

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.
Haruka Okamoto
Jesper Gromada

<120> Anti-Glucagon Antibodies and Uses
Thereof

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<150> 62/050,889

<151> 2014-09-16

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ccaggcaagg ggctggaatg ggtgacattt atatcatatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaagtga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagaagca 300
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Asn Tyr
 20          25          30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35          40          45
Thr Phe Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65          70          75          80
Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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Ala Lys Glu Ala Val Leu Ala Ala Leu Phe Asp Tyr Trp Gly Gln Gly
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 gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
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 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 Ser Asn Asn Gln Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

		35				40			45								
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val		
	50					55					60						
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr		
65					70					75					80		
Ile	Asn	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln		
				85					90					95			
Tyr	Tyr	Ser	Thr	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys		
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<400> 13
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ccagtcaagg ggctggagtg ggtggcattt atatcaaagc ataagagtaa tacattctat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgttt 240
ctggaaatga acagcctgac agctgaggac acggctgttt attactgtgc gaaagagtcc 300
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<400> 18

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Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asn	Thr	Tyr
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Val	Lys	Gly	Leu	Glu	Trp	Val
		35				40						45			
Ala	Phe	Ile	Ser	Asn	Asp	Lys	Ser	Asn	Thr	Phe	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe
65					70				75					80	
Leu	Glu	Met	Asn	Ser	Leu	Thr	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Lys	Glu	Ser	Ile	Leu	Ala	Ala	Leu	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105					110		
Thr	Leu	Val	Thr	Val	Ser	Ser									
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 Gly Phe Thr Phe Asn Thr Tyr Gly
 1 5

<210> 21
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<400> 21
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<210> 22
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<400> 22
Ile Ser Asn Asp Lys Ser Asn Thr
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tggtaccaac agaaaccaag acagcctctt aaactactca tttactgggc atctattcgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
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Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser
			20					25					30		
Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Arg	Gln
		35					40					45			
Pro	Leu	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Ile	Arg	Glu	Ser	Gly	Val
	50				55						60				
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
65					70					75					80
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln
				85					90					95	
Phe	Tyr	Ser	Val	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
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<400> 31
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<400> 32
Gln Gln Phe Tyr Ser Val Pro Thr
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ccagtcaagg ggctggagtg ggtggctttt atatcaaatg ataagaataa taaattctat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaggga cagctatat 240
ctgcaaatga acagcctgac acctgaggac acggctgttt attactgtgc gaaagagtcc 300

attttagcag ccctctttga ctactggggc caggggaaccc tggtcaccgt ctctca 357

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20 25 30
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35 40 45
Ala Phe Ile Ser Asn Asp Lys Asn Asn Lys Phe Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asp Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Thr Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
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Gly Phe Thr Phe Ser Thr Phe Gly
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 <400> 37
 atatcaaagt ataagaataa taaa 24

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 Ile Ser Asn Asp Lys Asn Asn Lys
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 Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr
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tggtaccagc agaaaccagg acagcctctt aaacttctca tttactgggc atctattcgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaatt ttatactggt 300
cccacttttg gcctggggac caagctggag atcaaa 336

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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Leu Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Phe Tyr Thr Val Pro Thr Phe Gly Leu Gly Thr Lys Leu Glu Ile Lys
100 105 110

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1 5 10

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Gln Gln Phe Tyr Thr Val Pro Thr
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<400> 49

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cctggcaagg ggctggaatg ggtggcagtt acatcatctg atggacttaa taaattctat 180
tcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtct 240
ctgcaaatta cgggcctgag agctgaggac acggctgtgt attactgtgc gaaagagtcc 300
atattagcag ccctctttga ctactggggc caggaaccc tggtcaccgt ctctca 357
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<400> 50

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 1          5          10          15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Tyr
 20          25          30
Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35          40          45
Ala Val Thr Ser Ser Asp Gly Leu Asn Lys Phe Tyr Ser Asp Ser Val
 50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser
 65          70          75          80
Leu Gln Ile Thr Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85          90          95
Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr Trp Gly Gln Gly
 100          105          110
Thr Leu Val Thr Val Ser Ser
 115
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1 5

