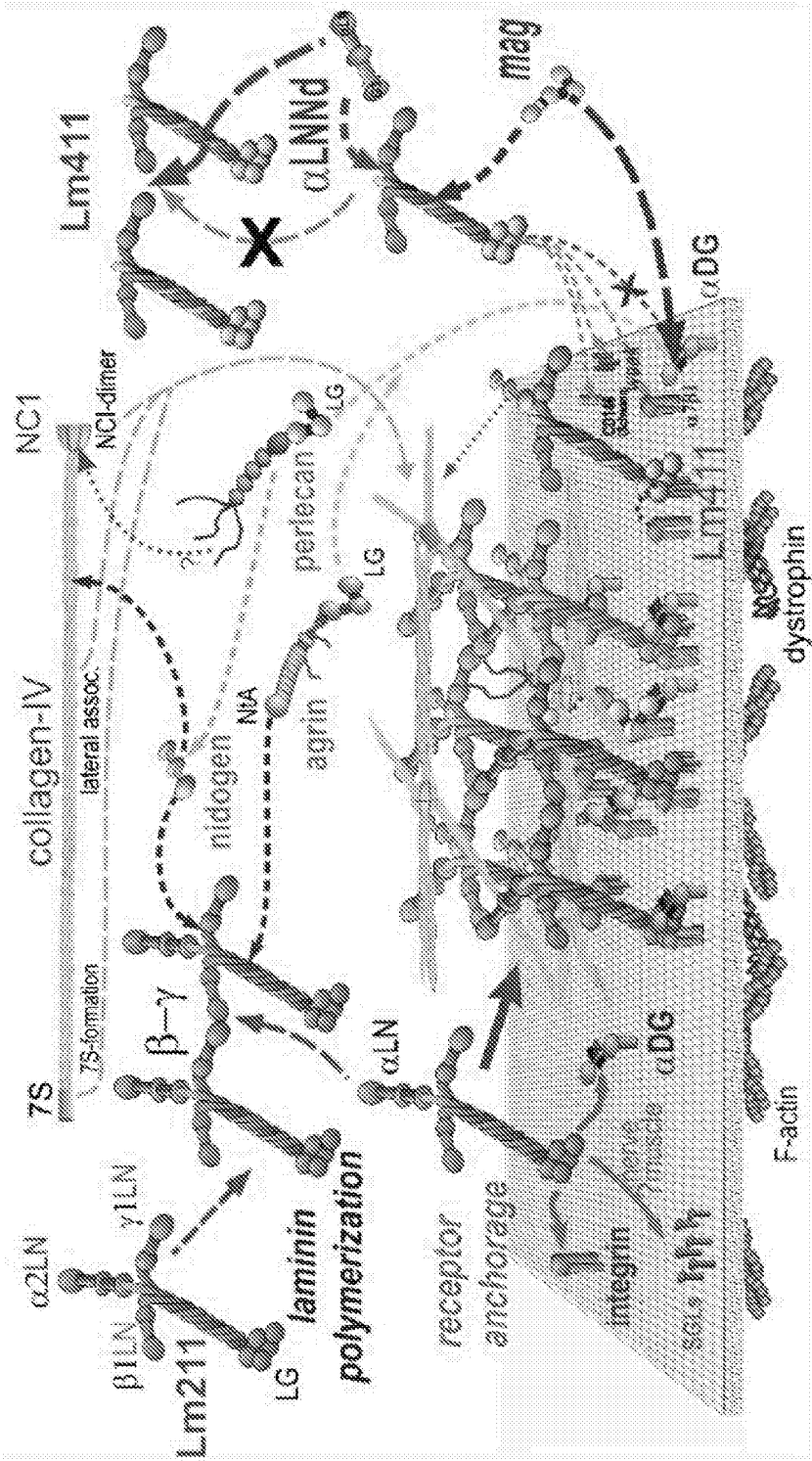


FIG.2

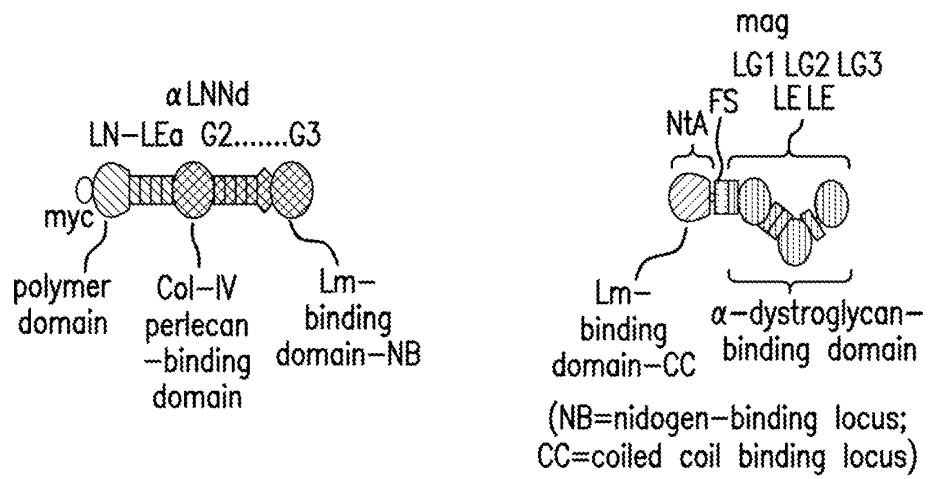


FIG.3A

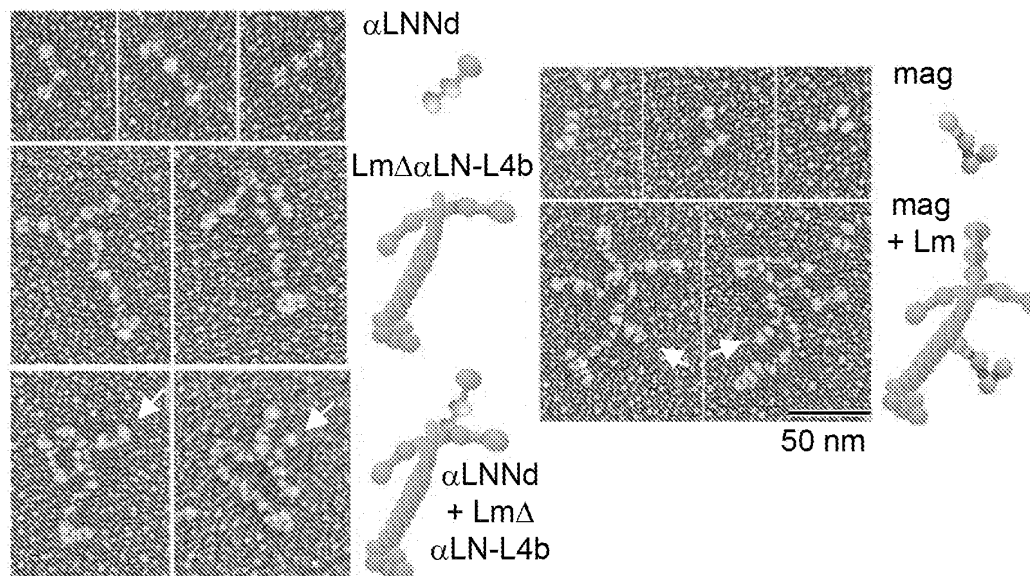


FIG.3B

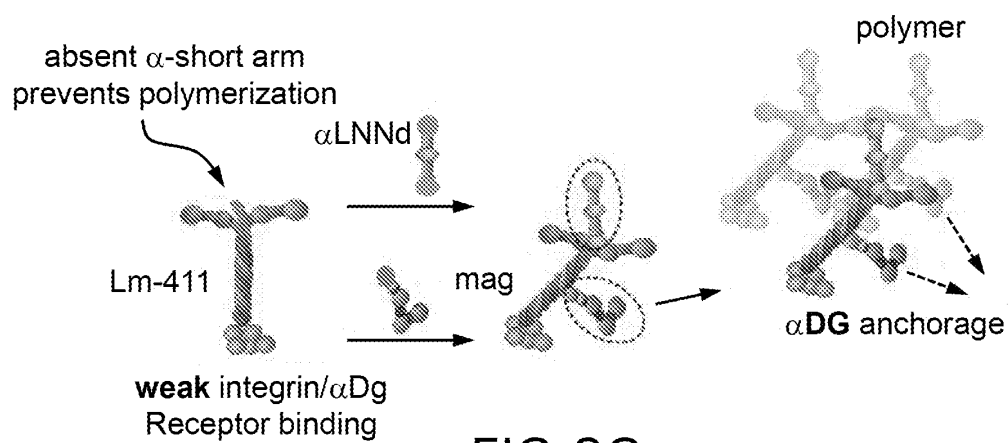


FIG.3C

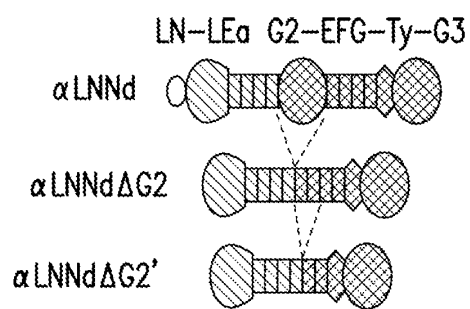


FIG.3D

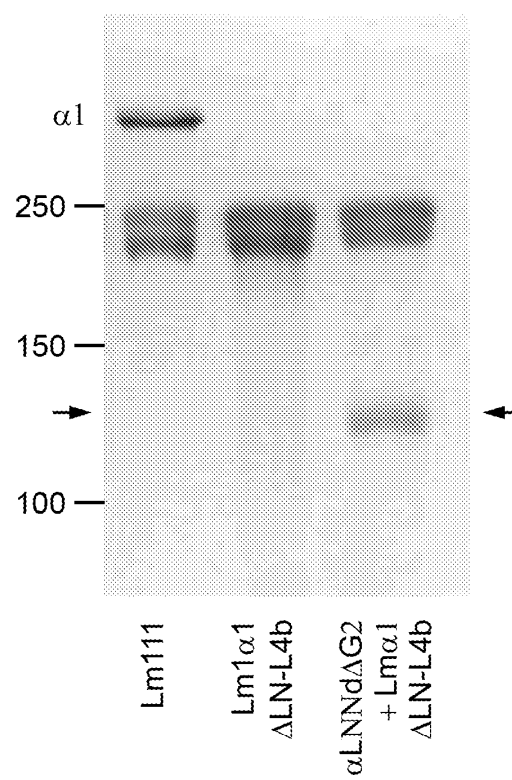


FIG.3E

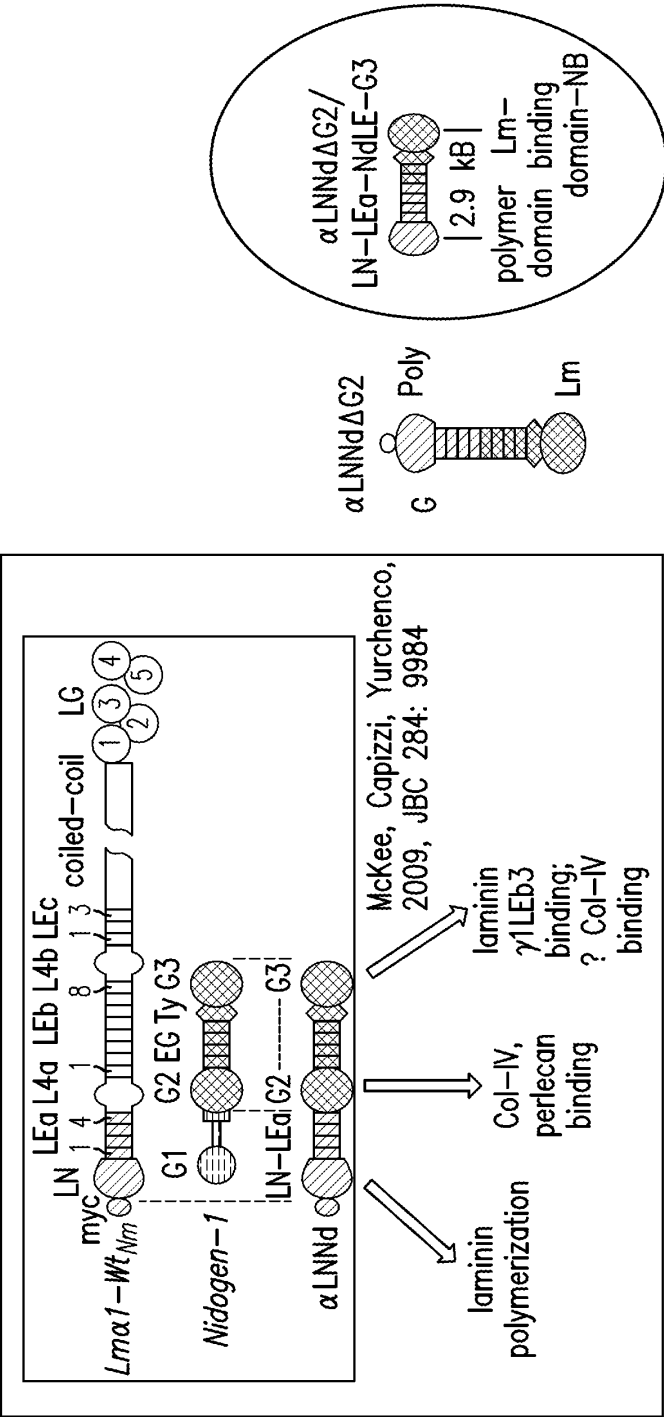


FIG.4

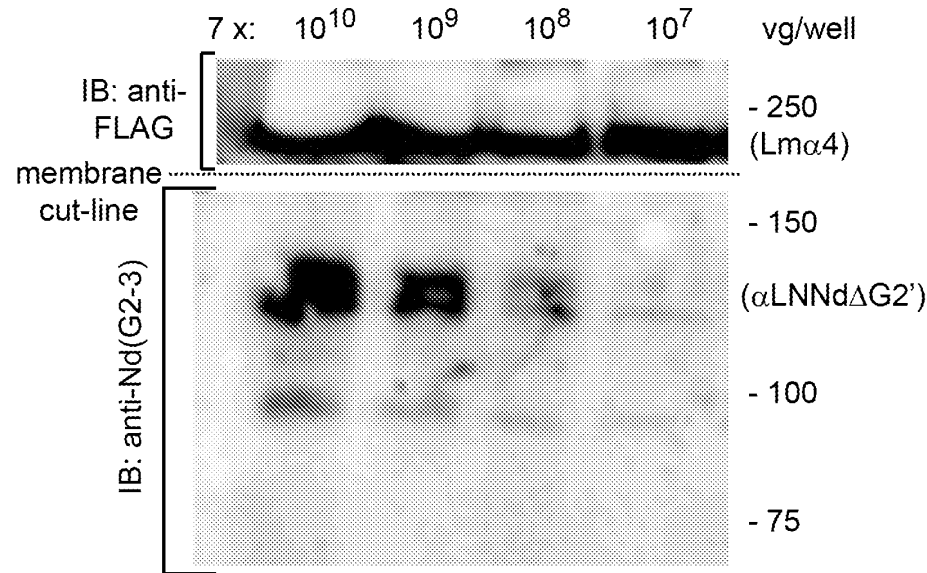


FIG.5A

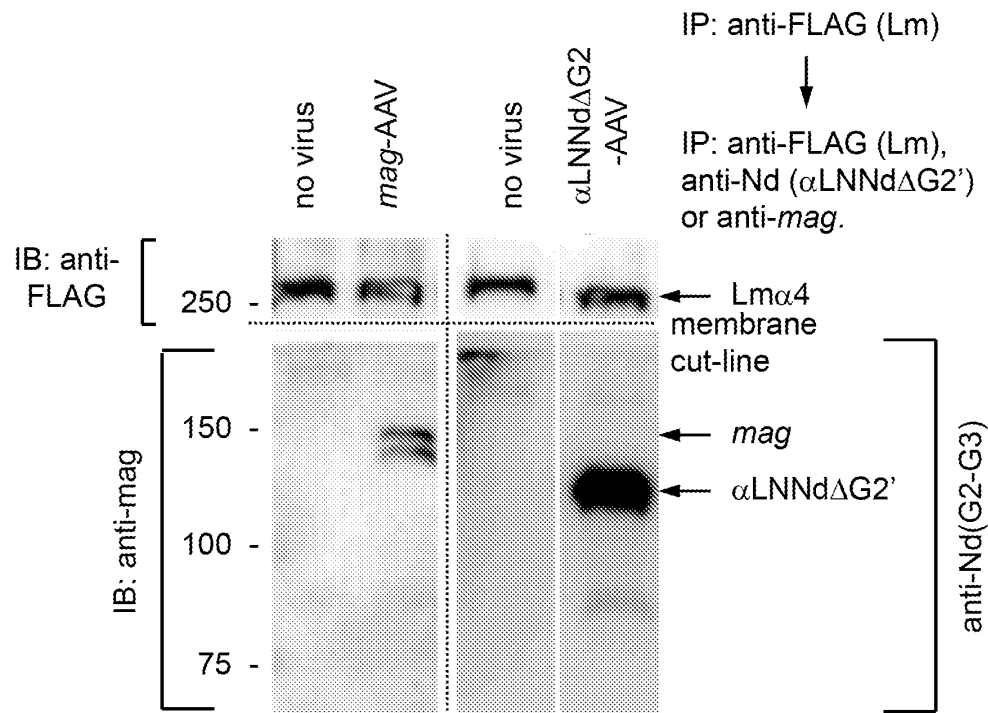


FIG.5B

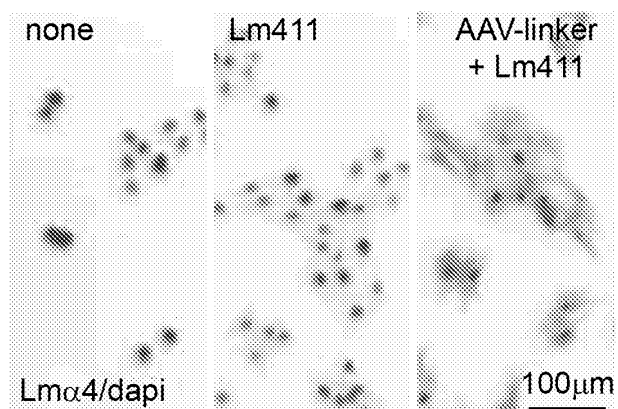


FIG.5C

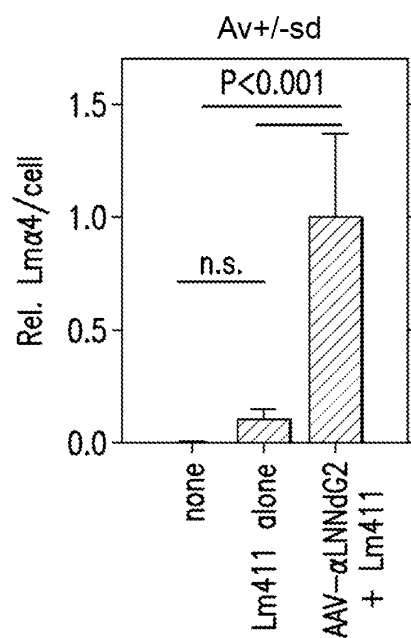


FIG.5D

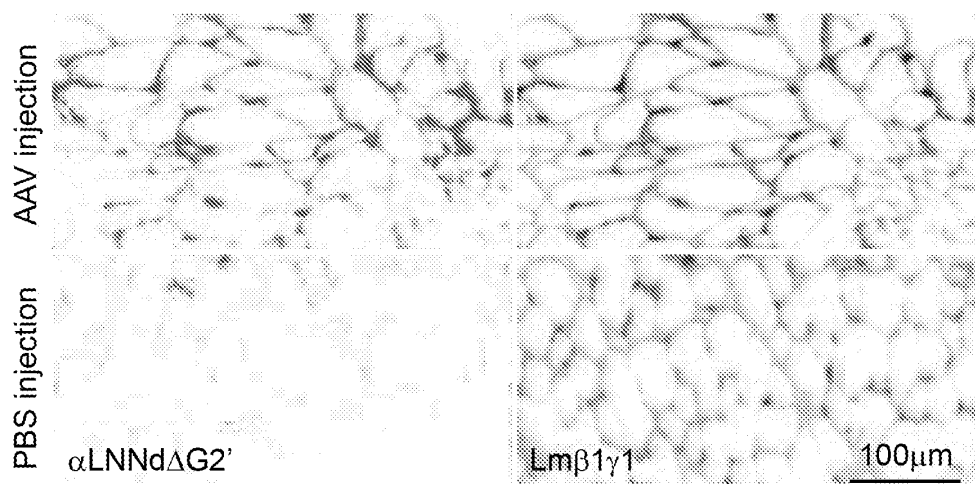


FIG.5E

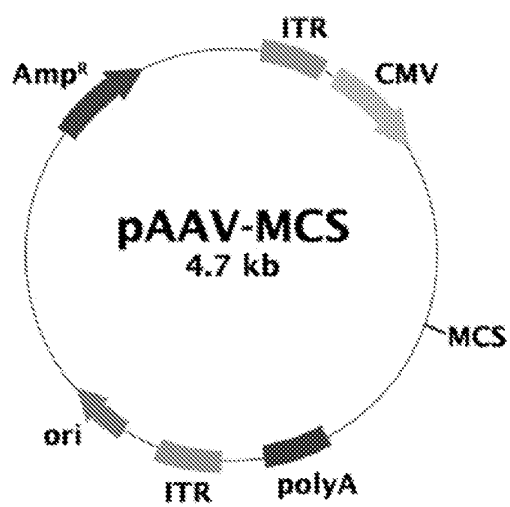


FIG.6

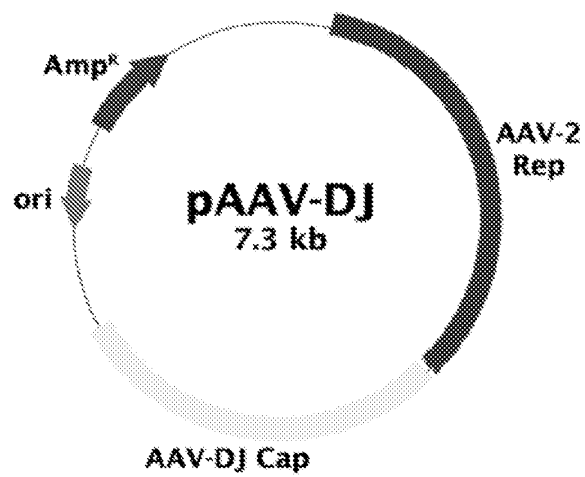


