

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> Anti-C5 Antibodies and Uses Thereof

<130> 10168W001

<150> 62/349,705

<151> 2016-06-14

<150> 62/405,561

<151> 2016-10-07

<150> 62/422,107

<151> 2016-11-15

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tcagactccg tgaagggccg attcatcatc tccagagaca attccaggaa gacagtgtat 240
ctgcaaatga acagcctgag aggcgaggac acggctgttt attactgtgc gagagatgcc 300
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Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Tyr
             20             25             30
Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
             35             40             45
Ala Val Ile Trp Asp Asp Gly Asn Asn Ile Asn Tyr Ser Asp Ser Val
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Leu	Gln	Met	Asn	Ser	Leu	Arg	Gly	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
				85					90					95			
Ala	Arg	Asp	Ala	Pro	Ile	Ala	Pro	Val	Pro	Asp	Tyr	Trp	Gly	Gln	Gly		
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aggttcagcg gcagtggatc tgggacagag ttcactctca ccatcagcag cctgcagcct 240
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			20					25				30			
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Lys	Ala	Ser	Ser	Leu	Asp	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80
Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Thr	Tyr	Ser	Tyr
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ccagggaagg	ggctggagtg	ggtttcatat	attagcagta	gtggtaatac	cataaaatat	180
gcagactcta	tgaagggccg	attcaccatc	tccagggaca	acgccaagaa	atcactgttt	240
gtggaaatga	acagcctgag	agccgaggac	acggccgtgt	attactgtgc	gaggtataaa	300
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30
 Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Tyr Ile Ser Ser Ser Gly Asn Thr Ile Lys Tyr Ala Asp Ser Met
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Phe
 65 70 75 80
 Val Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Tyr Lys Ser Ser Ser Asp Tyr Phe Asp His Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
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24

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<220>
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<400> 20
 Gly Phe Thr Phe Ser Asp Tyr Tyr
 1 5

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<400> 21
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Ala Arg Tyr Lys Ser Ser Ser Asp Tyr Phe Asp His
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ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgc catcccagcc 180
aggttcagtg gcagtggtgc tgggacagac ttcactctca ccatcagcag cctagagcct 240
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Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Arg	Ser	Tyr
			20					25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile
		35					40					45			
Tyr	Asp	Ala	Ser	Asn	Arg	Ala	Thr	Ala	Ile	Pro	Ala	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro
65					70					75				80	
Glu	Asp	Leu	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Ser	Gly	Asn	Trp	Pro	Leu
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

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Asp Ala Ser

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<210> 31

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<212> DNA

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<210> 32

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Gln Gln Ser Gly Asn Trp Pro Leu Thr

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5

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ccaggcaagg ggctggagtg ggtggcagtt atctgggatg atggaaataa taaatattat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attcgaagaa cacgctgtat 240
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 Ser Leu Arg Leu Ser Cys Gly Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Trp Asp 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 Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Ser Glu Val Ala Pro Val Gly Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
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<400> 36
 Gly Phe Thr Phe Ser Thr Tyr Gly
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<210> 38

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<400> 38

Ile Trp Asp Asp Gly Asn Asn Lys
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<210> 39

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<212> DNA

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Ala Arg Asp Ser Glu Val Ala Pro Val Gly Asp Tyr
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gggaaggccc ctaaactcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
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		20					25						30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35				40						45			
Tyr	Lys	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55				60					
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65				70				75						80	
Asp	Asp	Phe	Ala	Ala	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Asp	Tyr	Ser	Tyr
			85					90						95	
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys					
			100					105							

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ccagggaagg ggctggactg gattggccgt attagaaaca aagctaacgc ttataacaca 180
gaatacgccg cgtctgtgag aggcagattc accatctcaa gagatgattc acagaattta 240
ctgtatctgc aaatgaacag cctgaaaacc gatgacacgg ccgtatatta ttgtgttaga 300
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp His
20 25 30
Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Ile
35 40 45
Gly Arg Ile Arg Asn Lys Ala Asn Ala Tyr Asn Thr Glu Tyr Ala Ala
50 55 60
Ser Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Gln Asn Leu
65 70 75 80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Asp Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Val Arg Val Trp Asn Tyr Ala Tyr Phe Ala Met Asp Val Trp
100 105 110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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<400> 52
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ggggaagccc ctaacctcct gatctccgct gcatccagtt tacacagtgg ggtcccttca 180
aggttcagtg gcagtgggtc tgggacagat ttcactctca ccatcggcag tctgcagcct 240
gaagattttg cgacttacta ctgtcaacag acgtacaata ccatattcac tttcggccct 300
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Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Asn Leu Leu Ile
35 40 45
Ser Ala Ala Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Gly Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asn Thr Ile Phe
85 90 95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

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 ccagggaagg gactggagtg ggtctcagct attagtggtc gtggtgatag tacatactac 180
 gcagactccg tgaagggccg gctcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag agccgaggac acggccgtat attactgtgt gaaagagggg 300
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 35 40 45
 Ser Ala Ile Ser Gly Arg Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Leu Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Lys Glu Gly Glu Gln Leu Val Tyr Trp Tyr Phe Asp Leu Trp Gly
 100 105 110
 Arg Gly Thr Leu Val Thr Val Ser Ser
 115 120

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1 5

<210> 69
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24

<210> 70
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<213> Artificial Sequence

<220>
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<400> 70
Ile Ser Gly Arg Gly Asp Ser Thr
1 5

<210> 71
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
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<400> 71
gtgaaagagg gggagcaact cgtctactgg tacttcgatc tc

42

<210> 72
<211> 14
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<213> Artificial Sequence

<220>

<223> synthetic

<400> 72

Val Lys Glu Gly Glu Gln Leu Val Tyr Trp Tyr Phe Asp Leu
1 5 10

<210> 73

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 73

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atcacttgcc gggcaagtca gaccattagc aactttttac attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttt caacttactt ctgtcaacag agttacacta ccccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 74

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 74

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

<210> 75

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 75
cagaccatta gcaacttt 18

<210> 76
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 76
Gln Thr Ile Ser Asn Phe
1 5

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

<220>
<223> synthetic

<400> 77
gctgcatcc 9

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

<220>
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<400> 78
Ala Ala Ser
1

<210> 79
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 79
caacagagtt acactacccc gctcact 27

<210> 80
<211> 9
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<213> Artificial Sequence

<220>

<223> synthetic

<400> 80

Gln Gln Ser Tyr Thr Thr Pro Leu Thr

1

5

<210> 81

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 81

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tcctgtgcag cctctggatt cacctttaac agatatgcca tgacctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct ataagtggta gtggtagcag cacatactac 180
acagactccg tgaaaggccg gttcaccatc tccagagaca attccaagaa ttcggtggat 240
ctgcaaatgc acagcctgag agtcgaagac acggccatat attattgtgc gagaggggact 300
acagtcacta cgggggtacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 360
tca 363
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<210> 82

<211> 121

<212> PRT

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<220>

<223> synthetic

<400> 82

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 1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Arg Tyr
 20          25          30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35          40          45
Ser Ala Ile Ser Gly Ser Gly Ser Ser Thr Tyr Tyr Thr Asp Ser Val
 50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Val Asp
 65          70          75          80
Leu Gln Met His Ser Leu Arg Val Glu Asp Thr Ala Ile Tyr Tyr Cys
 85          90          95
Ala Arg Gly Thr Thr Val Thr Thr Gly Tyr Gly Met Asp Val Trp Gly
100          105          110
Gln Gly Thr Thr Val Thr Val Ser Ser
115          120
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<210> 83

<211> 24
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<220>
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<400> 83
ggattcacct ttaacagata tgcc

24

<210> 84
<211> 8
<212> PRT
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<220>
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<400> 84
Gly Phe Thr Phe Asn Arg Tyr Ala
1 5

<210> 85
<211> 24
<212> DNA
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<220>
<223> synthetic

<400> 85
ataagtggta gtggtagcag caca

24

<210> 86
<211> 8
<212> PRT
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<220>
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<400> 86
Ile Ser Gly Ser Gly Ser Ser Thr
1 5

<210> 87
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 87
gcgagagggga ctacagtcac tacggggtac ggtatggacg tc 42

<210> 88
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 88
Ala Arg Gly Thr Thr Val Thr Thr Gly Tyr Gly Met Asp Val
1 5 10

<210> 89
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 89
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
ttcacttgcc aggcgagtca ggacattacc aattctttaa attggtatca acagaaacct 120
gggagagccc ctaagctcct gatctacgat gcatcgtatt tgaaggcagg ggtcccatca 180
agattcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240
gaagatattg caacatatta ctgtcaacaa tatgatgac tcccatacac ttttggccag 300
gggaccaagc tggagatcaa a 321

<210> 90
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

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

<210> 91
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 91
caggacatta ccaattct

18

<210> 92
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 92
Gln Asp Ile Thr Asn Ser
1 5

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

<220>
<223> synthetic

<400> 93
gatgcatcg

9

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

<220>
<223> synthetic

<400> 94
Asp Ala Ser
1

<210> 95
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 95

caacaatatg atgatctccc atacact

27

<210> 96

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 96

Gln Gln Tyr Asp Asp Leu Pro Tyr Thr

1

5

<210> 97

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 97

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtga ctccgtcagt agttcctact ggacctggat ccggcagccc 120
ccagggaagg gactggagtg gattggctat atctattaca gtgggagttc caactacaac 180
ccctccctca agagtcgagc caccatttca gtagacacgt ccaagaacca gttctccctg 240
aagctgagtt ctgtgaccgc tgcggacacg gccgtatatt actgtgagag agaagggaac 300
gtggatacaa ctatgatatt tgactactgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 98

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 98

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

Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85					90					95	
Arg	Glu	Gly	Asn	Val	Asp	Thr	Thr	Met	Ile	Phe	Asp	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
		115					120								

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

<220>
 <223> synthetic

<400> 99
 ggtgactccg tcagtagttc ctac

24

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

<220>
 <223> synthetic

<400> 100
 Gly Asp Ser Val Ser Ser Ser Tyr
 1 5

<210> 101
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 101
 atctattaca gtgggagttc c

21

<210> 102
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 102
 Ile Tyr Tyr Ser Gly Ser Ser
 1 5

<210> 103
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 103
gcgagagaag ggaacgtgga tacaactatg atatttgact ac 42

<210> 104
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 104
Ala Arg Glu Gly Asn Val Asp Thr Thr Met Ile Phe Asp Tyr
1 5 10

<210> 105
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 105
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atcacttgcc gggcaagtca gggcattaga aatgatttag gctggatatca acagaaacca 120
gggaaagccc ctaaactcct gatctatgct gcatccagtt taaaaagtgg ggtcccatcg 180
aggttcgccg gccgtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacaa gatttcaatt acccgtggac gttcggccaa 300
gggaccaagg tggaatcaa a 321