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<210> 54
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<400> 54
Thr Ser Ser Asp Gly Leu Asn Lys
1 5

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<400> 56

Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr
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 tggtaccagc agaaaccagg acagcctcct aagctgctct ttactgggc atctaccgg 180
 gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
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 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Phe Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 His Tyr Thr Thr Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

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36

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1 5 10

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<400> 61
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ccgggcaagg ggctggagtg ggtggcattt atatcatatg atggaaataa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgttt 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagagtcc 300
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
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Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 69
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 69
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24

<210> 70
<211> 8
<212> PRT
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<220>
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<400> 70
Ile Ser Tyr Asp Gly Asn Asn Lys
1 5

<210> 71
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 71

gcgaaagagt ccattttagc agccctcttt gactac

36

<210> 72

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

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<400> 72

Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr

1

5

10

<210> 73

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 73

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atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120
tggtaccagc agaaacctgg acagcctcct aagctgctca tttactgggc atctaccggg 180
gaatccggggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca ctttattact gtcaacaata ttataatact 300
cccacttttg gccaggggac caagctggag atcaaa 336

<210> 74

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 74

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Leu Tyr Tyr Cys Gln Gln
85 90 95
Tyr Tyr Asn Thr Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 75
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 75
cagagtgttt tatacagctc caacaataag aactac

36

<210> 76
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 76
Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 77
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 77
tgggcatct

9

<210> 78
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 78
Trp Ala Ser
1

<210> 79
<211> 24
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<220>
<223> Synthetic

<400> 79
caacaatatt ataatactcc cact

24

<210> 80
<211> 8
<212> PRT
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<220>
<223> Synthetic

<400> 80
Gln Gln Tyr Tyr Asn Thr Pro Thr
1 5

<210> 81
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 81
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tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccagggt 120
ccagtcaagg ggctggagtg ggtggcattt atatcatatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctccaaatga acagcctgac agctgaggac acggctgttt attactgtgc gaaagagtcc 300
attttagcag ccctctttga ctactggggc cagggaaccc tggtcaccgt ctctca 357

<210> 82
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 82
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Val Lys Gly Leu Glu Trp Val
35 40 45
Ala Phe Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu	Gln	Met	Asn	Ser	Leu	Thr	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Lys	Glu	Ser	Ile	Leu	Ala	Ala	Leu	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105					110		
Thr	Leu	Val	Thr	Val	Ser	Ser									
			115												

<210> 83
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 83
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24

<210> 84
 <211> 8
 <212> PRT
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<220>
 <223> Synthetic

<400> 84
 Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

<210> 85
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 85
 atatcatatg atggaagtaa taaa

24

<210> 86
 <211> 8
 <212> PRT
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<220>
 <223> Synthetic

<400> 86
 Ile Ser Tyr Asp Gly Ser Asn Lys
 1 5

<210> 87
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 87
 gcgaaagagt ccattttagc agccctcttt gactac 36

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

<220>
 <223> Synthetic

<400> 88
 Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr
 1 5 10

<210> 89
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 89
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 atcaactgca agtccagcca gagtggttta tacagttcca acaataagaa ctacttagct 120
 tggtagcagc agaaaccaag acagcctcct aagctgctca tttactgggc atctattcgg 180
 gaatccggggg tccctgaccg attcagtggc agcgggtctg ggacagattt cattctcacc 240
 atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaatt ttatagtatt 300
 cccacttttg gccaggggac caagctggag atcaaa 336

<210> 90
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 90
 Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser

			20					25					30				
Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Arg	Gln		
		35					40					45					
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Ile	Arg	Glu	Ser	Gly	Val		
	50					55					60						
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Ile	Leu	Thr		
65					70					75					80		
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln		
			85						90					95			
Phe	Tyr	Ser	Ile	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
			100					105					110				

<210> 91
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 91
 cagagtgttt tatacagttc caacaataag aactac

