

53161000003Sequence

SEQUENCE LISTING

<110> Aduro Biotech, Inc.

<120> EPIDERMAL GROWTH FACTOR RECEPTOR VARIANT
III-MESOTHELIN FUSIONS AND METHODS OF USING THE SAME

<130> 5316.1000-003

<150> 62/146,559

<151> 2015-04-13

<150> 62/243,397

<151> 2015-10-19

<160> 32

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 2744

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion

<400> 1

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cacaatttgc	tacgttaatt	gatagattcg	ttaaaggccg	tggtcaatta	gataaagata	2160
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tagatttatc ggttcaagaa gcattaagtg gtacaccgtg tttattaggt ccagggtccag 2700
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<213> Artificial Sequence

<220>

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ctgctaattcc aatttttaac ggaataaaatt agtgaaaatg aaggccgaat tttccttggt 180
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<213> Artificial Sequence

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<223> promoter

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gatgaatggg aagaagaata cgaaactgca cgtgaagtaa gtacacgtga tattgaggaa 180
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<210> 4

<211> 63

<212> DNA

<213> Artificial Sequence

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<221> misc_feature

<222> 33, 42

<223> n = A,T,C or G

<220>

<223> EGFRVIII Consensus Sequence

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<211> 486

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion

<400> 5

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gcatcacgag cacttgaaga gaaaaaagga aactatgttg tgaccgatca tggtagctgc 180
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53161000003Sequence

aagggttaact	atgtcgtaac	agatcatgga	agttgtgctg	acggaagtgt	taaagcgctcg	300
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catggtagtt	gtggtgatgg	ctcgatcaaa	ttgtcaaaag	ttctaccggc	ttctcgctgcg	420
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<210> 6
<211> 1764
<212> DNA
<213> Artificial Sequence

<220>
<223> fragment

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tcaggtttta	gtacagaacg	tgtccgtgag	ttagcagttg	catttagcaca	aaaaaacgtt	180
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cgtttcgttg	cagaatcagc	agaagtgtta	ttaccgagat	tagtttcatg	cccaggacct	540
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<213> Artificial Sequence

<220>
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53161000003Sequence

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<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion

<400> 8

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			20					25					30		
Ser	Glu	Asp	Ser	Ser	Leu	Asn	Thr	Asp	Glu	Trp	Glu	Glu	Glu	Tyr	Glu
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Thr	Ala	Arg	Glu	Val	Ser	Ser	Arg	Asp	Ile	Glu	Glu	Leu	Glu	Lys	Ser
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			85					90						95	
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Cys	Leu	Ala	325	Leu	Leu	Leu	Phe	Leu	330	Asn	Pro	Asp	Ala	Phe	Ser	Gly	Pro	
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<210> 9
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<220>
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<400> 9
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 Asp His Gly Ser Cys
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<210> 10
 <211> 162
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fragment

<400> 10
 Ala Ser Lys Val Leu Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Gly
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 Asn Tyr Val Val Thr Asp His Gly Ser Cys Ala Asp Gly Ser Val Lys
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 Thr Ser Ala Ser Lys Val Ala Pro Ala Ser Arg Ala Leu Glu Glu Lys
 35 40 45
 Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys Gly Asp Gly Ser
 50 55 60
 Ile Lys Leu Ser Lys Val Leu Pro Ala Ser Arg Ala Leu Glu Glu Lys
 65 70 75 80
 Lys Gly Asn Tyr Val Thr Asp His Gly Ser Cys Ala Asp Gly Ser
 85 90 95
 Val Lys Ala Ser Lys Val Ala Pro Ala Ser Arg Ala Leu Glu Glu Lys
 100 105 110
 Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys Gly Asp Gly Ser
 115 120 125
 Ile Lys Leu Ser Lys Val Leu Pro Ala Ser Arg Ala Leu Glu Glu Lys
 130 135 140
 Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys Ala Asp Gly Ser
 145 150 155 160
 Val Lys

<210> 11
 <211> 588
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fragment

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 Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu Asp Gly
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 Val Leu Thr Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu
 20 25 30