FIG.7

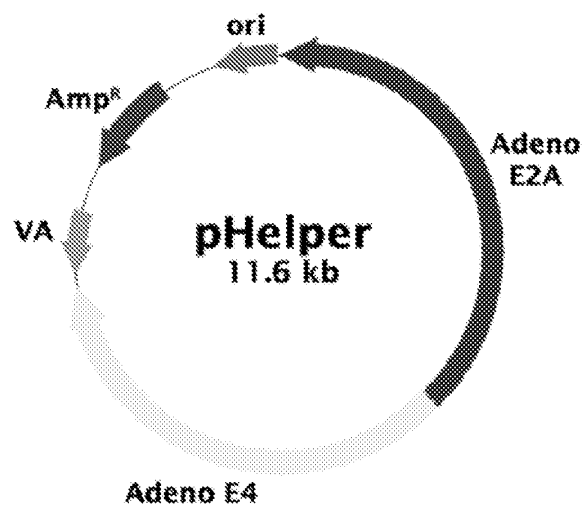


FIG.8

	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	MRWIFFLLCLAGRALARQGLFPAILNLASNAHISTNATCGEKGPEMFCKLVEHVPGRP				60
Sbjct	1	MRWIFFLLCLAGRALA+QRLFPAILNLA+NAHIS NATCGEKGPEMFCKLVEHVPGRP				60
Query	61	VRNPQCRICDGNSANPRERHPISHAIDGTNNWWQSPSIQNGREYHWVTITLDRQVFQVA				120
Sbjct	61	VRHAQCRVCDGNSNPRERHPISHAIDGTNNWWQSPSIQNGREYHWVTITLDRQVFQVA				120
Query	121	YVIIKAANAPRPGNWILERSLDGTTFSWQYYAVSDSECLSRYNITPRRGPTTYRADDEV				180
Sbjct	121	YIIKAANAPRPGNWILERSVDGVKFKPWQYYAVSDTECLTRYKITPRRGPTTYRADNEV				180
Query	181	ICTSYYSRLVPLEHGEIHTSLINGRPSADDLSPKLLEFTSARYIRLRLQRIRTLNLADLMT				240
Sbjct	181	ICTSYYSKLVPLEHGEIHTSLINGRPSADDPSPQLLEFTSARYIRLRLQRIRTLNLADLMT				240