<210> 106
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 106
Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

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

<210> 107
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 107
 cagggcatta gaaatgat 18

<210> 108
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 108
 Gln Gly Ile Arg Asn Asp
 1 5

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

<220>
 <223> synthetic

<400> 109
 gctgcatcc 9

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

<220>
 <223> synthetic

<400> 110

Ala Ala Ser
1

<210> 111
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 111
ctacaagatt tcaattaccc gtggacg 27

<210> 112
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 112
Leu Gln Asp Phe Asn Tyr Pro Trp Thr
1 5

<210> 113
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 113
gccatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca acagaaacca 120
gggaaagccc ctaaactcct gatctatgct gcatccagtt tacaaagtgg ggtcccatcg 180
aggttcgccg gccgtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcatcaa gatttcaatt acccgtggac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 114
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 114
Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

<210> 115
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 115
 cagggcatta gaaatgat

18

<210> 116
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 116
 Gln Gly Ile Arg Asn Asp
 1 5

<210> 117
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 117
 gctgcatcc

9

<210> 118
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 118

Ala Ala Ser

1

<210> 119

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 119

catcaagatt tcaattaccc gtggacg

27

<210> 120

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 120

His Gln Asp Phe Asn Tyr Pro Trp Thr

1

5

<210> 121

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 121

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtga ctccgtcagt agttcctact ggacctggat ccggcagccc 120
ccagggaagg gactggagtg gattggctat atctattaca gtgggagttc caactacaac 180
ccctccctca agagtcgagc caccatttca gtagacacgt ccaagaacca gttctccctg 240
aagctgagtt ctgtgaccgc tgcggacacg gccgtatatt actgtgagag agaacataac 300
gtggatacaa ctatgatatt tgactactgg ggccaggga ccctgggtcac cgtctcctca 360

<210> 122

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 122
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Val Ser Ser Ser
 20 25 30
 Tyr Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Tyr Ser Gly Ser Ser Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Glu His Asn Val Asp Thr Thr Met Ile Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 123
 ggtgactccg tcagtagttc ctac 24

<210> 124
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 124
 Gly Asp Ser Val Ser Ser Ser Tyr
 1 5

<210> 125
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 125
 atctattaca gtgggagttc c 21

<210> 126
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 126
Ile Tyr Tyr Ser Gly Ser Ser
1 5

<210> 127
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 127
gcgagagaac ataacgtgga tacaactatg atatttgact ac 42

<210> 128
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 128
Ala Arg Glu His Asn Val Asp Thr Thr Met Ile Phe Asp Tyr
1 5 10

<210> 129
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 129
gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca acagaaacca 120
gggaaagccc ctaaactcct gatctatgct gcatccagtt tacaaagtgg ggtcccatcg 180
aggttcgccg gccgtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacaa gatttcaatt acccgtggca cttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 130
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

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

<210> 131
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 131
cagggcatta gaaatgat 18

<210> 132
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 132
Gln Gly Ile Arg Asn Asp
1 5

<210> 133
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 133
gctgcatcc

9

<210> 134
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
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<400> 134
Ala Ala Ser
1

<210> 135
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 135
ctacaagatt tcaattaccc gtggcac

27

<210> 136
<211> 9
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<220>
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<400> 136
Leu Gln Asp Phe Asn Tyr Pro Trp His
1 5

<210> 137
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
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<400> 137
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtga ctccgtcagt agttcctact ggacctggat ccggcagccc 120
ccagggaagg gactggagtg gattggctat atctattaca gtgggagttc caactacaac 180
ccctccctca agagtcgagc caccatttca gtagacacgt ccaagaacca gttctccctg 240
aagctgagtt ctgtgaccgc tgcggacacg gccgtatatt actgtgagag agaagggaac 300
gtggatacaa ctatgatata tgactactgg ggccaggga ccttggtcac cgtctcctca 360

<210> 138
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 138
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Val Ser Ser Ser
 20 25 30
 Tyr Trp Thr Trp Ile Arg Gln Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Tyr Ser Gly Ser Ser Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Glu Gly Asn Val Asp Thr Thr Met Ile His Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 139
 ggtgactccg tcagtagttc ctac

24

<210> 140
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 140
 Gly Asp Ser Val Ser Ser Ser Tyr
 1 5

<210> 141
 <211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 141
atctattaca gtgggagttc c

21

<210> 142
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 142
Ile Tyr Tyr Ser Gly Ser Ser
1 5

<210> 143
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 143
gcgagagaag ggaacgtgga tacaactatg atacatgact ac

42

<210> 144
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 144
Ala Arg Glu Gly Asn Val Asp Thr Thr Met Ile His Asp Tyr
1 5 10

<210> 145
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 145

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
 acctgcactg tctctggtga ctccgtcagt agttcctact ggacctggat ccggcagccc 120
 ccagggaagg gactggagtg gattggctat atctattaca gtgggagttc caactacaac 180
 ccctccctca agagtcgagc caccatttca gtagacacgt ccaagaacca gttctccctg 240
 aagctgagtt ctgtgaccgc tgcggacacg gccgtatatt actgtgagag agaaggggaa 300
 gtggatcaca ctatgatatt tgactactgg ggccaggga ccttggtcac cgtctcctca 360

<210> 146
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 146
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Val Ser Ser Ser
 20 25 30
 Tyr Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Tyr Ser Gly Ser Ser Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Glu Gly Asn Val Asp His Thr Met Ile Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 147
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 147
 ggtgactccg tcagtagttc ctac 24

<210> 148
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 148

Gly Asp Ser Val Ser Ser Ser Tyr
1 5

<210> 149
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 149
atctattaca gtgggagttc c 21

<210> 150
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 150
Ile Tyr Tyr Ser Gly Ser Ser
1 5

<210> 151
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 151
gcgagagaag ggaacgtgga tcacactatg atatttgact ac 42

<210> 152
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 152
Ala Arg Glu Gly Asn Val Asp His Thr Met Ile Phe Asp Tyr
1 5 10

<210> 153
<211> 360
<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 153

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caggtgcagc  tgggtggagtc  tggggggaggc  ttgggtcaagc  ctggagggtc  cctgagactc  60
tcctgtgcag  cctctggatt  caccttcagt  gactcctaca  tgtcctggat  ccgtcaggct  120
ccagggaagg  gactagagtg  gatttcatac  attggtagta  gtggtaatac  cttttactac  180
gcagactctg  tgaagggccg  gttcaccatt  tccagagaca  acgccaacaa  tttactgtat  240
ctgcaaata  ccagcctgag  agccgaggac  acggccgtgt  attactgtgc  gagagaagaa  300
ggcgattttt  ggagtgccgt  tgactcctgg  ggccagggaa  ccctggtcac  cgtctcctca  360
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<210> 154

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 154

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser
 20           25           30
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35           40           45
Ser Tyr Ile Gly Ser Ser Gly Asn Thr Phe Tyr Tyr Ala Asp Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Asn Asn Leu Leu Tyr
 65           70           75           80
Leu Gln Met Thr Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85           90           95
Ala Arg Glu Glu Gly Asp Phe Trp Ser Ala Val Asp Ser Trp Gly Gln
100          105          110
Gly Thr Leu Val Thr Val Ser Ser
115          120
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<210> 155

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 155

ggattcacct tcagtgactc ctac

24

<210> 156

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 156

Gly Phe Thr Phe Ser Asp Ser Tyr
1 5

<210> 157

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 157

attggtagta gtggaatac cttt

24

<210> 158

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 158

Ile Gly Ser Ser Gly Asn Thr Phe
1 5

<210> 159

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 159

gcgagagaag aaggcgattt ttggagtgcc gttgactcc

39

<210> 160

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 160

Ala Arg Glu Glu Gly Asp Phe Trp Ser Ala Val Asp Ser

1

5

10

<210> 161
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 161
gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120
ggtaaagccc ctaaactcct gatccatact gcatccactt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcaa cctgcagcct 240
gaagattttg caacttatta ctgtcaacag cttaatagtt acccattcac tttcggccct 300
gggaccaaaag tggatatcaa a 321

<210> 162
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 162
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
His Thr Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Phe
85 90 95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 163
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 163
cagggcatta gcagttat

18

<210> 164
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 164
Gln Gly Ile Ser Ser Tyr
1 5

<210> 165
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 165
actgcatcc

9

<210> 166
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 166
Thr Ala Ser
1

<210> 167
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 167
caacagctta atagttaccc attcact

27

<210> 168
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 168

Gln Gln Leu Asn Ser Tyr Pro Phe Thr
1 5

<210> 169

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 169

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cagggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcggt ggccatgccca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg gctggcagtt atatcatctg atggcagtaa taaacagtat 180
gcagattctg tgaagggccg attcaccatc tccagggaca atcccaagaa cacgctgtat 240
ctgcaaatga acagtctgag agttggggac acggctatatt attactgtgc gaaagagggtg 300
gcacctcggtt attattatta cggtctggac gtctggggcc aagggaccac ggtcaccgtc 360
tcctca 366
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<210> 170

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 170

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gly His
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Ala Val Ile Ser Ser Asp Gly Ser Asn Lys Gln Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Val Gly Asp Thr Ala Ile Tyr Tyr Cys
85 90 95
Ala Lys Glu Val Ala Pro Arg Tyr Tyr Tyr Tyr Gly Leu Asp Val Trp
100 105 110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120
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<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
 <223> synthetic

<400> 171
 ggattcacct tcggtggcca tgcc 24

<210> 172
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 172
 Gly Phe Thr Phe Gly Gly His Ala
 1 5

<210> 173
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 173
 atatcatctg atggcagtaa taaa 24

<210> 174
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 174
 Ile Ser Ser Asp Gly Ser Asn Lys
 1 5

<210> 175
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 175
 gcgaaagagg tggcacctcg ttattattat tacggtctgg acgtc 45

<210> 176

<211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 176
 Ala Lys Glu Val Ala Pro Arg Tyr Tyr Tyr Tyr Gly Leu Asp Val
 1 5 10 15

<210> 177
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 177
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 atcacttgcc gggcgagtc ggacattagc aatttttttag cctggtatca gcagaaacca 120
 gggaagggtc ctaaactcct gatctatact gcatccactt tacaatcagg ggtcccatct 180
 cggttcagtg gcagtggatc tgggacagat ttcactctca ccgtcagcag cctacagcct 240
 gaagatgttg caacttatta ctgtcaaaag tatgccggcg ccctcacttt cggccctggg 300
 accaaagtgg atatcaaa 318

<210> 178
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 178
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Phe
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
 35 40 45
 Tyr Thr Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Ala Gly Ala Leu Thr
 85 90 95
 Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 179
 <211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 179
caggacatta gcaatttt

18

<210> 180
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 180
Gln Asp Ile Ser Asn Phe
1 5