53161000003Sequence

Leu	Gly	Phe	Pro	Cys	Ala	Glu	Val	Ser	Gly	Leu	Ser	Thr	Glu	Arg	Val
		35					40					45			
Arg	Glu	Leu	Ala	Val	Ala	Leu	Ala	Gln	Lys	Asn	Val	Lys	Leu	Ser	Thr
	50					55					60				
Glu	Gln	Leu	Arg	Cys	Leu	Ala	His	Arg	Leu	Ser	Glu	Pro	Pro	Glu	Asp
65					70					75					80
Leu	Asp	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Leu	Phe	Leu	Asn	Pro	Asp	Ala
				85					90					95	
Phe	Ser	Gly	Pro	Gln	Ala	Cys	Thr	Arg	Phe	Phe	Ser	Arg	Ile	Thr	Lys
			100					105					110		
Ala	Asn	Val	Asp	Leu	Leu	Pro	Arg	Gly	Ala	Pro	Glu	Arg	Gln	Arg	Leu
		115					120					125			
Leu	Pro	Ala	Ala	Leu	Ala	Cys	Trp	Gly	Val	Arg	Gly	Ser	Leu	Leu	Ser
	130					135					140				
Glu	Ala	Asp	Val	Arg	Ala	Leu	Gly	Gly	Leu	Ala	Cys	Asp	Leu	Pro	Gly
145					150					155					160
Arg	Phe	Val	Ala	Glu	Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu	Val	Ser
				165					170					175	
Cys	Pro	Gly	Pro	Leu	Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg	Ala	Ala
			180					185					190		
Leu	Gln	Gly	Gly	Gly	Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp	Ser	Val
		195					200					205			
Ser	Thr	Met	Asp	Ala	Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly	Gln	Pro
	210					215					220				
Ile	Ile	Arg	Ser	Ile	Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg	Gln	Arg
225					230					235					240
Ser	Ser	Arg	Asp	Pro	Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile	Leu	Arg
				245					250					255	
Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser	Gly	Lys
			260					265					270		
Lys	Ala	Arg	Glu	Ile	Asp	Glu	Ser	Leu	Ile	Phe	Tyr	Lys	Lys	Trp	Glu
		275					280					285			
Leu	Glu	Ala	Cys	Val	Asp	Ala	Ala	Leu	Leu	Ala	Thr	Gln	Met	Asp	Arg
	290					295					300				
Val	Asn	Ala	Ile	Pro	Phe	Thr	Tyr	Glu	Gln	Leu	Asp	Val	Leu	Lys	His
305					310					315					320
Lys	Leu	Asp	Glu	Leu	Tyr	Pro	Gln	Gly	Tyr	Pro	Glu	Ser	Val	Ile	Gln
				325					330					335	
His	Leu	Gly	Tyr	Leu	Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile	Arg	Lys
			340					345					350		
Trp	Asn	Val	Thr	Ser	Leu	Glu	Thr	Leu	Lys	Ala	Leu	Leu	Glu	Val	Asn
		355					360					365			
Lys	Gly	His	Glu	Met	Ser	Pro	Gln	Val	Ala	Thr	Leu	Ile	Asp	Arg	Phe
	370					375					380				
Val	Lys	Gly	Arg	Gly	Gln	Leu	Asp	Lys	Asp	Thr	Leu	Asp	Thr	Leu	Thr
385					390					395					400
Ala	Phe	Tyr	Pro	Gly	Tyr	Leu	Cys	Ser	Leu	Ser	Pro	Glu	Glu	Leu	Ser
				405					410					415	
Ser	Val	Pro	Pro	Ser	Ser	Ile	Trp	Ala	Val	Arg	Pro	Gln	Asp	Leu	Asp
			420					425					430		
Thr	Cys	Asp	Pro	Arg	Gln	Leu	Asp	Val	Leu	Tyr	Pro	Lys	Ala	Arg	Leu
		435					440					445			
Ala	Phe	Gln	Asn	Met	Asn	Gly	Ser	Glu	Tyr	Phe	Val	Lys	Ile	Gln	Ser
	450					455					460				
Phe	Leu	Gly	Gly	Ala	Pro	Thr	Glu	Asp	Leu	Lys	Ala	Leu	Ser	Gln	Gln
465					470					475					480
Asn	Val	Ser	Met	Asp	Leu	Ala	Thr	Phe	Met	Lys	Leu	Arg	Thr	Asp	Ala
				485					490					495	
Val	Leu	Pro	Leu	Thr	Val	Ala	Glu	Val	Gln	Lys	Leu	Leu	Gly	Pro	His
			500					505					510		
Val	Glu	Gly	Leu	Lys	Ala	Glu	Glu	Arg	His	Arg	Pro	Val	Arg	Asp	Trp
		515					520					525			
Ile	Leu	Arg	Gln	Arg	Gln	Asp	Asp	Leu	Asp	Thr	Leu	Gly	Leu	Gly	Leu
	530					535					540				
Gln	Gly	Gly	Ile	Pro	Asn	Gly	Tyr	Leu	Val	Leu	Asp	Leu	Ser	Val	Gln
545					550					555					560
Glu	Ala	Leu	Ser	Gly	Thr	Pro	Cys	Leu	Leu	Gly	Pro	Gly	Pro	Val	Leu
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53161000003Sequence
 Thr Val Leu Ala Leu Leu Leu Ala Ser Thr Leu Ala
 580 585