Query	241	LSHREPKELDPIVTRYYYSIKDISVGGMCICYGHASSCPWDETTKKLQCCEHNTCGES				300
Sbjct	241	LSHRDRLDPIVTRYYYSIKDISVGGMCICYGHASSCPWDEEAKQLQCCEHNTCGES				300
Query	301	CNRCCPGYHQPWPGTVSSGNTCEACNCHNAKDCYYDESVAKQKSLNTAGQFRGGV				360
Sbjct	301	CDRCCPGYHQPWPGTISSGNEECNCHNAKDCYYDSSVAKERRSLNTAGQYSGGV				360
Query	361	CINCLQNTMGINCETCIDQYYRPHKVSPYDEPCRPCNCDPVGSLSSVCIKDDLHSDLHN				420
Sbjct	361	CVNCSQNTTGINCETCIDQYYRPHKVSPYDDHPCRPCNCDPVGSLSSVCIKDDRHLN				420
Query	421	GKQPGQCPCKEGYTGEKCDRCQLGYKDYPTCVSCGCPVGSASDEPCTGPCVCKENVEGK				480
Sbjct	421	GKWPQCPCPKGYAGDKCDRCQFGYRGFPNCIPDCRTVGSNLNEDPCIEPCLCKKNVEGK				480
Query	481	ACDRCKPGFYNLKEKNPRGCSECFGVSVDVCPINYCETGLHNCIPQRAQCIYTGSSY				540