<210> 181
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 181
actgcatcc

9

<210> 182
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 182
Thr Ala Ser
1

<210> 183
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 183

caaaagtatg ccggcgccct cact

24

<210> 184

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 184

Gln Lys Tyr Ala Gly Ala Leu Thr

1

5

<210> 185

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 185

gaggtgcagc tgggtggagtc tggggggaggc ttggcacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacgtttaga agctatgcca tgagctgggt ccgccaggct 120
ccagggaagg ggccggagtg ggtctcaggt ataggtggta atggtgttac cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgttt 240
ctgcaaataa atagcctgag agccgaggac acggccgtat attattgtgt gcaggggggt 300
ttaggtgggt attttacagg ctactggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 186

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 186

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val
35 40 45
Ser Gly Ile Gly Gly Asn Gly Val Thr Thr 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
Val Gln Gly Gly Leu Gly Gly Tyr Phe Thr Gly Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser

<210> 187
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 187
 ggattcacgt ttagaagcta tgcc

24

<210> 188
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 188
 Gly Phe Thr Phe Arg Ser Tyr Ala
 1 5

<210> 189
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 189
 ataggtggta atggtgttac caca

24

<210> 190
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 190
 Ile Gly Gly Asn Gly Val Thr Thr
 1 5

<210> 191
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 191

gtgcaggggg gtttaggtgg ttatatttaca ggctac

36

<210> 192

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 192

Val Gln Gly Gly Leu Gly Gly Tyr Phe Thr Gly Tyr
1 5 10

<210> 193

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 193

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagtattagt acctatttaa attggtatca gcagaatcca 120
gggaaagccc ctaaactcct gatctttgat gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagagg tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagtg ccccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 194

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 194

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

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Ala	Pro	Leu
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

<210> 195
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 195
 cagagtatta gtacctat 18

<210> 196
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 196
 Gln Ser Ile Ser Thr Tyr
 1 5

<210> 197
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 197
 gatgcatcc 9

<210> 198
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 198
 Asp Ala Ser
 1

<210> 199

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 199
caacagagtt acagtgcccc gctcact

27

<210> 200
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 200
Gln Gln Ser Tyr Ser Ala Pro Leu Thr
1 5

<210> 201
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 201
caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt ggttatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcactt atatggcttg atggaagtaa tgactactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgttatat 240
ctgcaaatga acagactgag agccgaggac acggctgtgt attactgtgc gagagatggc 300
ccggttgctg ctatacccga ctactggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 202
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 202
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 Gly Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Leu Ile Trp Leu Asp Gly Ser Asn Asp 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	Arg	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
				85					90					95			
Ala	Arg	Asp	Gly	Pro	Val	Ala	Ala	Ile	Pro	Asp	Tyr	Trp	Gly	Gln	Gly		
			100					105					110				
Thr	Leu	Val	Thr	Val	Ser	Ser											
			115														

<210> 203
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 203
 ggattcacct tcagtgggta tggc 24

<210> 204
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 204
 Gly Phe Thr Phe Ser Gly Tyr Gly
 1 5

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 205
 atatggcttg atggaagtaa tgac 24

<210> 206
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 206

Ile Trp Leu Asp Gly Ser Asn Asp
1 5

<210> 207
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 207
gcgagagatg gcccggttgc tgctataccc gactac 36

<210> 208
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 208
Ala Arg Asp Gly Pro Val Ala Ala Ile Pro Asp Tyr
1 5 10

<210> 209
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 209
gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggccagtc gagtattagt aggtggttgg cctggatatca gctgaaacca 120
gggaaagccc ctaagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagac ttcactctca ccatcagcag cctgcaacct 240
gatgatcttg caacttatta ctgccaacag tataatactt attcgtacac ttttgccag 300
gggaccaagc tggagatcaa a 321

<210> 210
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 210
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

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

<210> 211
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 211
 cagagtatta gtaggtgg 18

<210> 212
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 212
 Gln Ser Ile Ser Arg Trp
 1 5

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

<220>
 <223> synthetic

<400> 213
 aaggcgtct 9

<210> 214
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 214

Lys Ala Ser

1

<210> 215

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 215

caacagtata atacttattc gtacact

27

<210> 216

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 216

Gln Gln Tyr Asn Thr Tyr Ser Tyr Thr

1

5

<210> 217

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 217

gaggtgcagc tgggtggagtc tggggggaggt gtggtacggc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gaatatggca tgacttgggt ccgccaagtt 120
ccagggaagg ggctggagtg ggtctctggt attacttgga atggtggttt cacagattat 180
acagactctg tgaagggccg attcaccagc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaataga acagtctgag agccgaggac acggccttgt attactgtgc gagagatgga 300
tatagcagct cgtgggggggc ttatgatata tggggccaag ggacaatggt caccgtctct 360
tca 363

<210> 218

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 218
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Tyr
 20 25 30
 Gly Met Thr Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Trp Asn Gly Gly Phe Thr Asp Tyr Thr Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ser Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Gly Tyr Ser Ser Ser Trp Gly Ala Tyr Asp Ile Trp Gly
 100 105 110
 Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 219
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 219
 ggattcacct ttgatgaata tggc

24

<210> 220
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 220
 Gly Phe Thr Phe Asp Glu Tyr Gly
 1 5

<210> 221
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 221
 attacttgga atggtggttt caca

24

<210> 222
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 222
Ile Thr Trp Asn Gly Gly Phe Thr
1 5

<210> 223
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
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<400> 223
gcgagagatg gatatagcag ctcgtggggg gcttatgata ta 42

<210> 224
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 224
Ala Arg Asp Gly Tyr Ser Ser Ser Trp Gly Ala Tyr Asp Ile
1 5 10

<210> 225
<211> 321
<212> DNA
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<220>
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<400> 225
gacatccaga tgaccagtc tccatcatcc ctgtctgcat ctgtgggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc acctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccata 180
aggttcagtg gcagtggatc tgggactgat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caagttattt ctgtcaacag agttacagta ccccgtagac ttttggccag 300
gggaccaagc tggagatcaa a 321

<210> 226
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 226
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Leu Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Ser Tyr Phe Cys Gln Gln Ser Tyr Ser Thr Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 227
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 227
cagagcatta gcacctat 18

<210> 228
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 228
Gln Ser Ile Ser Thr Tyr
1 5

<210> 229
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 229
gctgcatcc

9

<210> 230
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 230
Ala Ala Ser
1

<210> 231
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 231
caacagagtt acagtacccc gtacact

27

<210> 232
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 232
Gln Gln Ser Tyr Ser Thr Pro Tyr Thr
1 5

<210> 233
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
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<400> 233
gaagtgcagc tgggtggagtc tggggggaggc gtggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttaat gattatgcc a tgcactgggt ccgtcaagct 120
ccagggaagg gtctggagtg ggtctctctt attagtggag atggttggtaa cacatactat 180
gcagactctg tgaagggccg actcaccatc tccagagaca acagcaaaaa ctccctgtat 240
ctgcaaatga acagtctgag aacagaggac accgccttat attactgtgc aaaagataag 300
ggctggaact tcggttactt cgatctctgg ggccgtggca ccctggtcac tgtctcctca 360

<210> 234
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 234
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Leu Ile Ser Gly Asp Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Leu Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Lys Gly Trp Asn Phe Gly Tyr Phe Asp Leu Trp Gly Arg
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 235
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 235
 ggattcacct ttaatgatta tgcc

24

<210> 236
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 236
 Gly Phe Thr Phe Asn Asp Tyr Ala
 1 5

<210> 237
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 237
attagtggag atggtggtaa caca

24

<210> 238
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 238
Ile Ser Gly Asp Gly Gly Asn Thr
1 5

<210> 239
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 239
gcaaaagata agggctggaa cttcggttac ttcgatctc

39

<210> 240
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 240
Ala Lys Asp Lys Gly Trp Asn Phe Gly Tyr Phe Asp Leu
1 5 10

<210> 241
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 241

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 atcacttgcc gggcaagtca gaacattgac acctatttaa attggtatca gcagaaacca 120
 gggaaagccc ctaaactcct gatctatgat gcatccagtt tacaaagtgg ggtcccatca 180
 cggttcagtg gcagcggatc tgggacagat ttcactctca ccatcaccag tctgcaacct 240
 gaagattttg ccacttacta ctgtcaacag aatgacaata ttcttcaccc tctcactttc 300
 ggcggaggga ccaaggtgga gatcaaaa 327

<210> 242
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 242
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Thr Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asp Thr Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asp Asn Ile Leu His
 85 90 95
 Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 243
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 243
 cagaacattg acacctat 18

<210> 244
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 244
 Gln Asn Ile Asp Thr Tyr
 1 5

<210> 245
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 245
gatgcatcc

9

<210> 246
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 246
Asp Ala Ser
1

<210> 247
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 247
caacagaatg acaatattct tcaccctctc act

33

<210> 248
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 248
Gln Gln Asn Asp Asn Ile Leu His Pro Leu Thr
1 5 10

<210> 249
<211> 369
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 249

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gaggtgcagc tgggtggagtc tggggggaggc ttggtccaac cggggggggtc cctgagactc 60
tcctgtgcag cctctggatt ccactctaata agatattgga tggactgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtggccaac ataaagcaag atggaagtga ggaaaactat 180
gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactttat 240
ctgcaaataga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatcga 300
agcacctcgt ggggtcccta ctggttcttc gatctctggg gccgtggcac cctggtcact 360
gtctcctca 369
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<210> 250

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 250

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe His Ser Asn Arg Tyr
20          25          30
Trp Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35          40          45
Ala Asn Ile Lys Gln Asp Gly Ser Glu Glu Asn Tyr Val Asp Ser Val
50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65          70          75          80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85          90          95
Ala Arg Asp Arg Ser Thr Ser Trp Val Pro Tyr Trp Phe Phe Asp Leu
100         105         110
Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115         120
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<210> 251

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 251

ggattccact ctaatagata ttgg

24

<210> 252

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 252

Gly Phe His Ser Asn Arg Tyr Trp
1 5

<210> 253

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 253

ataaagcaag atggaagtga ggaa

24

<210> 254

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 254

Ile Lys Gln Asp Gly Ser Glu Glu
1 5

<210> 255

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 255

gcgagagatc gaagcacctc gtgggtccct tactggttct tcgatctc

48

<210> 256

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 256

Ala Arg Asp Arg Ser Thr Ser Trp Val Pro Tyr Trp Phe Phe Asp Leu
1 5 10 15

<210> 257
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 257
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
caaggacac gactggagat taaa 324

<210> 258
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 258
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 259
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 259
cagagcatta gcagctat