<210> 12
 <211> 88
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion

<400> 12
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 1 5 10 15
 Ala Asn Cys Ile Thr Ile Asn Pro Asp Ile Ile Phe Ala Ala Thr Asp
 20 25 30
 Ser Glu Asp Ser Ser Leu Asn Thr Asp Glu Trp Glu Glu Tyr Glu
 35 40 45
 Thr Ala Arg Glu Val Ser Ser Arg Asp Ile Glu Glu Leu Glu Lys Ser
 50 55 60
 Asn Lys Val Lys Asn Thr Asn Lys Ala Asp Gln Asp Asn Lys Arg Lys
 65 70 75 80
 Ala Lys Ala Glu Lys Gly Gly Ser
 85

<210> 13
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fragment

<400> 13
 ccagctagtc gtgcattaga ggagaaaaag gggaattacg tggtgacgga tcatggatcg 60
 tgt 63

<210> 14
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fragment

<400> 14
 cctgcatcac gagcacttga agagaaaaaa ggaaactatg ttgtgaccga tcatggtagc 60
 tgc 63

<210> 15
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fragment

<400> 15
 ccagcatcta gagctttaga ggaaaagaag ggtaactatg tcgtaacaga tcatggaagt 60
 tgt 63

<210> 16
 <211> 63
 <212> DNA
 <213> Artificial Sequence

53161000003Sequence

<220>

<223> fragment

<400> 16

ccagcttctc gcgcattaga agaaaagaaa ggcaattatg ttgtaacaga ccatggtagt 60
tgt 63

<210> 17

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> fragment

<400> 17

ccggcttctc gtgcgctaga agagaagaaa ggaaattacg tagttacaga ccacggctct 60
tgc 63

<210> 18

<211> 231

<212> DNA

<213> Artificial Sequence

<220>

<223> promoter

<400> 18

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taatgacgtc aaaaggatag caagactaga ataaagctat aaagcaagca tataatattg 120
cgtttcattc ttagaagcga atttcgccaa tattataatt atcaaaagag aggggtggca 180
aacgggtattt ggcattatta ggttaaaaaa tgtagaagga gagtgaacc c 231

<210> 19

<211> 1323

<212> DNA

<213> Artificial Sequence

<220>

<223> LLO441 sequence

<400> 19

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caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120
ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatgaa 180
atcgataagt atatacaagg attggattac aataaaaaaca atgtattagt ataccacgga 240
gatgcagtga caaatgtgcc gccaaagaaaa ggttacaaag atggaaatga atatatgtt 300
gtggagaaaa agaagaaatc catcaatcaa aataatgcag acattcaagt tgtgaatgca 360
atttcgagcc taacctatcc aggtgctctc gtaaaagcga attcgggaatt agtagaaaat 420
caaccagatg ttctccctgt aaaacgtgat tcattaacac tcagcattga tttgccaggt 480
atgactaatc aagacaataa aatagttgta aaaaatgcc aataatcaaa cgtaacaac 540
gcagtaaata cattagtgga aagatggaat gaaaaatat ctcaagctta tccaaatgta 600
agtgcacaaa ttgattatga tgacgaaatg gcttacagt aatcacaaat aattgcgaaa 660
tttggtagag catttaaagc tgtaaataat agcttgaatg taaacttcgg cgcaatcagt 720
gaagggaaaa tgcaagaaga agtcattagt tttaacaaa tttactataa cgtgaatgtt 780
aatgaacctc caagaccttc cagatttttc ggcaaagctg ttactaaaga gcagttgcaa 840
gcgcttggag tgaatgcaga aaatcctcct gcatatatct caagtgtggc gtatggccgt 900
caagtttatt tgaaattatc aactaattcc catagtacta aagtaaaagc tgcttttgat 960
gctgccgtaa gcggaataatc tgtctcaggt gatgtagaac taacaaatat catcaaaaat 1020
tcttccttca aagccgtaat ttacggaggt tccgcaaaa atgaagttca aatcatcgac 1080
ggcaacctcg gagacttacg cgatattttg aaaaaaggcg ctacttttaa tcgagaaaaca 1140
ccaggagttc ccattgctta tacaacaaa ttcctaaaag acaatgaatt agctgttatt 1200
aaaaacaact cagaatatat tgaaacaact tcaaaagctt atacagatgg aaaaattaac 1260
atcgatcact ctggaggata cgttgctcaa ttcaacattt cttgggatga agtaaattat 1320
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<210> 20