FIG.9

Sbjct	481	CDRCKPGFYNLKE+NP GCSECFGVS VCPINYCETGLHNCIPQRAQCIY GSSSY NCDRCKPGFYNLKERNPEGCECFGVSVCPIINYCETGLHNCIPQRAQCIYMGSSSY	540
Query	541	TCSCLPGFSGDGACQDVEQCPSRCHPDAFCYNTPGSFTCQCKPGYQGDGFRCPGEVE TCSCLPGFSGDG+AC+DVDECQ SRCHPDAFCYNTPGSFTCQCKPGYQGDGFRCPGEV	600
Sbjct	541	TCSCLPGFSGDGRACRDVEQCQHSRCHPDAFCYNTPGSFTCQCKPGYQGDGFRCPGEVS	600
Query	601	KTRCQHEREHILGAAGATDPQRP IPPGLFVPECDAGHYAPTQCHGSTGYCWCVD RDGRE KTRCQ EREHILGAAG D QRP G+VFP+CD +GHY PTQCH STGYCWCVD RDGRE	660
Sbjct	601	KTRCQLEREHILGAAGADAQRPTLQGMFVPCDEYGHVPTQCHHSTGYCWCVD RDGRE	660
Query	661	VEGTRTRPGMTPPCLSTVAPPIHQGPVPTAVIPLPPGTHLLFAQTGKIERLPLEGNTMR +EG+RT PGM PPCLSTVAPPIHQGP VPTAVIPLPPGTHLLFAQTGKIERLPLE NTM+	720
Sbjct	661	LEGSRTPPGMRPPCLSTVAPPIHQGPVPTAVIPLPPGTHLLFAQTGKIERLPLERNTMK	720
Query	721	KTEAKAFLHVPKVIIGLAFDCVDKVVYWDITEPSIGRASLHGGEPTTIIRQDLGSPEG KTE KAFLH+PAKVIIGLAFDCVDK+VYWDI+EPSIGRASLHGGEPTTIIRQDLGSPEG	780
Sbjct	721	KTERKAFLHIPAKVIIGLAFDCVDKVVYWDISEPSIGRASLHGGEPTTIIRQDLGSPEG	780
Query	781	IAVDHLGRNIFWTDNLDRIEVAKLDGTQRRVLFETDLVNPRGIVTDSVRGNLYWTDWNR IA+DHLGR IFWTDNLDRIEVAK+DGTQRRVLF+T LVNPRGIVTD VRGNLYWTDWNR	840
Sbjct	781	IALDHLGRTIFWTDNLDRIEVAKMDGTQRRVLFDTGLVNPRGIVTDPVRGNLYWTDWNR	840
Query	841	DNPKIETSYMDGTNRRILVQDDLGLPNGLTFDAFSSQLCWVDAGTNRAECLNPQSRRK DNPKIETS+MDGTNRRIL QD+LGLPNGLTFDAFSSQLCWVDAGT+RAECLNP+QP RRK	900
Sbjct	841	DNPKIETSHMDGTNRRILAQDNLGLPNGLTFDAFSSQLCWVDAGTHRAECLNPAQGRRK	900
Query	901	ALEGLQYPFAVTSYGKNLYFTDWKMNSVVALDLAISKETDAFQPHKQTRLYGITTALSQC LEGLQYPFAVTSYGKNLY+TDWK NSV+A+DLAISKE D F PHKQTRLYGIT ALSQC	960
Sbjct	901	VLEGLQYPFAVTSYGKNLYYTDWKTNSVIAMDLAISKEMDTFHPHKQTRLYGITIALSQC	960
Query	961	PQGHNYCSVNNGGCTHLCLATPGSRTCRCPDNTLGVD CIEQK PQGHNYCSVNNGGCTHLCL TPGSRTCRCPDNTLGVD CIE+K	1002
Sbjct	961	PQGHNYCSVNNGGCTHLCLPTPGSRTCRCPDNTLGVD CIERK	1002

FIG.9 continued

1 ATGAGGGCCT GGAATCTTCTT TCTGCTTTGCTG GGGCTCTGGC AGCGCAGAGA GGCCTGTGTTTCTG CTAATCTTGGC AGCAATGCTC ACATCAGCAC
 M R A W I F F L L C L A 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 AGGGGGCGGA GATGTTCTGC AAATCTGTGG AGCATGTGCC AGTGGGGCC GTCCGAAACC CACAGTGGCG GATCTGTGAT GGCACACGG
 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 CAAGCCCCAG AGAAGCCCAT CCAATATCAC ATGCCATAGA TGGCACCAGT AACTGGTGGC AAAGTCCGAG CATTGAGAAT 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 TTAAGCTGC CAATGCCCT CGACCTGGAA ACTGGATTTT GGAGGTTCT CTGGATGGCA CCAGCTTCAG
 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 CCCCCTGGCAG TATTATGCAG TCAGCGACTC AGAGTGTGTTG TCTGTTTACA ATATACTCC AAGACGAGG 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 CCTATTATC CAGATTGGTG CCACITGAGC ATGGAGAGAT TCATACATCA CTCATCAATG GCAGACCAAG CCTGAGGAT CTTCACCCA AGTGTGGA 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 TTCGCTTCG CTTCGACGCC ATTAGAAGCC TCAATGCAGA TCTCATGACC CTTAGCCACC GGGAACTAA AGAAGTGGAT 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 TTATTATCA ATAAGGACA TTTCTGTGG AGGATGTGT ATCTGCTATG GCCATGCTAG TAGTGGCCA TGGGATGAAA CTACAAGAA 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 ATAATCTTG CGGGAGAGC TGTACAGGT GCTGTCTCTGG GTACCATCAG CAGCCTGGA GCGCGGAAC CGTGTCTCC GGCATACAT GTGAAGCATG TAATTGTAC
 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 AATAAGCCA AAGACTGTTA CTATGATGAA AGTGTGCAA AGCAGAGAA AAGTTTGAAT ACTGCTGGAC AGTTCAGAGG AGGAGGGGT TGCATAAAT 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 ACAAGTGTG TCCTTAAGAG GATGAGCCTT GCGGCCCCCTG 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 TGTCTGTAIT AAGGATGACC TCCATTCTGA CTTACACAAAT GGGAGACAGC CAGGTCAGTG CCCATGTAG GAAGGTATA CAGGAGAAA 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 TTACCGGACC TGTGCTCTCT GTGGTGGAA CCCAGTGGC AGTGCAGTG ATGAGCCCTG CACAGGGCC TGTGTTGTA AGGAAAGCT
 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 TGAGGGGAG GCCTGTGATC GCTGCAAGCC AGGATCTAT AACTTGAAGG AAAAAACCC CCGGGCTGC TCCGAGTGT TCTGCTTTGG CGTTCTGAT GTCTGCCCA
 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 TGAACACTGGC CTTTCATAACT GCCACATACC CCACGGGGGCC CAGTGTATCT ACACAGGAGG CTCCTCCTAC ACTGTTCTCT GCTTGGCAGG CTTTCTGGG
 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 GATGGCAAG CCTGCCAAGA TGTAGTCAA TGGCAGCAA GCGGATGCA CCCTGACGCC TTCTGCTACA AGACTCCAGG CTCCTTTCACG TGGCAGTGCA AACTGGTTA
 D G 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 TCAGGAGAC GGCCTCCGTT GCGTGCCCGG AGAGTGGAG AAAACCGGT GCCAGCAGA GCGAGAACAC ATTCTGGGG CAGCGGGGC GACAGACCA CAGGACCCA
 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 TTCTCCGGG GCTGTTGTT CTTGAGTGG ATGGCAGG GCACTAGCG CCCACCCAGT GCCAGGCGAC CACCGGCTAC TGTGGTGGG TGGATCGGA CGGCCGGGAG
 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 ACCCGCCCGT GTCTGAGTAC AGTGGCTCCC CCGATTACG AAGGACCTGC GGTGCCCTACC GCGGTGATCC 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 TGGACCCAT TTACTTTTG CCCAGACTGG GAAGATTGAG CCGCTGCCCC TGGAGGGAAA TACCATGAGG AAGACAGAAG CAAGCGCTT CCTTCATGTC CCGGCTAAG
 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 TTACTGGAGG GACATCACTG AGCCTTCCAT TGGAGAGCT AGTCTACATG GTGGAGAGCC AACCCCATC
 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 ATCTTGAAG TCCAGAAGGT ATCGCTGTG ATCACCCTTG 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 CAGGAGCGC CCGGTGCTCT TTGAGACTGA CTTGGTGAAT CCCAGAGGCA TTGTAAACGA TTCCGTGAGA GGAACCTTT ACTGGACAGA CTGGACAGA 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 AGATTGAAC TTCCTACATG GACGGCAGCA ACCGGAGGAT CCTTGTGAG GATGACCTGG GCTTGGCCAA TGGACTGACC TTGGATGGGT 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 GCGCGAATCG CTGAACCCCA GTCAGCCCGAG CAGAGGCAAG GCTCTCGAAG GGTCCAGTA TCTTTTGGT 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 CAATTCCAA GGAGAGGAT GCTTTCCAA 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 ATAACACTG CTCAGTGAAC AATGGCGGT GCACCCACCT ATGCTTGGCC ACCCCAGGA GCAGGACCTG CCGTTGGCCT
 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 GACACACCT TGGGAGTGA CTGTATCGAA CAGAAATGA
 D N T L G V D C I E Q K .