18

<210> 260
<211> 6
<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 260

Gln Ser Ile Ser Ser Tyr

1

5

<210> 261

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 261

gctgcatcc

9

<210> 262

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 262

Ala Ala Ser

1

<210> 263

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 263

caacagagtt acagtacccc tccgatcacc

30

<210> 264

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 264

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr

1

5

10

<210> 265

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 265

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gaagtgcagc  tgggtggagtc  tggggggaggc  gtggtacagc  gggggggagtc  cctgagactc  60
tcctgttcag  cctctgactt  catctttaaa  gattatgcca  tgtactgggt  ccgtcaaatt  120
ccagggaagg  gtctagagtg  gatctctctt  attagtgggt  atggtgacac  tacatggtat  180
ggagactctg  tgaagggccg  attcaccatc  tccagagaca  acaacgaaaa  ctccctcttt  240
ctgcaaatga  acgatctgag  aactgaggac  accgccatgt  actactgtgc  aagagatatg  300
gggtggaact  tctttcagtt  gcaatactgg  ggccaggga  ccctggtcac  cgtctcctca  360

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<210> 266

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 266

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Arg Gly Glu
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ser Ala Ser Asp Phe Ile Phe Lys Asp Tyr
      20           25           30
Ala Met Tyr Trp Val Arg Gln Ile Pro Gly Lys Gly Leu Glu Trp Ile
      35           40           45
Ser Leu Ile Ser Gly Asp Gly Asp Thr Thr Trp Tyr Gly Asp Ser Val
      50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Asn Glu Asn Ser Leu Phe
65           70           75           80
Leu Gln Met Asn Asp Leu Arg Thr Glu Asp Thr Ala Met Tyr Tyr Cys
      85           90           95
Ala Arg Asp Met Gly Trp Asn Phe Phe Gln Leu Gln Tyr Trp Gly Gln
      100          105          110
Gly Thr Leu Val Thr Val Ser Ser
      115          120

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<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 267
gacttcatct ttaaagatta tgcc 24

<210> 268
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 268
Asp Phe Ile Phe Lys Asp Tyr Ala
1 5

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 269
attagtgggtg atgggtgacac taca 24

<210> 270
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 270
Ile Ser Gly Asp Gly Asp Thr Thr
1 5

<210> 271
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 271
gcaagagata tgggggtggaa cttctttcag ttgcaatac 39

<210> 272
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 272

Ala Arg Asp Met Gly Trp Asn Phe Phe Gln Leu Gln Tyr
1 5 10

<210> 273

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 273

dcaggtgcag ctgcaggagt cgggccccgc actggtgaag ccttcacaga ccctgtccct 60
cacctgcact gtctctgggtg gctccatcat cagaggtagt acctactgga gttgggtccg 120
ccaattccca gggaagggcc tggagtggat tggatacagt tattacagtg ggaccgccta 180
ctataatccg tccctcgaga gtcgagctac catttctgta gacacgtcta agaaccagtt 240
ctccctgaac ctgaagtctg tgacggccgc ggacacggcc gtgtattatt gtacaagaga 300
aataggagtg gctggtctct ttgacatctg gggccaggga accctggtca ccgtctcctc 360
a 361

<210> 274

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 274

Gln Val Gln Leu Gln Glu Ser Gly Pro Ala Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ile Arg Gly
20 25 30
Ser Thr Tyr Trp Ser Trp Val Arg Gln Phe Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ser Tyr Tyr Ser Gly Thr Ala Tyr Tyr Asn Pro Ser
50 55 60
Leu Glu Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Asn Leu Lys Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Thr Arg Glu Ile Gly Val Ala Gly Leu Phe Asp Ile Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 275

<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 275
ggtggctcca tcacagagg tagtacctac

30

<210> 276
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 276
Gly Gly Ser Ile Ile Arg Gly Ser Thr Tyr
1 5 10

<210> 277
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 277
agttattaca gtgggaccgc c

21

<210> 278
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 278
Ser Tyr Tyr Ser Gly Thr Ala
1 5

<210> 279
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 279

acaagagaaa taggagtggc tggctctctt gacatc

36

<210> 280

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 280

Thr	Arg	Glu	Ile	Gly	Val	Ala	Gly	Leu	Phe	Asp	Ile
1				5				10			

<210> 281

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 281

gaaatagttt	tgacacagag	tcccggcaca	ctgtcactct	ctcccgggga	aagagccacc	60
ttgtcatgta	gagcaagtca	gtcagtctct	agctcttata	tcgcctggta	ccagcagaag	120
ccgggacagg	cccctagact	gctgatctac	ggggcaagtt	ccagggccac	cggaatcccc	180
gaccggttca	gtggaagcgg	aagcggaacc	gattttactt	tgacgatttc	tagactggag	240
ccagaggatt	tcgccgttta	ctattgtcaa	cagtacggaa	gcagcccgtg	gacgtttggc	300
cagggcacga	aggtagaaat	caag				324

<210> 282

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 282

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

<210> 283
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 283
agagcaagtc agtcagtctc tagctcttat ctcgcc

36

<210> 284
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 284
Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 285
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 285
ggggcaagtt ccagggccac c

21

<210> 286
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 286
Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 287
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 287

caacagtacg gaagcagccc gtggacg

27

<210> 288

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 288

Gln Gln Tyr Gly Ser Ser Pro Trp Thr

1

5

<210> 289

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 289

caggagcagt tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgtaagg cttctggata caccttcacc ggctactata tacattgggt gcgacaggcc 120
cctggactag ggcttgaatg gatgggatgg atcaacccta acagtgggtg cacaaaatat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcaa tacagcctac 240
atggagctga aaagactgaa atctgacgac tcggccgtat attactgtgc gagagacgcc 300
cctcccatg atgtttttga tatctggggc caaggacat tggtcaccgt ctcttca 357

<210> 290

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 290

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

Ala Arg Asp Ala Pro Pro His Asp Val Phe Asp Ile Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 291
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 291
ggatacacct tcaccggcta ctat 24

<210> 292
<211> 8
<212> PRT
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<220>
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<400> 292
Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

<210> 293
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 293
atcaacccta acagtgggtg caca 24

<210> 294
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 294
Ile Asn Pro Asn Ser Gly Gly Thr
1 5

<210> 295

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

<220>
<223> synthetic

<400> 295
gcgagagacg cccctcccca tgatgttttt gatatc 36

<210> 296
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 296
Ala Arg Asp Ala Pro Pro His Asp Val Phe Asp Ile
1 5 10

<210> 297
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 297
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggatatca gcagaaacca 120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaattgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacag cataatagtt acccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 298
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 298
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ile Gly Val Pro Ser Arg Phe Ser Gly

50						55						60					
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro		
65					70					75					80		
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	His	Asn	Ser	Tyr	Pro	Leu		
				85					90					95			
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys							
			100					105									

<210> 299
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 299
 cagggcatta gaaatgat
 18

<210> 300
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 300
 Gln Gly Ile Arg Asn Asp
 1 5

<210> 301
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 301
 gctgcatcc
 9

<210> 302
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 302
 Ala Ala Ser
 1

<210> 303
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 303
ctacagcata atagttaccc gctcact

27

<210> 304
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 304
Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 305
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 305
cagggtgcagc tgcaagagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt agtggtgctt accactggag ctggatccgc 120
cagcacccag ggaagggcct agagtggatt ggatacatct attacaatgg ggacacctac 180
tataatccgt cctcaagag tcgctgtacc atttcagtgg acacgtctaa gaaccaattc 240
ttcctgaagg tgacctctgt gactgccgcg gacacggcca tgtattactg tgcgggagaa 300
aagcagctga ctgcttttga tatctggggc caaggacat tggtcaccgt ctcttca 357

<210> 306
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 306
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

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

<210> 307
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
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<400> 307
ggtaggtcca tcagtagtgg tgcttaccac

30

<210> 308
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 308
Gly Gly Ser Ile Ser Ser Gly Ala Tyr His
1 5 10

<210> 309
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 309
atctattaca atggggacac c

21

<210> 310
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 310

Ile Tyr Tyr Asn Gly Asp Thr
1 5

<210> 311

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 311

gcgggagaaa agcagctgac tgcttttgat atc 33

<210> 312

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 312

Ala Gly Glu Lys Gln Leu Thr Ala Phe Asp Ile
1 5 10

<210> 313

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 313

gtcatccaga tgaccagtc tccatcctcc ctgtctgcat ctgttggaga cagagtcacc 60
ataacttgcc gggcgagtca ggacattaat aatttttttaa attggtatca acagaaatta 120
gggaaagccc ctaaactcct gatctccgat gcatccaatt tgcagacagg agtcccgtca 180
aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240
gaagatattg ctgcatatta ctgtcaacaa tatgatcatt tcccgtatac ttttggccag 300
gggaccagac tggagaacaa t 321

<210> 314

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 314
Val Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asn Asn Phe
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Leu Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Ser Asp Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Ile Ala Ala Tyr Tyr Cys Gln Gln Tyr Asp His Phe Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Arg Leu Glu Asn Asn
100 105

<210> 315
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 315
caggacatta ataatttt 18

<210> 316
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 316
Gln Asp Ile Asn Asn Phe
1 5

<210> 317
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 317
gatgcatcc 9

<210> 318
<211> 3
<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 318

Asp Ala Ser

1

<210> 319

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 319

caacaatatg atcatttccc gtatact

27

<210> 320

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 320

Gln Gln Tyr Asp His Phe Pro Tyr Thr

1

5

<210> 321

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 321

gaggtgcagt tgggtggagtc tggggggaggt gtggttcggc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatggca tgacctgggt ccgccaagct 120
ccaggaagg ggctggagtg ggtctctgggt attaattgga atggcgatag cacagagtat 180
tcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatac acagtctgag agccgaggac acggccttct atcactgtgc gagagagaat 300
aactggaact tctactttga ctactggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 322

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 322

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

<210> 323

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 323

ggattcacct ttgatgatta tggc

24

<210> 324

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 324

Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Gly		
1				5					

<210> 325

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 325

attaattgga atggcgatag caca

24

<210> 326

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 326

Ile Asn Trp Asn Gly Asp Ser Thr

1

5

<210> 327

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 327

gcgagagaga ataactggaa cttctacttt gactac

36

<210> 328

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 328

Ala Arg Glu Asn Asn Trp Asn Phe Tyr Phe Asp Tyr

1

5

10

<210> 329

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 329

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctcgagggga aagagccacc 60
ctctcctgta gggccagtc gagtggttag agcaacttag cctggtacca gcagaaactt 120
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ttgtcagcag tataataact ggccgtggac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 330
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 330
 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Arg Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Leu Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Trp
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 331
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 331
 cagagtgtta gcagcaac 18

<210> 332
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 332
 Gln Ser Val Ser Ser Asn
 1 5