36

<210> 92
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 92
 Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
 1 5 10

<210> 93
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 93
 tgggcatct

9

<210> 94
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 94
Trp Ala Ser
1

<210> 95
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 95
cagcaatttt atagtattcc cact 24

<210> 96
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 96
Gln Gln Phe Tyr Ser Ile Pro Thr
1 5

<210> 97
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 97
caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttttagt agctatggca tgcactgggt ccgccaggct 120
ccagtcaagg ggctggagtg ggtggcatTTT atatcaaTg ataaaagTaa taaatattat 180
gcagactcct tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaTga acagcctgac agctgaagac acggctgttt attactgtgc gaaagagtcc 300
attttagcag ccctctttga ctattggggc cagggaaacc tggtcaccgt ctctca 357

<210> 98
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 98
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Val Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Phe Ile Ser Asn Asp Lys Ser Asn Lys Tyr Tyr Ala Asp Ser Leu
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Thr Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 99
 ggattcacct ttagtagcta tggc

24

<210> 100
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 100
 Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

<210> 101
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 101
 atatcaaatg ataaaagtaa taaa

24

<210> 102
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 102
 Ile Ser Asn Asp Lys Ser Asn Lys
 1 5

<210> 103
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 103
 gcgaaagagt ccattttagc agccctcttt gactat 36

<210> 104
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 104
 Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr
 1 5 10

<210> 105
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 105
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 atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120
 tggtagcagc agaaaccaag acagcctcct aagctactca tttactgggc atctattcgg 180
 gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
 atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaatt ttatagtgtt 300
 cccacttttg gccaggggac caagctggag atcaaa 336

<210> 106

<211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 106
 Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Arg Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 Phe Tyr Ser Val Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 107
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 107
 cagagtgttt tatacagctc caacaataag aactac

36

<210> 108
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 108
 Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
 1 5 10

<210> 109
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 109
tgggcatct

9

<210> 110
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 110
Trp Ala Ser
1

<210> 111
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 111
caacaatttt atagtgttcc cact

24

<210> 112
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 112
Gln Gln Phe Tyr Ser Val Pro Thr
1 5

<210> 113
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 113
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tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
ccagtcaagg ggctggagtg ggtggcattt atatcatttg atggaagtaa taaatactat 180

acagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctccaaatga acagcctgac agctgaggac acggctatattt attactgtgc gaaagagtcc 300
 attttagcag ccctctttga ctactggggc caggggaaccc tggtcactgt ctctca 357

<210> 114
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 114
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Val Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Phe Ile Ser Phe Asp Gly Ser Asn Lys Tyr Tyr Thr Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Thr Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 115
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 115
 ggattcacct tcagtagcta tggc 24

<210> 116
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 116
 Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

<210> 117
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 117
atatcatttg atggaagtaa taaa

24

<210> 118
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 118
Ile Ser Phe Asp Gly Ser Asn Lys
1 5

<210> 119
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 119
gcgaaagagt ccattttagc agccctcttt gactac

36

<210> 120
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 120
Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr
1 5 10

<210> 121
<211> 336
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 121

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atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120
tggtaccagc agaaaccaag acagcctcct aacctgctca tttactgggc atctattcgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca ttttattact gtcagcaatt ttatagtatt 300
cccacttttg gccaggggac caagctggag atcaaa 336
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<210> 122

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 122

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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
      20           25           30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Arg Gln
      35           40           45
Pro Pro Asn Leu Leu Ile Tyr Trp Ala Ser Ile Arg Glu Ser Gly Val
      50           55           60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65           70           75           80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Phe Tyr Tyr Cys Gln Gln
      85           90           95
Phe Tyr Ser Ile Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
      100          105          110
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<210> 123

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 123

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<210> 124

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 124
 Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
 1 5 10

<210> 125
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 125
 tgggcatct

9

<210> 126
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 126
 Trp Ala Ser
 1

<210> 127
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 127
 cagcaatttt atagtattcc cact

24

<210> 128
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 128
 Gln Gln Phe Tyr Ser Ile Pro Thr
 1 5