FIG.10 continued

1 ATGAGGGCCT GGATCTCTTT TCTCCTTTGG CTGGCCGGGA GGGCTCTGGC AGGCAGAGA GGCCTGTTTC CTGCCATTCT CAATCTTGGC AGCAATGCTC ACATCAGCAC
 MR A W I F F L L C L A 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 AGGGCGCGGA GATGTTCTGC AAAGTTGGG AGCATGTGCC AGGTGGGCCC GTCCGAAACC CACAGTGGCG GATCTGTGAT GGCAGACGGG
 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 CAAACCCAG AGAACCCAT CCAATATCAC ATGCCATAGA TGGCACC AAT AACTGGTGGC AAAGTCCAG CATTGAGAAT GGCAGAGAAT 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 GACAGTCTT TCAAGTTGCA TATGTCATCA TTAAGCTGC CAATGCCCTT CGACCTGGAA ACTGGATTTT GGAGCGTTCT CTGGATGGCA CCACGTTTCAG
 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 CCCTGGCAG TATTATGCAG TCAGCGACTC AGAGTGTG TCTGTTTACA ATATACTCC AAGACGAGGG CCACCCACCT ACAGGCTGA 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 CCTATTATC CAGATTGGTG CCACTTGACC ATGGAGAGAT TCATACATCA CTCATCAATG GCAGACCAG CGCTGACCAT CTTTACCCCA AGTTGTGGA 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 TTGGCCTTCG CTTGCAAGCC ATTAGAAGCC TCAATGCAGA TCTCATGACC CTTAGCCACC GGGAACTAA 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 TTATTATCA ATAAAGACA TTCTGTGTTG AGCGATGTGT ATCTGCTATG GCCATGCTAG TAGCTGCCCA TGGGATGAAA CTACAAGAA 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 TGTAAACAGT CTTGTCTCTGG GTACCATCAG CAGCCCTGGA GGGCGGGAGC CTTGTCTCTCC GGCATATACAT GTGAAGCATG TAATGTAC
 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 AATAAGCCA AAGACTGTTA CTATGATGAA AGTGTGCAA AGCTGTGCAA AAGTTTGAAT ACTGCTGGAC AGTTGACAGG AGGAGGGGT 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 ACAAGTGTG TCCTTATGAG GATGAGCCTT GCGCGCCCTG TAAITGTGAC 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 TGTCTGTTT AAGCATGACC TCCATTCTGA CTTACACAAAT GGGAGCAGC CAGTTCAGTG CCCATGTAG GAAGTTATA CAGGAGAAA ATGTGATGCG
 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 TTGTCTCTCT GTGGTGGCAA CCCAGTGGGC AGTGCCAGTG ATGAGCCCTG CACAGGGCCC TGTGTTTGA AGGAAACGT
 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

FIG. 11

1431 TGAGGGGAG GCCTGTGATC GCTGCAAGCC AGGATTCTAT AACTTGAAGG AAAAAAACC CCGGGGCTGC TCGAGTGTCT TCTGCTTTGG CGTTTCTGAT GTCTGCCCA
 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 TGAACCTGGC CTTCACTACT GCGACATACC CCAGCGGGCC CAGTGTATCT ACACAGGAGG CTCCTCTCTAC ACCTGTCTCT GCTTGGCAGG CTTTCTGGG
 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 GATGGCAAG CCGTGGCAAGA TGTAGATGAA TGGCAGCAA GCGCATGTCA CCGTGACGCC TTCTGCTACA ACACTCCAGG CTCCTTTCAGG TGGCAGTGCA 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 TCAGGAGAC GCGTTCGTT CCGTGGCCGG AGAGTGGAG AAAACCGGT GCGACACGA GCGAGAACAC ATTCTGGGG CAGCGGGGC 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 TTCCTCGGG GCTGTTCGTT CCGTGTGGG ATGCGCAGG GCACTACGG CCCACCCAGT GCGACGGCAG CACCGCTAC TCGTGGTGG TGGATCGGA CCGCGCGGAG
 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 GTGGAGGCA CCAGGACAG GCGCGGGATG AGCGCCCGT GTCTGAGTAC AGTGGCTCC CCGATTACCC AAGGACCTGC GGTGCTACC GCGGTGATCC CCTTGGCTCC
 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 TGGAGCCAT TTACTCTTG CCCAGACTGG GAAGATTGAG CCGCTGCCCC TGGAGGGAAA TACCATGAGG AAGACAGAAG CAAAGCGTT CCTTCATGTC CCGGCTAAG
 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 TCATCATGG ACTGGCCTTT GACTGCGTGG ACAAGATGGT TTAAGTGGG GACATCACTG AGCCTTCCAT TGGAGAGCT AGTCTACATG GTGGAGAGCC AACCACTC
 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 ATTAGCAAG ATCTTGAAG TCCAGAAGGT ATCGCTGTG ATCAGCTTGG CCGCAACATC TTCTGGACAG ACTCTAACCT GATCGAATA 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 CAGCGACGC CCGGTGCTCT TTGAGACTGA CTTCGTGAAT CCCAGAGGCA TTCTAACGGA TTCCGTGAGA GGAACCTTT ACTGGACAGA CTGGAACAGA GATAACCCA
 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 AGATTGAAC TTCCTACATG GACGGCAGCA ACCGAGGAT CCTTGTGAG GATGACCTGG GCTTGGCCAA 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 GCGGGAATGC CTGAACCCCA GTCAGCCGAG CAGAGCCAG GCTCTCGAG GGTCTCCAGTA TCCTTTTGGT GTGACGAGCT ACGGGAGAA
 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 TCTGTATTC ACAGACTGA AGATGAATC CCGTGTGCT CTCATCTTG CAATTCGAA GGAGAGGAT GCTTTCGAG GACCCGCTG 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 CCAGCGCCT GTCTCAGTGT CCGCAAGGCC ATACTACTG CTCAGTGAAC AATGGCGGT GCACCCACT ATGCTTGGCC ACCCCAGGA GCGAGACCTG CCGTGGCCT
 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 TGGAGTTGA CTGTATGAA CAGAAATGA
 D N T L G V D C I E Q K .