<210> 333
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 333

ggtgcatcc

9

<210> 334

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 334

Gly Ala Ser

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<210> 335

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 335

cagcagtata ataactggcc gtggacg

27

<210> 336

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 336

Gln Gln Tyr Asn Asn Trp Pro Trp Thr

1

5

<210> 337

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 337

caggtccacc tggtacagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggctc 60

tcctgcaagg tttccggaaa caccctcact gaattatcca tgcactgggt gcgacaggct 120

cctggaaaag ggcttgagtg gatgggaggt tttgacctg aagatggtga cacaatctac 180

tcacagaagt tccagggcag agtcaccttg accgaggaca catctacaga cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgttc aacagtgggg 300
 ggacctacct ctgactgctg gggccaggga accctggtca ccgtctcctc a 351

<210> 338
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 338
 Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Val Ser Gly Asn Thr Leu Thr Glu Leu
 20 25 30
 Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Phe Asp Pro Glu Asp Gly Asp Thr Ile Tyr Ser Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Leu Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ser Thr Val Gly Gly Pro Thr Ser Asp Cys Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser
 115

<210> 339
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 339
 ggaaacaccc tcactgaatt atcc 24

<210> 340
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 340
 Gly Asn Thr Leu Thr Glu Leu Ser
 1 5

<210> 341

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

<220>
<223> synthetic

<400> 341
tttgatcctg aagatggtga caca

24

<210> 342
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 342
Phe Asp Pro Glu Asp Gly Asp Thr
1 5

<210> 343
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 343
tcaacagtgg ggggacctac ctctgactgc

30

<210> 344
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 344
Ser Thr Val Gly Gly Pro Thr Ser Asp Cys
1 5 10

<210> 345
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 345
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120
gggaaagccc ctaaggtcct gatcttcgat gcatccaatt tagaaccagg ggtcccatca 180
aggttcagtg gaagtggatc tgggacagat tttactttca ccatcatcag cctgcagcct 240
gaagatattg caacatatta ctgtcaacaa tatgataatc tcccgatcac cttcggccag 300
gggacacgac tggacattaa a 321

<210> 346
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 346
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45
Phe Asp Ala Ser Asn Leu Glu Pro Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ile Ser Leu Gln Pro
65 70 75 80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Ile
85 90 95
Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Lys
100 105

<210> 347
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 347
caggacatta gcaactat 18

<210> 348
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 348
Gln Asp Ile Ser Asn Tyr
1 5

<210> 349
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 349
gatgcatcc

9

<210> 350
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 350
Asp Ala Ser
1

<210> 351
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 351
caacaatatg ataatctccc gatcacc

27

<210> 352
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 352
Gln Gln Tyr Asp Asn Leu Pro Ile Thr
1 5

<210> 353
<211> 447
<212> PRT
<213> Artificial Sequence

<220>

<223> HC

<400> 353

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Asp	Ser	Val	Ser	Ser	Ser
			20					25					30		
Tyr	Trp	Thr	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Tyr	Ile	Tyr	Tyr	Ser	Gly	Ser	Ser	Asn	Tyr	Asn	Pro	Ser	Leu	Lys
	50					55					60				
Ser	Arg	Ala	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu
65					70					75					80
Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
			85					90						95	
Arg	Glu	Gly	Asn	Val	Asp	Thr	Thr	Met	Ile	Phe	Asp	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
		115					120					125			
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
	130					135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
			165					170						175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195				200						205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
	210					215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225				230						235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
			245					250						255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
		260						265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
	275					280						285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
	290					295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
			325					330						335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
		340						345					350		
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
	355						360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385				390						395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg

				405					410					415		
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	
			420					425					430			
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys		
		435					440					445				

<210> 354
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC

<400> 354

Ala	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5				10						15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Asp	
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Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	
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<220>
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Val	Gly	Ala	Ser	Glu	Asn	Ile	Val	Ile	Gln	Val	Tyr	Gly	Tyr	Thr	Glu
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Asn	Ser	Ala	Ile	Leu	Thr	Ile	Gln	Pro	Lys	Gln	Leu	Pro	Gly	Gly	Gln
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Asn	Pro	Val	Ser	Tyr	Val	Tyr	Leu	Glu	Val	Val	Ser	Lys	His	Phe	Ser
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Lys	Ser	Lys	Arg	Met	Pro	Ile	Thr	Tyr	Asp	Asn	Gly	Phe	Leu	Phe	Ile
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His	Thr	Asp	Lys	Pro	Val	Tyr	Thr	Pro	Asp	Gln	Ser	Val	Lys	Val	Arg
	130					135					140				
Val	Tyr	Ser	Leu	Asn	Asp	Asp	Leu	Lys	Pro	Ala	Lys	Arg	Glu	Thr	Val
145					150					155					160
Leu	Thr	Phe	Ile	Asp	Pro	Glu	Gly	Ser	Glu	Val	Asp	Met	Val	Glu	Glu
				165					170					175	
Ile	Asp	His	Ile	Gly	Ile	Ile	Ser	Phe	Pro	Asp	Phe	Lys	Ile	Pro	Ser
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Asn	Pro	Arg	Tyr	Gly	Met	Trp	Thr	Ile	Lys	Ala	Lys	Tyr	Lys	Glu	Asp
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Phe	Ser	Thr	Thr	Gly	Thr	Ala	Tyr	Phe	Glu	Val	Lys	Glu	Tyr	Val	Leu
	210					215					220				
Pro	His	Phe	Ser	Val	Ser	Ile	Glu	Pro	Glu	Tyr	Asn	Phe	Ile	Gly	Tyr
225					230					235					240
Lys	Asn	Phe	Lys	Asn	Phe	Glu	Ile	Thr	Ile	Lys	Ala	Arg	Tyr	Phe	Tyr
			245						250					255	
Asn	Lys	Val	Val	Thr	Glu	Ala	Asp	Val	Tyr	Ile	Thr	Phe	Gly	Ile	Arg
			260					265					270		
Glu	Asp	Leu	Lys	Asp	Asp	Gln	Lys	Glu	Met	Met	Gln	Thr	Ala	Met	Gln
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Lys	Tyr	Leu	Tyr	Ile	Ala	Val	Thr	Val	Ile	Glu	Ser	Thr	Gly	Gly	Phe
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Lys	Leu	Asn	Leu	Val	Ala	Thr	Pro	Leu	Phe	Leu	Lys	Pro	Gly	Ile	Pro
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Tyr	Pro	Ile	Lys	Val	Gln	Val	Lys	Asp	Ser	Leu	Asp	Gln	Leu	Val	Gly
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Gly	Val	Pro	Val	Thr	Leu	Asn	Ala	Gln	Thr	Ile	Asp	Val	Asn	Gln	Glu
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Thr	Ser	Asp	Leu	Asp	Pro	Ser	Lys	Ser	Val	Thr	Arg	Val	Asp	Asp	Gly
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Val	Ala	Ser	Phe	Val	Leu	Asn	Leu	Pro	Ser	Gly	Val	Thr	Val	Leu	Glu
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Phe	Asn	Val	Lys	Thr	Asp	Ala	Pro	Asp	Leu	Pro	Glu	Glu	Asn	Gln	Ala