<210> 129

<211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 129
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 tcctgtgcag cctctggatt caccttttagg acctatggca tgcactgggt ccgccaggct 120
 ccagtcaagg ggctggagtg ggtggcattt atatcaaagg atggaagtga taaatactat 180
 gtagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgttt 240
 ctgcaaatga acagcctgac agctgaggac acggctgttt attattgtgc gaaagagtcc 300
 attttagcag ccctctttga ctactggggc caggggaacc tggtcactgt ctctca 357

<210> 130
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 130
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Thr Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Val Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Phe Ile Ser Lys Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 65 70 75 80
 Leu Gln Met Asn Ser Leu Thr Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 131
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 131
 ggattcacct ttaggaccta tggc

24

<210> 132
 <211> 8

<212> PRT
<213> Artificial Sequence

<220>
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<400> 132
Gly Phe Thr Phe Arg Thr Tyr Gly
1 5

<210> 133
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 133
atatcaaagg atggaagtga taaa

24

<210> 134
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 134
Ile Ser Lys Asp Gly Ser Asp Lys
1 5

<210> 135
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 135
gcgaaagagt ccattttagc agccctcttt gactac

36

<210> 136
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 136
Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Tyr
1 5 10

<210> 137
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
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<400> 137
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atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120
tggtaccagc agaaaccaag acagcctcct aaactcctca ttactgggc atctaatacgg 180
gaatccggggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaatt ttatagtgtt 300
cccacttttg gccaggggac caagctggag atcaaa 336

<210> 138
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 138
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Arg Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Asn Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Phe Tyr Ser Val Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 139
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 139
cagagtgttt tatacagctc caacaataag aactac

36

<210> 140
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 140
Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 141
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 141
tgggcatct

9

<210> 142
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 142
Trp Ala Ser
1

<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 143
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24

<210> 144
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<400> 144

Gln Gln Phe Tyr Ser Val Pro Thr
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<210> 145

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 145

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tcctgtgcag cctctggatt caccttttagt agctatggca tgcactgggt ccgccaggct 120
ccagtcaagg ggctggagtg ggtggcattt atatcaaagta ataaaagtaa taaatactat 180
gcagactccg tgaaggggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaataga acagcctgac agctgaggac acggctgttt attactgtgc gaaagagtcc 300
atttttagcag ccctctttga ctcctggggc caggggaaccc tggtcaccgt ctcctca 357

<210> 146

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 146

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Val Lys Gly Leu Glu Trp Val
35 40 45
Ala Phe Ile Ser Asn Asp Lys Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Thr Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Ser Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 147

<211> 24

<212> DNA
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<220>
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<400> 147
ggattcacct ttagtagcta tggc

24

<210> 148
<211> 8
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<220>
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<400> 148
Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 149
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic

<400> 149
atatcaaatg ataaaagtaa taaa

24

<210> 150
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<212> PRT
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<220>
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<400> 150
Ile Ser Asn Asp Lys Ser Asn Lys
1 5

<210> 151
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 151
gcgaaagagt ccatttttagc agccctcttt gactcc 36

<210> 152
<211> 12
<212> PRT
<213> Artificial Sequence

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<400> 152
Ala Lys Glu Ser Ile Leu Ala Ala Leu Phe Asp Ser
1 5 10

<210> 153
<211> 336
<212> DNA
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<400> 153
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tggtaccagc agaaaccaag acagcctcct aagctgctca tttactgggc atctattcgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg gggcagattt cactctcacc 240
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cccacttttg gccaggggac caagctggag atcaaa 336

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<211> 112
<212> PRT
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<220>
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<400> 154
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Arg Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Ala Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Phe Tyr Ser Val Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

100

105

110

<210> 155
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<212> DNA
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<220>
<223> Synthetic

<400> 155
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36

<210> 156
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 156
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1 5 10

<210> 157
<211> 9
<212> DNA
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<400> 157
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9

<210> 158
<211> 3
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<400> 158
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<210> 159
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<220>