FIG.11 continued

ATGAGGGCCTGGATCTTCTTTCTCTTTGCTGGCCGGGAGGGCTCTGGCACAGCAGAGAGGCTTGTTCCTG
CCATTCTCAACCTGGCCACCAATGCCACATCAGCGCCAATGCTACCTGTGGAGAGAAGGGGCTGAGATGT
CTGCAAACTCGTGGAGCACGTGCCGGGCCGCTGTTGACACGCCCAATGCCGGGTCTGTGACGGTAACAG
TACGAATCTAGAGAGCGCCATCCGATATCACACGCAATCGATGGCACCAACAACTGGTGGCAGAGCCCCAG
TATTCAGAATGGGAGAGAGTATCACTGGGTCACTGTCAACCCTGGACTTACGGCAGGTCTTTCAAGTTGCATAC
ATCATCATTAAGCTGCCAATGCCCCCTGGCCTGGAACTGGATTTGGAGCGCTCCGTGGATGGCGTCAAGT
TCAAACCTGGCAGTACTATGCCGTGAGCGATACAGAGTGTGGACCCGCTACAAAATAACTCCACGGCGGGG
ACCTCCCACTTACAGAGCAGACAACGAAGTCATCTGCACCTCGTATTATTCAAAGCTGGTGCCACTTGAACATG
GAGAGATTACACATCACTCATCAATGGCAGACCCAGCGCTGACGACCCCTACCCCAAGTTGCTGGAATTCAC
CTCAGCACGGTACATTGCGCTTCTGCTTTCAGCGCATCAGAACTCAACGCAGACCTCATGACCCTTAGCCATC
GGGACCTCAGAGACCTTGACCCATTGTGACAAGACGTTATTACTATTCGATAAAAGACATTTCCGTGGAGG
CATGTGCAATTTGCTACGGCCATGCCAGCAGCTGCCCGTGGGATGAAGAAGCAAAGCAACTACAGTGTCACTG
TGAACACAATACGTGTGGCGAGAGCTGCCAGAGGTGCTGTCTGGCTACCATCAGCAGCCCTGGAGGCCCCG
AACCATTCTCCGGCAACGAGTGTGAGGAATGCAACTGTCAACAAGCCAAAGATTGTACTATGACAGC
AGTGTTCGAAAGGAGAGGAGAAGCCTGAACACTGCCGGGCAGTACAGTGGAGGAGGGGTTTGTGCAACTG
CTCGCAGAATACCACAGGGATCAACTGTGAAACCTGTATCGACAGTATTACAGACCTCACAAGGTATCTCCTT
ATGATGACCACTTGTCCGTCCCTGTAACTGTGACCTGTGGGCTCTGAGTTCGTCTGTATCAAGGATGAC
CGCCATGCCGATTTAGCCAATGGAAAGTGGCCAGGTCAAGTGTCCATGTAGGAAGGTTATGCTGGAGATAAA
TGTGACCGCTGCCAGTTTGGCTACCGGGGTTTCCCAAAATTCATCCCTGTGACTGCAAGGATGTCCGCAACC
TGAATGAGGATCCATGCATAGAGCGGTGCTTTGTAAGAAAAATGTTGAGGGTAAGAACTGTGATCGCTGCA
AGCCAGGATTCTACAACCTGAAGGAACGAAACCCGAGGGCTGCTCCGAGTGCTTCTGCTTCGGTGTCTG
TGTCTGTCCCATCAACTACTGTGAACTGGTCTCCACAACCTGTGATATCCCCAGCGAGCCCACTGCATCTATA
TGGGTGGTTCCTCTACACCTGCTCTGTCTGCTGGCTTCTCTGGGGATGGCAGAGCCTGCCGAGAGCTGGA
TGAATGCCAGCACAGCCGATGTCAACCCGATGCTTCTGTACACACACAGGCTCTTTCATGTCACTGCA
AGCCTGGCTATCAGGGGGATGGCTTCCGATGCATGCCCGGAGAGGTGAGCAAAACCGGTGTCAACTGGAA
CGAGAGCACATCCTTGGAGCAGCGCGGGGAGATGCACAGCGGCCACCTGCAGGGGATGTTTGTGCT
CAGTGTGATGAATATGGACACTATGTACCCACCAAGTGTCAACACAGCACTGGCTACTGCTGGTGTGGACC
GAGATGGTGGGAGCTGGAGGGTAGCCGTACCCACCTGGGATGAGGCCCCGTGTCTGAGTACAGTGGCT
CCTCCTATTCACAGGGACCACTAGTACCTACAGCTGTATCCCCCTGCCTCCAGGGACACACTTACTCTTGT
CAGACTGGAAAGATTGAACGCTGCCCTGGAAAGAAACACCATGAAGAAGACAGAACGCAAGGCCCTTCTC
CATATCCCTGCAAAAGTCATCATTGGACTGGCTTTGACTGCGTGGACAAGGTGGTTTACTGGACAGACATCA
GCGAGCCTTCCATTGGGAGAGCCAGCCTCCACGGTGGAGAGCCAACCAACCATTCGACAAGATCTTGGAA
GCCCTGAAGGCATTGCCCTTGACCATCTTGGTGAACCATCTTCTGGACGGACTCTCAGTTGGATCGAATAGA
AGTTGCAAGATGGATGGCACCCAGCGCCGAGTGTGTTGACACGGGTTTGGTGAATCCAGAGGCATTGT
GACAGACCCGTAAGAGGGAACCTTTATTGGACAGATTGGAACAGAGATAATCCCAAAATTGAGACTTCTCAC
ATGGATGGCACCAACCGGAGGATTCTCGACAGGACAACCTGGGCTTGCCCAATGGTCTGACCTTTGATGCAT
TCTCATCTCAGCTTGTCTGGGTGGATGCAGGCACCCATAGGGCAGAATGCCTGAACCCAGCTCAGCCTGGCAG
ACGCAAAAGTTCTCGAAGGGCTCCAGTATCCTTTCGCTGTGACTAGCTATGGGAAGAATTTGACTACACAGAC
TGGAAGACGAATTCAGTGATTGCCATGGACCTTGTATATCCAAAGAGATGGATACCTTCCACCCACACAAGC
AGACCCGGCTATATGGCATCAACCATCGCCCTGTCCAGTGTCCCAAGGCCACAATTACTGCTCAGTGAATAAT
GGTGGATGTACCCACCTGTGCTTGCCTCCAGGGAGCAGGACCTGCCGATGTCTGACAACACCTGGGAG
TTGACTGCATTGAACGGAATGA

FIG.12

MRAWIFFLLCLAGRALAQQRGLFPAILNLATNAHISANATCGEKGPMEFCKLVEHVPGRPVRHAQCRVCDGNSTN
PRERHPISHAIDGTNNWWQSPSIQNGREYHWVTVTLDLRQVFQVAYIIHKAANAPRPGNWILERSVDGVKFKPW
QYYAVSDTECLTRYKITPRRGPPTYRADNEVICTSYYSKLVPLEHGEIHTSLINGRPSADDPSPQLLEFTSARYIRLRQ
RIRTLNADLMTLSHRDLROLDPIVTRYYYSIKDISVGGMCICYGHASSCPWDEEAKQLQCCEHNTCGESCDRCC
PGYHQQPWRPGTISSGNECEECNCHNKAKDCYYDSSVAKERRSLNTAGQYSGGGVCVNCNQNTTGINCETCIDQ
YYRPHKVSPYDDHPCRPCNCDPVGSLSSVCIKDDRHADLANGKWPGQCPCRKGYAGDKCDRCQFGYRGFPNCIP
CDCRTVGS LNEDPCIEPCLCKKNVEGKNCDRCKPGFYNLKERNPEGCSECFGVSGVCPINYCETGLHNCDIPQRA
QCIYMGSSSYTCCLPGFSGDGRACRDVDECQHSRCHPD AFCYNTPGSFTCQCKPGYQGDGFRCMPGEVSKTRC
QLEREHILGAAGGADAQRPTLQGMFVPQCDEYGHYVPTQCHHSTGYCWCVDRDGRELEGSRTPPGMRPPCLST
VAPPIHQGPVVPTAVIPLPPGTHLLFAQTGKIERLPLERNTMKKTERKAFLHIPAKVIIGLAFDCVDKVVYWTDISPS
IGRASLHGGEPTTIHQDLGSPEGIALDHLGRTIFWTDSQLDRIEVAKMDGTQRRVLFDTGLVNPRGIVTDPVRGNL
YWTOWNRDNPKIETSHMDGTNRRILAQDNLGLPNGLTFDAFSSQLCWVDAGTHRAECLNPAQPGRRKVLEGLQ
YPPAVTSYGKNLYTDWKTNSVIAMDLAISKEMDTFHPHKQTRLYGITIALSQCPQGHNYCSVNNGGCTHLCCLPTP
GSRTCRCPDNTLGVDIERK