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Arg	Glu	Gly	Tyr	Arg	Ala	Ile	Ala	Tyr	Ser	Ser	Leu	Ser	Gln	Ser	Tyr
	450					455					460				
Leu	Tyr	Ile	Asp	Trp	Thr	Asp	Asn	His	Lys	Ala	Leu	Leu	Val	Gly	Glu
465					470					475					480
His	Leu	Asn	Ile	Ile	Val	Thr	Pro	Lys	Ser	Pro	Tyr	Ile	Asp	Lys	Ile
			485						490					495	
Thr	His	Tyr	Asn	Tyr	Leu	Ile	Leu	Ser	Lys	Gly	Lys	Ile	Ile	His	Phe
			500					505					510		
Gly	Thr	Arg	Glu	Lys	Phe	Ser	Asp	Ala	Ser	Tyr	Gln	Ser	Ile	Asn	Ile
		515					520					525			
Pro	Val	Thr	Gln	Asn	Met	Val	Pro	Ser	Ser	Arg	Leu	Leu	Val	Tyr	Tyr
	530					535					540				
Ile	Val	Thr	Gly	Glu	Gln	Thr	Ala	Glu	Leu	Val	Ser	Asp	Ser	Val	Trp
545					550					555					560
Leu	Asn	Ile	Glu	Glu	Lys	Cys	Gly	Asn	Gln	Leu	Gln	Val	His	Leu	Ser
			565						570					575	
Pro	Asp	Ala	Asp	Ala	Tyr	Ser	Pro	Gly	Gln	Thr	Val	Ser	Leu	Asn	Met
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Ala	Thr	Gly	Met	Asp	Ser	Trp	Val	Ala	Leu	Ala	Ala	Val	Asp	Ser	Ala
		595					600					605			
Val	Tyr	Gly	Val	Gln	Arg	Gly	Ala	Lys	Lys	Pro	Leu	Glu	Arg	Val	Phe
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Asn	Asn	Ala	Asn	Val	Phe	His	Leu	Ala	Gly	Leu	Thr	Phe	Leu	Thr	Asn
				645					650					655	
Ala	Asn	Ala	Asp	Asp	Ser	Gln	Glu	Asn	Asp	Glu	Pro	Cys	Lys	Glu	Ile
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Leu	Arg	Pro	Arg	Arg	Thr	Leu	Gln	Lys	Lys	Ile	Glu	Glu	Ile	Ala	Ala
		675					680					685			
Lys	Tyr	Lys	His	Ser	Val	Val	Lys	Lys	Cys	Cys	Tyr	Asp	Gly	Ala	Cys
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Val	Asn	Asn	Asp	Glu	Thr	Cys	Glu	Gln	Arg	Ala	Ala	Arg	Ile	Ser	Leu
705					710					715					720
Gly	Pro	Arg	Cys	Ile	Lys	Ala	Phe	Thr	Glu	Cys	Cys	Val	Val	Ala	Ser
			725						730					735	
Gln	Leu	Arg	Ala	Asn	Ile	Ser	His	Lys	Asp	Met	Gln	Leu	Gly	Arg	Leu
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His	Met	Lys	Thr	Leu	Leu	Pro	Val	Ser	Lys	Pro	Glu	Ile	Arg	Ser	Tyr
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Phe	Pro	Glu	Ser	Trp	Leu	Trp	Glu	Val	His	Leu	Val	Pro	Arg	Arg	Lys
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Gln	Leu	Gln	Phe	Ala	Leu	Pro	Asp	Ser	Leu	Thr	Thr	Trp	Glu	Ile	Gln
785					790					795					800
Gly	Val	Gly	Ile	Ser	Asn	Thr	Gly	Ile	Cys	Val	Ala	Asp	Thr	Val	Lys
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Ala	Lys	Val	Phe	Lys	Asp	Val	Phe	Leu	Glu	Met	Asn	Ile	Pro	Tyr	Ser
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Val	Val	Arg	Gly	Glu	Gln	Ile	Gln	Leu	Lys	Gly	Thr	Val	Tyr	Asn	Tyr
		835					840						845		
Arg	Thr	Ser	Gly	Met	Gln	Phe	Cys	Val	Lys	Met	Ser	Ala	Val	Glu	Gly
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Ile	Cys	Thr	Ser	Glu	Ser	Pro	Val	Ile	Asp	His	Gln	Gly	Thr	Lys	Ser
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Ser	Lys	Cys	Val	Arg	Gln	Lys	Val	Glu	Gly	Ser	Ser	Ser	His	Leu	Val	
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Thr	Phe	Thr	Val	Leu	Pro	Leu	Glu	Ile	Gly	Leu	His	Asn	Ile	Asn	Phe	
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Tyr	Arg	Ile	Pro	Leu	Asp	Leu	Val	Pro	Lys	Thr	Glu	Ile	Lys	Arg	Ile	
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Leu	Glu	Thr	Gly	Asn	His	Trp	Asn	Ile	Phe	His	Ser	Asp	Pro	Leu	Ile	
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Glu	Lys	Gln	Lys	Leu	Lys	Lys	Lys	Leu	Lys	Glu	Gly	Met	Leu	Ser	Ile	
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Ser	Ala	Ser	Thr	Trp	Leu	Thr	Ala	Phe	Ala	Leu	Arg	Val	Leu	Gly	Gln	
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Val	Asn	Lys	Tyr	Val	Glu	Gln	Asn	Gln	Asn	Ser	Ile	Cys	Asn	Ser	Leu	
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Ile	Lys	Ala	Asp	Asn	Phe	Leu	Leu	Glu	Asn	Thr	Leu	Pro	Ala	Gln	Ser	
	1170					1175					1180					
Thr	Phe	Thr	Leu	Ala	Ile	Ser	Ala	Tyr	Ala	Leu	Ser	Leu	Gly	Asp	Lys	
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Leu	Thr	Glu	Tyr	Ser	Leu	Leu	Val	Lys	Gln	Leu	Arg	Leu	Ser	Met	Asp	
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R885H change)
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Val	Ser	Tyr	Val	Tyr	Leu	Glu	Val	Val	Ser	Lys	His	Phe	Ser	Lys	Ser
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Lys	Arg	Met	Pro	Ile	Thr	Tyr	Asp	Asn	Gly	Phe	Leu	Phe	Ile	His	Thr
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Asp	Lys	Pro	Val	Tyr	Thr	Pro	Asp	Gln	Ser	Val	Lys	Val	Arg	Val	Tyr
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Phe	Ile	Asp	Pro	Glu	Gly	Ser	Glu	Val	Asp	Met	Val	Glu	Glu	Ile	Asp
145					150					155					160
His	Ile	Gly	Ile	Ile	Ser	Phe	Pro	Asp	Phe	Lys	Ile	Pro	Ser	Asn	Pro
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Arg	Tyr	Gly	Met	Trp	Thr	Ile	Lys	Ala	Lys	Tyr	Lys	Glu	Asp	Phe	Ser
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Thr	Thr	Gly	Thr	Ala	Tyr	Phe	Glu	Val	Lys	Glu	Tyr	Val	Leu	Pro	His
		195					200					205			
Phe	Ser	Val	Ser	Ile	Glu	Pro	Glu	Tyr	Asn	Phe	Ile	Gly	Tyr	Lys	Asn
	210					215					220				
Phe	Lys	Asn	Phe	Glu	Ile	Thr	Ile	Lys	Ala	Arg	Tyr	Phe	Tyr	Asn	Lys
225					230					235					240
Val	Val	Thr	Glu	Ala	Asp	Val	Tyr	Ile	Thr	Phe	Gly	Ile	Arg	Glu	Asp
				245					250					255	
Leu	Lys	Asp	Asp	Gln	Lys	Glu	Met	Met	Gln	Thr	Ala	Met	Gln	Asn	Thr
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Met	Leu	Ile	Asn	Gly	Ile	Ala	Gln	Val	Thr	Phe	Asp	Ser	Glu	Thr	Ala
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Val	Lys	Glu	Leu	Ser	Tyr	Tyr	Ser	Leu	Glu	Asp	Leu	Asn	Asn	Lys	Tyr
	290					295					300				
Leu	Tyr	Ile	Ala	Val	Thr	Val	Ile	Glu	Ser	Thr	Gly	Gly	Phe	Ser	Glu
305					310					315					320
Glu	Ala	Glu	Ile	Pro	Gly	Ile	Lys	Tyr	Val	Leu	Ser	Pro	Tyr	Lys	Leu
				325					330					335	
Asn	Leu	Val	Ala	Thr	Pro	Leu	Phe	Leu	Lys	Pro	Gly	Ile	Pro	Tyr	Pro
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Pro	Val	Thr	Leu	Asn	Ala	Gln	Thr	Ile	Asp	Val	Asn	Gln	Glu	Thr	Ser
	370					375					380				
Asp	Leu	Asp	Pro	Ser	Lys	Ser	Val	Thr	Arg	Val	Asp	Asp	Gly	Val	Ala
385					390					395					400
Ser	Phe	Val	Leu	Asn	Leu	Pro	Ser	Gly	Val	Thr	Val	Leu	Glu	Phe	Asn

				405				410				415			
Val	Lys	Thr	Asp	Ala	Pro	Asp	Leu	Pro	Glu	Glu	Asn	Gln	Ala	Arg	Glu
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Gly	Tyr	Arg	Ala	Ile	Ala	Tyr	Ser	Ser	Leu	Ser	Gln	Ser	Tyr	Leu	Tyr
		435					440					445			
Ile	Asp	Trp	Thr	Asp	Asn	His	Lys	Ala	Leu	Leu	Val	Gly	Glu	His	Leu
	450					455					460				
Asn	Ile	Ile	Val	Thr	Pro	Lys	Ser	Pro	Tyr	Ile	Asp	Lys	Ile	Thr	His
465					470					475					480
Tyr	Asn	Tyr	Leu	Ile	Leu	Ser	Lys	Gly	Lys	Ile	Ile	His	Phe	Gly	Thr
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Thr	Gly	Glu	Gln	Thr	Ala	Glu	Leu	Val	Ser	Asp	Ser	Val	Trp	Leu	Asn
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Ile	Glu	Glu	Lys	Cys	Gly	Asn	Gln	Leu	Gln	Val	His	Leu	Ser	Pro	Asp
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Ala	Asp	Ala	Tyr	Ser	Pro	Gly	Gln	Thr	Val	Ser	Leu	Asn	Met	Ala	Thr
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Ala	Asn	Val	Phe	His	Leu	Ala	Gly	Leu	Thr	Phe	Leu	Thr	Asn	Ala	Asn
625					630					635					640
Ala	Asp	Asp	Ser	Gln	Glu	Asn	Asp	Glu	Pro	Cys	Lys	Glu	Ile	Leu	Arg
			645					650						655	
Pro	Arg	Arg	Thr	Leu	Gln	Lys	Lys	Ile	Glu	Glu	Ile	Ala	Ala	Lys	Tyr
			660					665					670		
Lys	His	Ser	Val	Val	Lys	Lys	Cys	Cys	Tyr	Asp	Gly	Ala	Cys	Val	Asn
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Asn	Asp	Glu	Thr	Cys	Glu	Gln	Arg	Ala	Ala	Arg	Ile	Ser	Leu	Gly	Pro
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Glu	Ser	Trp	Leu	Trp	Glu	Val	His	Leu	Val	Pro	Arg	Arg	Lys	Gln	Leu
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Gln	Phe	Ala	Leu	Pro	Asp	Ser	Leu	Thr	Thr	Trp	Glu	Ile	Gln	Gly	Val
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Gly	Ile	Ser	Asn	Thr	Gly	Ile	Cys	Val	Ala	Asp	Thr	Val	Lys	Ala	Lys
785					790					795					800
Val	Phe	Lys	Asp	Val	Phe	Leu	Glu	Met	Asn	Ile	Pro	Tyr	Ser	Val	Val
			805					810						815	
Arg	Gly	Glu	Gln	Ile	Gln	Leu	Lys	Gly	Thr	Val	Tyr	Asn	Tyr	Arg	Thr
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Ser	Gly	Met	Gln	Phe	Cys	Val	Lys	Met	Ser	Ala	Val	Glu	Gly	Ile	Cys
		835					840					845			