<211> 441

53161000003Sequence

<212> PRT

<213> Artificial Sequence

<220>

<223> LLO441 sequence

<400> 20

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Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
      20      25      30
Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Ala Ser
      35      40      45
Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr
      50      55      60
Ile Gln Gly Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly
      65      70      75      80
Asp Ala Val Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn
      85      90      95
Glu Tyr Ile Val Glu Lys Lys Lys Ser Ile Asn Gln Asn Asn
      100      105      110
Ala Asp Ile Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly
      115      120      125
Ala Leu Val Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val
      130      135      140
Leu Pro Val Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly
      145      150      155      160
Met Thr Asn Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser
      165      170      175
Asn Val Asn Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys
      180      185      190
Tyr Ala Gln Ala Tyr Pro Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp
      195      200      205
Glu Met Ala Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala
      210      215      220
Phe Lys Ala Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser
      225      230      235      240
Glu Gly Lys Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr
      245      250      255
Asn Val Asn Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys
      260      265      270
Ala Val Thr Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn
      275      280      285
Pro Pro Ala Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu
      290      295      300
Lys Leu Ser Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp
      305      310      315      320
Ala Ala Val Ser Gly Lys Ser Val Ser Gly Asp Val Glu Leu Thr Asn
      325      330      335
Ile Ile Lys Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala
      340      345      350
Lys Asp Glu Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp
      355      360      365
Ile Leu Lys Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro
      370      375      380
Ile Ala Tyr Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile
      385      390      395      400
Lys Asn Asn Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp
      405      410      415
Gly Lys Ile Asn Ile Asp His Ser Gly Tyr Val Ala Gln Phe Asn
      420      425      430
Ile Ser Trp Asp Glu Val Asn Tyr Asp
      435      440

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<210> 21

<211> 1266

<212> DNA

53161000003Sequence

<213> Artificial Sequence

<220>

<223> fragment

<400> 21

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gaaatcgata agtatataca aggattggat tacaataaaa acaatgtatt agtataccac 180
ggagatgcag tgacaaatgt gccgccaaga aaaggttaca aagatggaaa tgaatatatt 240
gttgtggaga aaaagaagaa atccatcaat caaaataatg cagacattca agttgtgaat 300
gcaatttcga gcctaaccta tccagggtgct ctcgtaaaag cgaattcgga attagtagaa 360
aatcaaccag atgttctccc tgtaaaacgt gattcattaa cactcagcat tgatttgcca 420
ggtatgacta atcaagacaa taaaatagtt gtaaaaaatg ccactaaatc aaacgttaac 480
aacgcagtaa atacattagt ggaaagatgg aatgaaaaat atgctcaagc ttatccaaat 540
gtaagtgc aaattgatta tgatgacgaa atggcttaca gtgaatcaca attaattgcg 600
aaatttggtg cagcatttaa agctgtaaat aatagcttga atgtaaactt cggcgcaatc 660
agtgaaggga aaatgcaaga agaagtcatt agttttaaac aaatttacta taacgtgaat 720
gttaatgaac ctacaagacc ttccagattt ttcggcaaag ctgttactaa agagcagttg 780
cagtcgcttg gagtgaatgc agaaaatcct cctgcataata tctcaagtgt ggcgtatggc 840
cgtaagttt atttgaaatt atcaactaat tcccatagta ctaaagtaaa agctgctttt 900
gatgctgccg taagcggaaa atctgtctca ggtgatgtag aactaacaaa tatcatcaaa 960
aattcttcct tcaaagccgt aatttacgga ggttccgcaa aagatgaagt tcaaatacatc 1020
gacggcaacc tcggagactt acgcgatatt ttgaaaaaag gcgctacttt taatcgagaa 1080
acaccaggag ttcccattgc ttataacaaca aacttcctaa aagacaatga attagctgtt 1140
attaaaaaca actcagaata tattgaaaca acttcaaaag cttatacaga tggaaaaaatt 1200
aacatcgatc actctggagg atacgttgct caattcaaca tttcttgga tgaagtaaatt 1260
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<210> 22