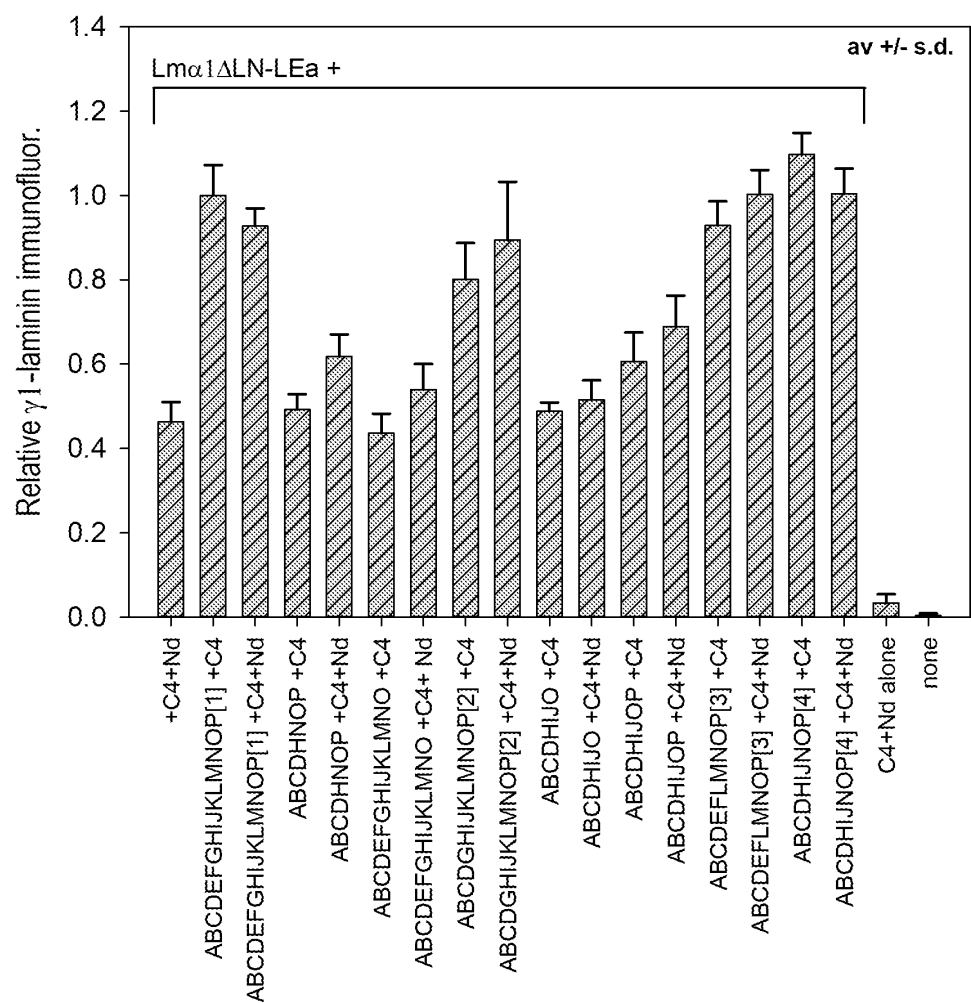
FIG.13

ATGAGGGGCTGGATCTTCTTTCTCTTTGCTGGCCGGGAGGGCTCTGGCACGGCAGAGAGGGCTGTTCTCTG
CCATTCTCAATCTTGCCAGCAATGCTCACATCAGCACCAATGCCACCTGTGGCGAGAAGGGGCGGAGATGTT
CTGCAAACTTGTGGAGCATGTGCCAGGTCGGCCCTCCGAAACCCACAGTGCAGGATCTGTGATGGCAACAG
CGCAAAACCCAGAGAACGCCATCCAATATCACATGCCATAGATGGCACCATAACTGGTGGCAAAAGTCCACG
ATTCAGAATGGGAGAGAATATCACTGGGTACAATCACTCTGGACTTAAGACAGGTCTTTCAAGTTGCATATG
TCATCATTAAAGCTGCCAATGCCCTCGACCTGGAACCTGGATTTTGGAGCGTTCTCTGGATGGCACCACGTTT
AGCCCCCTGGCAGTATTATGCAGTCAGCGACTCAGAGTGTTTGTCTCGTTACAATATAACTCCAAGACGAGGGC
CACCCACCTACAGGGCTGATGATGAAGTGATCTGCACCTCCTATTATCCAGATTGGTGCCACTTGAGCATGG
AGAGATTACATACACTCATCAATGGCAGACCAAGCGCTGACGATCTTTCACCCAAGTTGTTGGAATCACTT
CTGCACGATATATTCGCTTCGCTTGAACGCATTAGAACGCTCAATGCAGATCTCATGACCTTAGCCACCGG
GAACCTAAAGAACTGGATCCTATTGTTACCAGACGCTATTATTCAATAAAGGACATTTCTGTTGGAGGCAT
GTGTATCTGCTATGGCCATGCTAGTAGCTGCCATGGGATGAACTACAAAGAACTGCAGTGTCAATGTGAG
CATAAATCTTGGGGGAGAGCTGTAAACAGGTGCTGCTGGGTACCATCAGCAGCCCTGGAGGCCGGGAACC
GTGTCTCCGGCAATACATGTGAAGCATGTAATTGTCAACAATAAGCCAAAGACTGTTACTATGATGAAAGTG
TTGCAAGCAGAAGAAAAGTTTGAATACTGCTGGACAGTTCAGAGGAGGAGGGGTTTGCAATAATTGCTTGC
AGAACACCATGGGAATCAACTGTGAAACCTGTATTGATGGATATTATAGACCACACAAAGTGTCTCCTTATGA
GGATGAGCCTTGCCGCCCTGTAAATTGTGACCTGTGGGGTCCCTCAGTTCTGTCTGTATTAAGGATGACCTCC
ATTCGACTTACACAATGGGAAGCAGCCAGGTGAGTGCCTGTAAGGAAGGTTATACAGGAGAAAAATGTG
ATCTGTGCCAATCTGGCTATAAGGATTACCCGACCTGTGTCTCTGTGGGTGCAACCCAGTGGGCAGTGCCAG
TGATGAGCCCTGCACAGGGCCCTGTGTTTGTAAAGGAAAACGTTGAGGGGAAGGCTGTGATCGCTGCAAGCC
AGGATTCTATAACTTGAAGGAAAAAAACCCCGGGGCTGCTCCGAGTGCTTCTGCTTTGGCGTTTCTGATGTC
TGCCCCATCAACTACTGTGAACTGGCCTTACATACTGCGACATACCCAGCGGGCCAGTGTATCTACACAG
GAGGCTCCTCTACACCTGTTCTGCTTGGCAGGCTTTCTGGGGATGGCCAAGCCTGCCAAGATGTAGATGA
ATGCCAGCCAAGCCGATGTACCTTGACGCTTCTGTACAACACTCCAGGCTCTTTCAGTGCCAGTGCAAAAC
CTGGTTATCAGGGAGACGGCTTCCGTTGCGTGCCCGGAGAGGTGGAGAAAACCGGTGCCAGCAGAGCGA
GAACACATTCTCGGGCAGCGGGGCGACAGACCCACAGCGACCCATTCTCCGGGGCTGTTGTTCTGAG
TGCGATGCGCACGGGCACTACGCGCCACCCAGTGCCACGGCAGCACCAGGCTACTGCTGGTGCGTGATCGC
GACGGCCGCGAGGTGGAGGGCACCAGGACCAGGCCCGGGATGACGCCCCGTGTCTGAGTACAGTGGCTCC
CCCGATTACCAAGGACCTGCGGTGCTACCGCGTGATCCCTTGCTCTCTGGGACCCATTACTCTTTGCC
AGACTGGGAAGATTGAGCGCTGCCCTGGAGGGAAATACCATGAGGAAGACAGAAGCAAAGCGTTCCTT
CATGTCCCGCTAAAGTCATCATTGGACTGGCCTTTGACTGCGTGGACAAGATGGTTTACTGGACGGACATCA
CTGAGCCTTCCATTGGGAGAGCTAGTCTACATGGTGGAGAGCCAACCACCATCATTAGACAAGATCTTGGAG
TCCAGAAGGTATCGTGTGATCACCTTGGCCGCAACATCTTCTGGACAGACTCTAACCTGGATCGAATAGAA
GTGGCGAAGCTGGACGGCAGCAGCGCCGGGTGCTCTTGAGACTGACTTGGTGAATCCAGAGGCATTGTA
ACGGATTCCGTGAGAGGGAACCTTTACTGGACAGACTGGAACAGAGATAACCCCAAGATTGAAACTTCTAC
ATGGACGGCACGAACCGGAGGATCCTTGTGAGGATGACCTGGGCTTGCCCAATGGACTGACCTTCGATGCG
TTCTCATCTCAGCTGTCTGGGTGGATGCAGGCACCAATCGGGCGGAATGCCTGAACCCAGTCAGCCACGCA
GACGCAAGGCTCTCGAAGGGCTCCAGTATCTTTGTGTGACGAGCTACGGGAAGAATCTGTATTTACAGA
CTGGAAGATGAATTCGTTGGTCTGCTCGATCTTGCAATTTCCAAGGAGACGGATGCTTTCCAACCCACAAG
CAGACCCGGCTGTATGGCATCACCGGCCCTGTCTCAGTGTCCGCAAGGCCATAACTACTGCTCAGTGAACA
ATGGCGGCTGCACCCACCTATGCTTGGCCACCCAGGGAGCAGGACCTGCCGTTGCCCTGACAACACCTTGGG
AGTTGACTGTATCGAACAGAAATGA