Thr	Ser	Glu	Ser	Pro	Val	Ile	Asp	His	Gln	Gly	Thr	Lys	Ser	Ser	Lys
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Cys	Val	His	Gln	Lys	Val	Glu	Gly	Ser	Ser	Ser	His	Leu	Val	Thr	Phe
865					870					875					880
Thr	Val	Leu	Pro	Leu	Glu	Ile	Gly	Leu	His	Asn	Ile	Asn	Phe	Ser	Leu
				885					890					895	
Glu	Thr	Trp	Phe	Gly	Lys	Glu	Ile	Leu	Val	Lys	Thr	Leu	Arg	Val	Val
			900					905					910		
Pro	Glu	Gly	Val	Lys	Arg	Glu	Ser	Tyr	Ser	Gly	Val	Thr	Leu	Asp	Pro
		915					920					925			
Arg	Gly	Ile	Tyr	Gly	Thr	Ile	Ser	Arg	Arg	Lys	Glu	Phe	Pro	Tyr	Arg
	930					935					940				
Ile	Pro	Leu	Asp	Leu	Val	Pro	Lys	Thr	Glu	Ile	Lys	Arg	Ile	Leu	Ser
945					950					955					960
Val	Lys	Gly	Leu	Leu	Val	Gly	Glu	Ile	Leu	Ser	Ala	Val	Leu	Ser	Gln
				965					970					975	
Glu	Gly	Ile	Asn	Ile	Leu	Thr	His	Leu	Pro	Lys	Gly	Ser	Ala	Glu	Ala
			980					985					990		
Glu	Leu	Met	Ser	Val	Val	Pro	Val	Phe	Tyr	Val	Phe	His	Tyr	Leu	Glu
		995				1000					1005				
Thr	Gly	Asn	His	Trp	Asn	Ile	Phe	His	Ser	Asp	Pro	Leu	Ile	Glu	Lys
	1010					1015					1020				
Gln	Lys	Leu	Lys	Lys	Lys	Leu	Lys	Glu	Gly	Met	Leu	Ser	Ile	Met	Ser
1025					1030					1035					1040
Tyr	Arg	Asn	Ala	Asp	Tyr	Ser	Tyr	Ser	Val	Trp	Lys	Gly	Gly	Ser	Ala
				1045					1050					1055	
Ser	Thr	Trp	Leu	Thr	Ala	Phe	Ala	Leu	Arg	Val	Leu	Gly	Gln	Val	Asn
			1060					1065					1070		
Lys	Tyr	Val	Glu	Gln	Asn	Gln	Asn	Ser	Ile	Cys	Asn	Ser	Leu	Leu	Trp
		1075					1080					1085			
Leu	Val	Glu	Asn	Tyr	Gln	Leu	Asp	Asn	Gly	Ser	Phe	Lys	Glu	Asn	Ser
	1090					1095					1100				
Gln	Tyr	Gln	Pro	Ile	Lys	Leu	Gln	Gly	Thr	Leu	Pro	Val	Glu	Ala	Arg
1105					1110					1115					1120
Glu	Asn	Ser	Leu	Tyr	Leu	Thr	Ala	Phe	Thr	Val	Ile	Gly	Ile	Arg	Lys
				1125					1130					1135	
Ala	Phe	Asp	Ile	Cys	Pro	Leu	Val	Lys	Ile	Asp	Thr	Ala	Leu	Ile	Lys
			1140					1145					1150		
Ala	Asp	Asn	Phe	Leu	Leu	Glu	Asn	Thr	Leu	Pro	Ala	Gln	Ser	Thr	Phe
		1155					1160					1165			
Thr	Leu	Ala	Ile	Ser	Ala	Tyr	Ala	Leu	Ser	Leu	Gly	Asp	Lys	Thr	His
	1170					1175					1180				
Pro	Gln	Phe	Arg	Ser	Ile	Val	Ser	Ala	Leu	Lys	Arg	Glu	Ala	Leu	Val
1185					1190					1195					1200
Lys	Gly	Asn	Pro	Pro	Ile	Tyr	Arg	Phe	Trp	Lys	Asp	Asn	Leu	Gln	His
				1205					1210					1215	
Lys	Asp	Ser	Ser	Val	Pro	Asn	Thr	Gly	Thr	Ala	Arg	Met	Val	Glu	Thr
			1220					1225					1230		
Thr	Ala	Tyr	Ala	Leu	Leu	Thr	Ser	Leu	Asn	Leu	Lys	Asp	Ile	Asn	Tyr
		1235					1240					1245			
Val	Asn	Pro	Val	Ile	Lys	Trp	Leu	Ser	Glu	Glu	Gln	Arg	Tyr	Gly	Gly
	1250					1255					1260				
Gly	Phe	Tyr	Ser	Thr	Gln	Asp	Thr	Ile	Asn	Ala	Ile	Glu	Gly	Leu	Thr
1265					1270					1275					1280
Glu	Tyr	Ser	Leu	Leu	Val	Lys	Gln	Leu	Arg	Leu	Ser	Met	Asp	Ile	Asp

<212> PRT

<213> Artificial Sequence

<220>

<223> hC5 R885C

aa 1-1658: hC5 (aa 19-1676 of NM_001735.2 with
R885C change)

aa 1659-1686: myc-myc-hexahistidine tag

<400> 357

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

Val	Phe	Lys	Asp	Val	Phe	Leu	Glu	Met	Asn	Ile	Pro	Tyr	Ser	Val	Val
			805						810					815	
Arg	Gly	Glu	Gln	Ile	Gln	Leu	Lys	Gly	Thr	Val	Tyr	Asn	Tyr	Arg	Thr
			820					825					830		
Ser	Gly	Met	Gln	Phe	Cys	Val	Lys	Met	Ser	Ala	Val	Glu	Gly	Ile	Cys
		835					840					845			
Thr	Ser	Glu	Ser	Pro	Val	Ile	Asp	His	Gln	Gly	Thr	Lys	Ser	Ser	Lys
	850					855					860				
Cys	Val	Cys	Gln	Lys	Val	Glu	Gly	Ser	Ser	Ser	His	Leu	Val	Thr	Phe
865					870					875					880
Thr	Val	Leu	Pro	Leu	Glu	Ile	Gly	Leu	His	Asn	Ile	Asn	Phe	Ser	Leu
				885					890					895	
Glu	Thr	Trp	Phe	Gly	Lys	Glu	Ile	Leu	Val	Lys	Thr	Leu	Arg	Val	Val
			900					905					910		
Pro	Glu	Gly	Val	Lys	Arg	Glu	Ser	Tyr	Ser	Gly	Val	Thr	Leu	Asp	Pro
		915					920					925			
Arg	Gly	Ile	Tyr	Gly	Thr	Ile	Ser	Arg	Arg	Lys	Glu	Phe	Pro	Tyr	Arg
	930					935					940				
Ile	Pro	Leu	Asp	Leu	Val	Pro	Lys	Thr	Glu	Ile	Lys	Arg	Ile	Leu	Ser
945					950					955					960
Val	Lys	Gly	Leu	Leu	Val	Gly	Glu	Ile	Leu	Ser	Ala	Val	Leu	Ser	Gln
				965					970					975	
Glu	Gly	Ile	Asn	Ile	Leu	Thr	His	Leu	Pro	Lys	Gly	Ser	Ala	Glu	Ala
			980					985					990		
Glu	Leu	Met	Ser	Val	Val	Pro	Val	Phe	Tyr	Val	Phe	His	Tyr	Leu	Glu
		995					1000					1005			
Thr	Gly	Asn	His	Trp	Asn	Ile	Phe	His	Ser	Asp	Pro	Leu	Ile	Glu	Lys
	1010					1015					1020				
Gln	Lys	Leu	Lys	Lys	Lys	Leu	Lys	Glu	Gly	Met	Leu	Ser	Ile	Met	Ser
1025					1030					1035					1040
Tyr	Arg	Asn	Ala	Asp	Tyr	Ser	Tyr	Ser	Val	Trp	Lys	Gly	Gly	Ser	Ala
				1045					1050					1055	
Ser	Thr	Trp	Leu	Thr	Ala	Phe	Ala	Leu	Arg	Val	Leu	Gly	Gln	Val	Asn
			1060					1065					1070		
Lys	Tyr	Val	Glu	Gln	Asn	Gln	Asn	Ser	Ile	Cys	Asn	Ser	Leu	Leu	Trp
		1075					1080					1085			
Leu	Val	Glu	Asn	Tyr	Gln	Leu	Asp	Asn	Gly	Ser	Phe	Lys	Glu	Asn	Ser
	1090					1095					1100				
Gln	Tyr	Gln	Pro	Ile	Lys	Leu	Gln	Gly	Thr	Leu	Pro	Val	Glu	Ala	Arg
1105					1110					1115					1120
Glu	Asn	Ser	Leu	Tyr	Leu	Thr	Ala	Phe	Thr	Val	Ile	Gly	Ile	Arg	Lys
				1125					1130					1135	
Ala	Phe	Asp	Ile	Cys	Pro	Leu	Val	Lys	Ile	Asp	Thr	Ala	Leu	Ile	Lys
			1140					1145					1150		
Ala	Asp	Asn	Phe	Leu	Leu	Glu	Asn	Thr	Leu	Pro	Ala	Gln	Ser	Thr	Phe
		1155					1160					1165			
Thr	Leu	Ala	Ile	Ser	Ala	Tyr	Ala	Leu	Ser	Leu	Gly	Asp	Lys	Thr	His
	1170					1175					1180				
Pro	Gln	Phe	Arg	Ser	Ile	Val	Ser	Ala	Leu	Lys	Arg	Glu	Ala	Leu	Val
1185					1190					1195					1200
Lys	Gly	Asn	Pro	Pro	Ile	Tyr	Arg	Phe	Trp	Lys	Asp	Asn	Leu	Gln	His
				1205					1210					1215	
Lys	Asp	Ser	Ser	Val	Pro	Asn	Thr	Gly	Thr	Ala	Arg	Met	Val	Glu	Thr
			1220					1225					1230		
Thr	Ala	Tyr	Ala	Leu	Leu	Thr	Ser	Leu	Asn	Leu	Lys	Asp	Ile	Asn	Tyr

His His His His His His
1685

<210> 358
<211> 1686
<212> PRT
<213> Artificial Sequence

<220>
<223> M. fascicularis C5 R885H
aa 1-1658: M. fascicularis C5 (determined
in-house; NTBK#12480)
aa 1659-1686: myc-myc-hexahistidine tag

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Gln Glu Gln Thr Tyr Val Ile Ser Ala Pro Lys Ile Phe Arg Val Gly
1 5 10 15
Ala Ser Glu Asn Ile Val Ile Gln Val Tyr Gly Tyr Thr Glu Ala Phe
20 25 30
Asp Ala Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Lys Phe Ser Tyr
35 40 45
Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln Asn Ser
50 55 60
Ala Val Leu Thr Ile Gln Pro Lys Gln Leu Pro Gly Gly Gln Asn Gln
65 70 75 80
Val Ser Tyr Val Tyr Leu Glu Val Val Ser Lys His Phe Ser Lys Ser
85 90 95
Lys Lys Ile Pro Ile Thr Tyr Asp Asn Gly Phe Leu Phe Ile His Thr
100 105 110
Asp Lys Pro Val Tyr Thr Pro Asp Gln Ser Val Lys Val Arg Val Tyr
115 120 125
Ser Leu Asn Asp Asp Leu Lys Pro Ala Lys Arg Glu Thr Val Leu Thr
130 135 140
Phe Ile Asp Pro Glu Gly Ser Glu Ile Asp Met Val Glu Glu Ile Asp
145 150 155 160
His Ile Gly Ile Ile Ser Phe Pro Asp Phe Lys Ile Pro Ser Asn Pro
165 170 175
Arg Tyr Gly Met Trp Thr Ile Gln Ala Lys Tyr Lys Glu Asp Phe Ser
180 185 190
Thr Thr Gly Thr Ala Phe Phe Glu Val Lys Glu Tyr Val Leu Pro His
195 200 205
Phe Ser Val Ser Val Glu Pro Glu Ser Asn Phe Ile Gly Tyr Lys Asn
210 215 220
Phe Lys Asn Phe Glu Ile Thr Ile Lys Ala Arg Tyr Phe Tyr Asn Lys
225 230 235 240
Val Val Thr Glu Ala Asp Val Tyr Ile Thr Phe Gly Ile Arg Glu Asp
245 250 255
Leu Lys Asp Asp Gln Lys Glu Met Met Gln Thr Ala Met Gln Asn Thr
260 265 270
Met Leu Ile Asn Gly Ile Ala Gln Val Thr Phe Asp Ser Glu Thr Ala
275 280 285
Val Lys Glu Leu Ser Tyr Tyr Ser Leu Glu Asp Leu Asn Asn Lys Tyr
290 295 300
Leu Tyr Ile Ala Val Thr Val Ile Glu Ser Thr Gly Gly Phe Ser Glu