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> fragment

<400> 22

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          20           25           30
Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr Ile Gln Gly
          35           40           45
Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly Asp Ala Val
          50           55           60
Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn Glu Tyr Ile
65           70           75           80
Val Val Glu Lys Lys Lys Ser Ile Asn Gln Asn Asn Ala Asp Ile
          85           90           95
Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly Ala Leu Val
          100          105          110
Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val Leu Pro Val
          115          120          125
Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly Met Thr Asn
130          135          140
Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser Asn Val Asn
145          150          155          160
Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys Tyr Ala Gln
          165          170          175
Ala Tyr Pro Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp Glu Met Ala
          180          185          190
Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala Phe Lys Ala
          195          200          205
Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser Glu Gly Lys
210          215          220
Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr Asn Val Asn
225          230          235          240

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53161000003Sequence

Val	Asn	Glu	Pro	Thr	Arg	Pro	Ser	Arg	Phe	Phe	Gly	Lys	Ala	Val	Thr
				245					250					255	
Lys	Glu	Gln	Leu	Gln	Ala	Leu	Gly	Val	Asn	Ala	Glu	Asn	Pro	Pro	Ala
			260					265					270		
Tyr	Ile	Ser	Ser	Val	Ala	Tyr	Gly	Arg	Gln	Val	Tyr	Leu	Lys	Leu	Ser
		275					280					285			
Thr	Asn	Ser	His	Ser	Thr	Lys	Val	Lys	Ala	Ala	Phe	Asp	Ala	Ala	Val
	290					295					300				
Ser	Gly	Lys	Ser	Val	Ser	Gly	Asp	Val	Glu	Leu	Thr	Asn	Ile	Ile	Lys
305					310					315					320
Asn	Ser	Ser	Phe	Lys	Ala	Val	Ile	Tyr	Gly	Gly	Ser	Ala	Lys	Asp	Glu
			325						330					335	
Val	Gln	Ile	Ile	Asp	Gly	Asn	Leu	Gly	Asp	Leu	Arg	Asp	Ile	Leu	Lys
			340					345					350		
Lys	Gly	Ala	Thr	Phe	Asn	Arg	Glu	Thr	Pro	Gly	Val	Pro	Ile	Ala	Tyr
		355					360					365			
Thr	Thr	Asn	Phe	Leu	Lys	Asp	Asn	Glu	Leu	Ala	Val	Ile	Lys	Asn	Asn
	370					375					380				
Ser	Glu	Tyr	Ile	Glu	Thr	Ser	Lys	Ala	Tyr	Thr	Asp	Gly	Lys	Ile	
385					390				395					400	
Asn	Ile	Asp	His	Ser	Gly	Gly	Tyr	Val	Ala	Gln	Phe	Asn	Ile	Ser	Trp
			405						410					415	
Asp	Glu	Val	Asn	Tyr	Asp										
			420												

<210> 23
 <211> 1245
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fragment