FIG.14

MRAWIFFLLCLAGRALARQRLFPAILNLASNAHISTNATCGEKGPEMFCKLVEHVPGRPVVRNPQCRICDGNANP
RERHPISHAIDGTNNWWQSPSIQNGREYHWVTITLDRQVFQVAYVIIKAANAPRPGNWILERSLDGTTFPWQY
YAVSDSECLSRYNITPRRGPPTYRADDEVICTSYYSRLVPLEHGEIHTSLINGRPSADDLSPKLLEFTSARYIRLRLQIR
TLNADLMTLSHREPKELDPIVTRRRYYYSIKDISVGGMCICYGHASSCPWDETTKKLQCCQEHNTCGESCNRCPPGY
HQQPWRPGTVSSGNTCEACNCHNKAKDCYYDESVAKQKSLNTAGQFRGGGVCINCLQNTMGINCETCIDGYY
RPHKVSPEDEPCRPCNCDPVGSLSSVCIKDDLHSDLHNGKQPGQCPCKEGYTGEKCDRCQLGYKDYPTCVSCGC
NPVGSASDEPCTGPCVCKENVEGKACDRCKPGFYNLKEKNPRGCSECFGVSDVCPINYCETGLHNCDIPQRAQC
IYTGSSYTCSLPGFSGDGOACQDVDECQPSRCHPD AFCYNTPGSFTCQCKPGYQGDGFRCVPGEVEKTRCQHE
REHILGAAGATDPQRPIPPGLFVPECDAGHYAPTQCHGSTGYCWCVDROGREVEGTRTRPGMTTPCLSTVAPPI
HQPAPVPTAVIPLPPGTHLLFAQTGKIERLPLEGNTMRKTEAKAFLHVPKVIIGLAFDCVDKMOVYWDITEPSIGR
ASLHGGEPTTIIRQDLGSPGIAVDHLGRNIFWTDNLDRIEVAKLDGTQRRVLFETDLVNPRGIVTDSVRGNLYWT
DWNDRDNPKIETSYMDGTNRRILVQDDLGLPNGLTFDAFSSQLCWVDAGTNRAECLNPSQPSRRKALEGLQYPFA
VTSYGKNLYFTDWKMNSVVALDLAISKETDAFQPHKQTRLYGITTALSQCPCQGHNYCSVNNGGCTHLCLATPGSR
TCRCPDNTLGVDCEQK.

FIG.15



Common names of linkers (selected): [1] α LNNd; [2]; α LNNd Δ LEa3,4 [3] α LNNd Δ G2'; [4] α LNNd Δ 2EGF'

α LN Chimeric Linker Proteins

FIG. 16

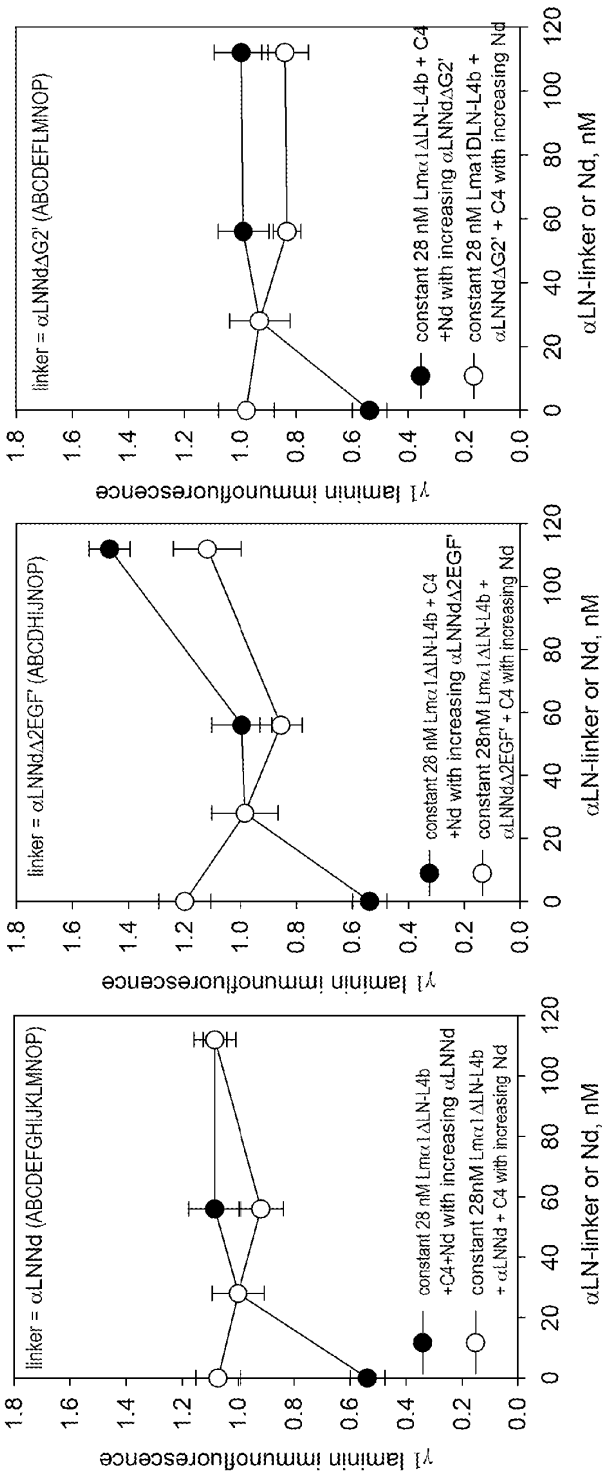


FIG. 17A

FIG. 17B

FIG. 17C

FIG. 18A

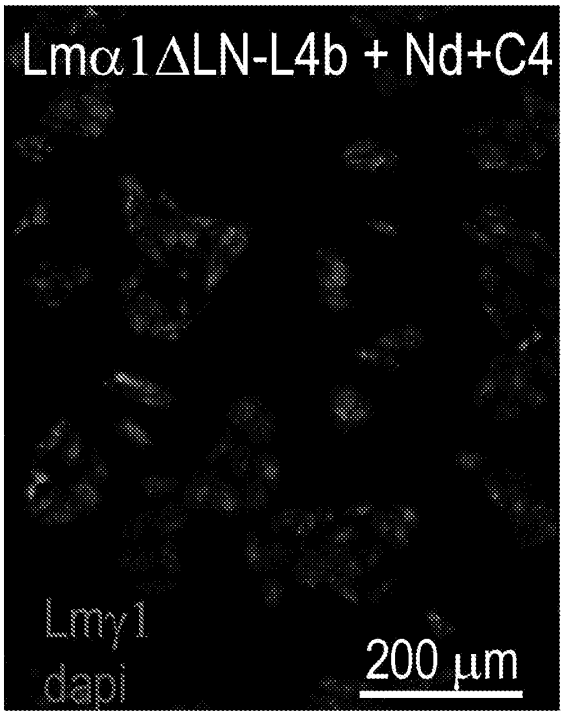
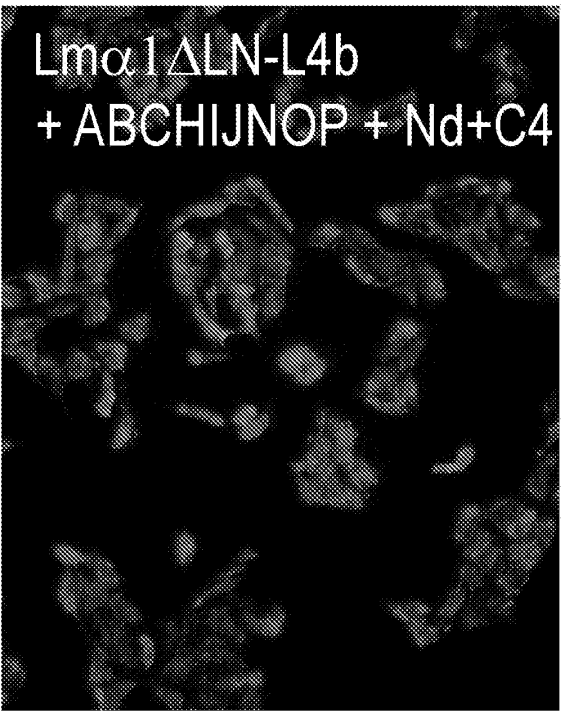


FIG. 18B

FIG. 18C