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<400> 159

cagcaatttt atagtgttcc cact

24

<210> 160

<211> 8

<212> PRT

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<220>

<223> Synthetic

<400> 160

Gln Gln Phe Tyr Ser Val Pro Thr

1

5

<210> 161

<211> 29

<212> PRT

<213> Artificial Sequence

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<223> GCG mature peptide: aa 53-81 of NP_002045.1

<400> 161

His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Ser

1

5

10

15

Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr

20

25

<210> 162

<211> 2076

<212> DNA

<213> Artificial Sequence

<220>

<223> PCSK9 DNA

<400> 162

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gctggtgcta gccttgcggt ccgaggagga cggcctggcc gaagcaccg agcacggaac 180
cacagccacc ttccaccgct gcgccaagga tccgtggagg ttgcctggca cctacgtggt 240
ggtgctgaag gaggagaccc acctctcgca gtcagagcgc actgcccgcc gcctgcaggc 300
ccaggctgcc cgccggggat acctcaccaa gatcctgcat gtcttccatg gccttcttcc 360
tggtctcctg gtgaagatga gtggcgacct gctggagctg gccttgaagt tgccccatgt 420
cgactacatc gaggaggact cctctgtctt tgcccagagc atcccgtgga acctggagcg 480
gattaccctt ccacggtacc gggcgggatga ataccagccc cccgacggag gcagcctggt 540

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ggaggtgtat ctcctagaca ccagcataca gagtgaccac cgggaaatcg agggcagggg 600
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cagcaagtgt gacagtcagt gcacccacct ggcaggggtg gtcagcggcc gggatgccgg 720
cgtggccaag ggtgccagca tgcgcagcct gcgctgtctc aactgccaaag ggaagggcac 780
ggtttagcggc accctcatag gcctggagtt tattcgaaa agccagctgg tccagcctgt 840
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gtcagcacta caggcagcac cagcgaagag gccgtgacag ccgttgccat ctgctgccgg 2040
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<210> 163
<211> 693
<212> PRT
<213> Artificial Sequence

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<220>
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<400> 163
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Glu Asp Glu Asp Gly Asp Tyr Glu Leu Val Leu Ala Leu Arg Ser
35          40          45
Glu Glu Asp Gly Leu Ala Glu Ala Pro Glu His Gly Thr Thr Ala Thr
50          55          60
Phe His Arg Cys Ala Lys Asp Pro Trp Arg Leu Pro Gly Thr Tyr Val
65          70          75          80
Val Val Leu Lys Glu Thr His Leu Ser Gln Ser Glu Arg Thr Ala
85          90          95
Arg Arg Leu Gln Ala Gln Ala Ala Arg Arg Gly Tyr Leu Thr Lys Ile
100         105         110
Leu His Val Phe His Gly Leu Leu Pro Gly Phe Leu Val Lys Met Ser
115         120         125
Gly Asp Leu Leu Glu Leu Ala Leu Lys Leu Pro His Val Asp Tyr Ile
130         135         140
Glu Glu Asp Ser Ser Val Phe Ala Gln Ser Ile Pro Trp Asn Leu Glu
145         150         155         160
Arg Ile Thr Pro Pro Arg Tyr Arg Ala Asp Glu Tyr Gln Pro Pro Asp