<400> 23

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ggatttgatt	acaataaaaa	caatgtatta	gtataccacg	gagatgcagt	gacaaatgtg	180
ccgccaagaa	aaggttacaa	agatggaaat	gaatatattg	ttgtggagaa	aaagaagaaa	240
tccatcaatc	aaaataatgc	agacattcaa	gttgatgaatg	caatttcgag	cctaacctat	300
ccaggtgctc	tcgtaaaagc	gaattcggaa	ttagtagaaa	atcaaccaga	tgttctccct	360
gtaaaacgtg	attcattaac	actcagcatt	gatttgccag	gtatgactaa	tcaagacaat	420
aaaatagttg	taaaaaatgc	cactaaatca	aacgttaaca	acgcagtaaa	tacattagtg	480
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gatgacgaaa	tggtttacag	tgaatcacaa	ttaattgcga	aatttggtac	agcatttaaa	600
gctgtaaata	atagcttgaa	tgtaaacctc	ggcgcaatca	gtgaagggaa	aatgcaagaa	660
gaagtcatta	gttttaaaaca	aatttactat	aacgtgaatg	ttaatgaacc	tacaagacct	720
tccagatttt	tcggcaaagc	tgttactaaa	gagcagttgc	aagcgcttgg	agtgaatgca	780
gaaaatcctc	ctgcataatc	ctcaagtgtg	gcgtatggcc	gtcaagttta	tttgaaatta	840
tcaactaatt	cccatagtac	taaagtataa	gctgcttttg	atgctgccgt	aagcggaaaa	900
tctgtctcag	gtgatgtaga	actaacaat	atcatcaaaa	attcttcctt	caaagccgta	960
atttacggag	gttccgcaaa	agatgaagtt	caaatcatcg	acggcaacct	cggagactta	1020
cgcgatattt	tgaaaaaagg	cgctactttt	aatcgagaaa	caccaggagt	tcccattgct	1080
tatacaacaa	acttcctaaa	agacaatgaa	ttagctgtta	ttaaaaacaa	ctcagaatat	1140
attgaaacaa	cttcaaaagc	ttatacagat	ggaaaaatta	acatcgatca	ctctggagga	1200
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<210> 24
 <211> 415
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fragment

<400> 24

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1				5					10					15	

53161000003Sequence

Pro	Ile	Ala	Gln	Gln	Thr	Glu	Ala	Lys	Asp	Ala	Ser	Ala	Phe	Asn	Lys
		20						25					30		
Glu	Glu	Ile	Asp	Lys	Tyr	Ile	Gln	Gly	Leu	Asp	Tyr	Asn	Lys	Asn	Asn
		35					40					45			
Val	Leu	Val	Tyr	His	Gly	Asp	Ala	Val	Thr	Asn	Val	Pro	Pro	Arg	Lys
	50					55					60				
Gly	Tyr	Lys	Asp	Gly	Asn	Glu	Tyr	Ile	Val	Val	Glu	Lys	Lys	Lys	Lys
65					70					75					80
Ser	Ile	Asn	Gln	Asn	Asn	Ala	Asp	Ile	Gln	Val	Val	Asn	Ala	Ile	Ser
			85						90					95	
Ser	Leu	Thr	Tyr	Pro	Gly	Ala	Leu	Val	Lys	Ala	Asn	Ser	Glu	Leu	Val
			100					105					110		
Glu	Asn	Gln	Pro	Asp	Val	Leu	Pro	Val	Lys	Arg	Asp	Ser	Leu	Thr	Leu
		115					120					125			
Ser	Ile	Asp	Leu	Pro	Gly	Met	Thr	Asn	Gln	Asp	Asn	Lys	Ile	Val	Val
	130					135					140				
Lys	Asn	Ala	Thr	Lys	Ser	Asn	Val	Asn	Asn	Ala	Val	Asn	Thr	Leu	Val
145					150					155					160
Glu	Arg	Trp	Asn	Glu	Lys	Tyr	Ala	Gln	Ala	Tyr	Pro	Asn	Val	Ser	Ala
			165						170					175	
Lys	Ile	Asp	Tyr	Asp	Asp	Glu	Met	Ala	Tyr	Ser	Glu	Ser	Gln	Leu	Ile
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Ser	Arg	Phe	Phe	Gly	Lys	Ala	Val	Thr	Lys	Glu	Gln	Leu	Gln	Ala	Leu
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Gly	Val	Asn	Ala	Glu	Asn	Pro	Pro	Ala	Tyr	Ile	Ser	Ser	Val	Ala	Tyr
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Asp	Val	Glu	Leu	Thr	Asn	Ile	Ile	Lys	Asn	Ser	Ser	Phe	Lys	Ala	Val
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 35 40 45
 Glu Glu Gln Pro Ser Glu Val Asn Thr Gly Pro Arg Tyr Glu Thr Ala
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 Arg Glu Val Ser Ser Arg Asp Ile Glu Glu Leu Glu Lys Ser Asn Lys
 65 70 75 80
 Val Lys Asn Thr Asn Lys Ala Asp Leu Ile Ala Met Leu Lys Ala Lys
 85 90 95
 Ala Glu Lys Gly
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