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		195					200					205					
Val	Pro	Glu	Glu	Asp	Gly	Thr	Arg	Phe	His	Arg	Gln	Ala	Ser	Lys	Cys		
	210				215						220						
Asp	Ser	His	Gly	Thr	His	Leu	Ala	Gly	Val	Val	Ser	Gly	Arg	Asp	Ala		
225				230						235				240			
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			245						250					255			
Gln	Gly	Lys	Gly	Thr	Val	Ser	Gly	Thr	Leu	Ile	Gly	Leu	Glu	Phe	Ile		
			260					265					270				
Arg	Lys	Ser	Gln	Leu	Val	Gln	Pro	Val	Gly	Pro	Leu	Val	Val	Leu	Leu		
		275					280					285					
Pro	Leu	Ala	Gly	Gly	Tyr	Ser	Arg	Val	Leu	Asn	Ala	Ala	Cys	Gln	Arg		
	290					295					300						
Leu	Ala	Arg	Ala	Gly	Val	Val	Leu	Val	Thr	Ala	Ala	Gly	Asn	Phe	Arg		
305				310						315					320		
Asp	Asp	Ala	Cys	Leu	Tyr	Ser	Pro	Ala	Ser	Ala	Pro	Glu	Val	Ile	Thr		
			325						330					335			
Val	Gly	Ala	Thr	Asn	Ala	Gln	Asp	Gln	Pro	Val	Thr	Leu	Gly	Thr	Leu		
			340					345					350				
Gly	Thr	Asn	Phe	Gly	Arg	Cys	Val	Asp	Leu	Phe	Ala	Pro	Gly	Glu	Asp		
		355					360					365					
Ile	Ile	Gly	Ala	Ser	Ser	Asp	Cys	Ser	Thr	Cys	Phe	Val	Ser	Gln	Ser		
	370					375					380						
Gly	Thr	Ser	Gln	Ala	Ala	Ala	His	Val	Ala	Gly	Ile	Ala	Ala	Met	Met		
385				390						395				400			
Leu	Ser	Ala	Glu	Pro	Glu	Leu	Thr	Leu	Ala	Glu	Leu	Arg	Gln	Arg	Leu		
			405						410					415			
Ile	His	Phe	Ser	Ala	Lys	Asp	Val	Ile	Asn	Glu	Ala	Trp	Phe	Pro	Glu		
		420						425					430				
Asp	Gln	Arg	Val	Leu	Thr	Pro	Asn	Leu	Val	Ala	Ala	Leu	Pro	Pro	Ser		
		435					440					445					
Thr	His	Gly	Ala	Gly	Trp	Gln	Leu	Phe	Cys	Arg	Thr	Val	Trp	Ser	Ala		
	450				455						460						
His	Ser	Gly	Pro	Thr	Arg	Met	Ala	Thr	Ala	Ile	Ala	Arg	Cys	Ala	Pro		
465				470						475				480			
Asp	Glu	Glu	Leu	Leu	Ser	Cys	Ser	Ser	Phe	Ser	Arg	Ser	Gly	Lys	Arg		
			485						490					495			
Arg	Gly	Glu	Arg	Met	Glu	Ala	Gln	Gly	Gly	Lys	Leu	Val	Cys	Arg	Ala		
		500						505					510				
His	Asn	Ala	Phe	Gly	Gly	Glu	Gly	Val	Tyr	Ala	Ile	Ala	Arg	Cys	Cys		
	515						520					525					
Leu	Leu	Pro	Gln	Ala	Asn	Cys	Ser	Val	His	Thr	Ala	Pro	Pro	Ala	Glu		
	530					535					540						
Ala	Ser	Met	Gly	Thr	Arg	Val	His	Cys	His	Gln	Gly	His	Val	Leu			
545				550						555				560			
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		580						585					590				
Arg	Glu	Ala	Ser	Ile	His	Ala	Ser	Cys	Cys	His	Ala	Pro	Gly	Leu	Glu		
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Cys	Lys	Val	Lys	Glu	His	Gly	Ile	Pro	Ala	Pro	Gln	Glu	Gln	Val	Thr		
	610					615					620						
Val	Ala	Cys	Glu	Glu	Gly	Trp	Thr	Leu	Thr	Gly	Cys	Ser	Ala	Leu	Pro		

625					630					635					640
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Val	Arg	Ser	Arg	Asp	Val	Ser	Thr	Thr	Gly	Ser	Thr	Ser	Glu	Glu	Ala
			660					665					670		
Val	Thr	Ala	Val	Ala	Ile	Cys	Cys	Arg	Ser	Arg	His	Leu	Ala	Gln	Ala
		675					680					685			
Ser	Gln	Glu	Leu	Gln											
	690														