305					310					315					320
Glu	Ala	Glu	Ile	Pro	Gly	Ile	Lys	Tyr	Val	Leu	Ser	Pro	Tyr	Lys	Leu
				325					330					335	
Asn	Leu	Val	Ala	Thr	Pro	Leu	Phe	Leu	Lys	Pro	Gly	Ile	Pro	Tyr	Ser
			340					345					350		
Ile	Lys	Val	Gln	Val	Lys	Asp	Ala	Leu	Asp	Gln	Leu	Val	Gly	Gly	Val
		355					360					365			
Pro	Val	Thr	Leu	Asn	Ala	Gln	Thr	Ile	Asp	Val	Asn	Gln	Glu	Thr	Ser
	370					375				380					
Asp	Leu	Glu	Pro	Arg	Lys	Ser	Val	Thr	Arg	Val	Asp	Asp	Gly	Val	Ala
385					390					395					400
Ser	Phe	Val	Val	Asn	Leu	Pro	Ser	Gly	Val	Thr	Val	Leu	Glu	Phe	Asn
				405					410					415	
Val	Lys	Thr	Asp	Ala	Pro	Asp	Leu	Pro	Asp	Glu	Asn	Gln	Ala	Arg	Glu
			420					425					430		
Gly	Tyr	Arg	Ala	Ile	Ala	Tyr	Ser	Ser	Leu	Ser	Gln	Ser	Tyr	Leu	Tyr
		435				440					445				
Ile	Asp	Trp	Thr	Asp	Asn	His	Lys	Ala	Leu	Leu	Val	Gly	Glu	Tyr	Leu
	450				455						460				
Asn	Ile	Ile	Val	Thr	Pro	Lys	Ser	Pro	Tyr	Ile	Asp	Lys	Ile	Thr	His
465					470					475					480
Tyr	Asn	Tyr	Leu	Ile	Leu	Ser	Lys	Gly	Lys	Ile	Ile	His	Phe	Gly	Thr
				485					490					495	
Arg	Glu	Lys	Leu	Ser	Asp	Ala	Ser	Tyr	Gln	Ser	Ile	Asn	Ile	Pro	Val
			500					505					510		
Thr	Gln	Asn	Met	Val	Pro	Ser	Ser	Arg	Leu	Leu	Val	Tyr	Tyr	Ile	Val
		515					520					525			
Thr	Gly	Glu	Gln	Thr	Ala	Glu	Leu	Val	Ser	Asp	Ser	Val	Trp	Leu	Asn
	530					535					540				
Ile	Glu	Glu	Lys	Cys	Gly	Asn	Gln	Leu	Gln	Val	His	Leu	Ser	Pro	Asp
545					550					555					560
Ala	Asp	Thr	Tyr	Ser	Pro	Gly	Gln	Thr	Val	Ser	Leu	Asn	Met	Val	Thr
				565					570					575	
Gly	Met	Asp	Ser	Trp	Val	Ala	Leu	Thr	Ala	Val	Asp	Ser	Ala	Val	Tyr
			580					585					590		
Gly	Val	Gln	Arg	Arg	Ala	Lys	Lys	Pro	Leu	Glu	Arg	Val	Phe	Gln	Phe
		595				600						605			
Leu	Glu	Lys	Ser	Asp	Leu	Gly	Cys	Gly	Ala	Gly	Gly	Gly	Leu	Asn	Asn
	610					615					620				
Ala	Asn	Val	Phe	His	Leu	Ala	Gly	Leu	Thr	Phe	Leu	Thr	Asn	Ala	Asn
625					630					635					640
Ala	Asp	Asp	Ser	Gln	Glu	Asn	Asp	Glu	Pro	Cys	Lys	Glu	Ile	Ile	Arg
				645					650					655	
Pro	Arg	Arg	Met	Leu	Gln	Glu	Lys	Ile	Glu	Glu	Ile	Ala	Ala	Lys	Tyr
			660					665					670		
Lys	His	Leu	Val	Val	Lys	Lys	Cys	Cys	Tyr	Asp	Gly	Val	Arg	Ile	Asn
		675					680					685			
His	Asp	Glu	Thr	Cys	Glu	Gln	Arg	Ala	Ala	Arg	Ile	Ser	Val	Gly	Pro
	690					695					700				
Arg	Cys	Val	Lys	Ala	Phe	Thr	Glu	Cys	Cys	Val	Val	Ala	Ser	Gln	Leu
705					710					715					720
Arg	Ala	Asn	Asn	Ser	His	Lys	Asp	Leu	Gln	Leu	Gly	Arg	Leu	His	Met
				725					730					735	
Lys	Thr	Leu	Leu	Pro	Val	Ser	Lys	Pro	Glu	Ile	Arg	Ser	Tyr	Phe	Pro
			740					745					750		

1185					1190					1195				1200	
Lys	Gly	Asn	Pro	Pro	Ile	Tyr	Arg	Phe	Trp	Lys	Asp	Ser	Leu	Gln	His
				1205					1210					1215	
Lys	Asp	Ser	Ser	Val	Pro	Asn	Thr	Gly	Thr	Ala	Arg	Met	Val	Glu	Thr
			1220					1225					1230		
Thr	Ala	Tyr	Ala	Leu	Leu	Thr	Ser	Leu	Asn	Leu	Lys	Asp	Ile	Asn	Tyr
		1235					1240					1245			
Val	Asn	Pro	Ile	Ile	Lys	Trp	Leu	Ser	Glu	Glu	Gln	Arg	Tyr	Gly	Gly
	1250					1255					1260				
Gly	Phe	Tyr	Ser	Thr	Gln	Asp	Thr	Ile	Asn	Ala	Ile	Glu	Gly	Leu	Thr
1265					1270					1275				1280	
Glu	Tyr	Ser	Leu	Leu	Val	Lys	Gln	Leu	Arg	Leu	Asn	Met	Asp	Ile	Asp
			1285					1290						1295	
Val	Ala	Tyr	Lys	His	Lys	Gly	Pro	Leu	His	Asn	Tyr	Lys	Met	Thr	Asp
			1300					1305					1310		
Lys	Asn	Phe	Leu	Gly	Arg	Pro	Val	Glu	Val	Leu	Leu	Asn	Asp	Asp	Leu
	1315						1320					1325			
Val	Val	Ser	Thr	Gly	Phe	Gly	Ser	Gly	Leu	Ala	Thr	Val	His	Val	Thr
	1330					1335					1340				
Thr	Val	Val	His	Lys	Thr	Ser	Thr	Ser	Glu	Glu	Val	Cys	Ser	Phe	Tyr
1345					1350					1355				1360	
Leu	Lys	Ile	Asp	Thr	Gln	Asp	Ile	Glu	Ala	Ser	His	Tyr	Arg	Gly	Tyr
			1365					1370						1375	
Gly	Asn	Ser	Asp	Tyr	Lys	Arg	Ile	Val	Ala	Cys	Ala	Ser	Tyr	Lys	Pro
			1380					1385					1390		
Ser	Arg	Glu	Glu	Ser	Ser	Ser	Gly	Ser	Ser	His	Ala	Val	Met	Asp	Ile
	1395						1400					1405			
Ser	Leu	Pro	Thr	Gly	Ile	Asn	Ala	Asn	Glu	Glu	Asp	Leu	Lys	Ala	Leu
	1410					1415					1420				
Val	Glu	Gly	Val	Asp	Gln	Leu	Phe	Thr	Asp	Tyr	Gln	Ile	Lys	Asp	Gly
1425					1430					1435				1440	
His	Val	Ile	Leu	Gln	Leu	Asn	Ser	Ile	Pro	Ser	Ser	Asp	Phe	Leu	Cys
			1445					1450						1455	
Val	Arg	Phe	Arg	Ile	Phe	Glu	Leu	Phe	Glu	Val	Gly	Phe	Leu	Ser	Pro
			1460					1465					1470		
Ala	Thr	Phe	Thr	Val	Tyr	Glu	Tyr	His	Arg	Pro	Asp	Lys	Gln	Cys	Thr
	1475						1480						1485		
Met	Phe	Tyr	Ser	Thr	Ser	Asn	Ile	Lys	Ile	Gln	Lys	Val	Cys	Glu	Gly
	1490					1495					1500				
Ala	Thr	Cys	Lys	Cys	Ile	Glu	Ala	Asp	Cys	Gly	Gln	Met	Gln	Lys	Glu
1505					1510					1515				1520	
Leu	Asp	Leu	Thr	Ile	Ser	Ala	Glu	Thr	Arg	Lys	Gln	Thr	Ala	Cys	Asn
			1525					1530						1535	
Pro	Glu	Ile	Ala	Tyr	Ala	Tyr	Lys	Val	Ile	Ile	Thr	Ser	Ile	Thr	Thr
			1540					1545					1550		
Glu	Asn	Val	Phe	Val	Lys	Tyr	Lys	Ala	Thr	Leu	Leu	Asp	Ile	Tyr	Lys
	1555						1560					1565			
Thr	Gly	Glu	Ala	Val	Ala	Glu	Lys	Asp	Ser	Glu	Ile	Thr	Phe	Ile	Lys
	1570					1575					1580				
Lys	Val	Thr	Cys	Thr	Asn	Ala	Glu	Leu	Val	Lys	Gly	Arg	Gln	Tyr	Leu
1585					1590					1595				1600	
Ile	Met	Gly	Lys	Glu	Ala	Leu	Gln	Ile	Lys	Tyr	Asn	Phe	Thr	Phe	Arg
			1605					1610						1615	
Tyr	Ile	Tyr	Pro	Leu	Asp	Ser	Leu	Thr	Trp	Ile	Glu	Tyr	Trp	Pro	Arg
			1620					1625					1630		

Asp	Thr	Thr	Cys	Ser	Ser	Cys	Gln	Ala	Phe	Leu	Ala	Asn	Leu	Asp	Glu
		1635					1640					1645			
Phe	Ala	Glu	Asp	Ile	Phe	Leu	Asn	Gly	Cys	Glu	Gln	Lys	Leu	Ile	Ser
	1650					1655					1660				
Glu	Glu	Asp	Leu	Gly	Gly	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu
1665					1670					1675					1680
His	His	His	His	His	His										
				1685											

<210> 359

<211> 1676

<212> PRT

<213> Artificial Sequence

<220>

<223> hC5 P01031

<400> 359

Met	Gly	Leu	Leu	Gly	Ile	Leu	Cys	Phe	Leu	Ile	Phe	Leu	Gly	Lys	Thr
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Trp	Gly	Gln	Glu	Gln	Thr	Tyr	Val	Ile	Ser	Ala	Pro	Lys	Ile	Phe	Arg
		20					25						30		
Val	Gly	Ala	Ser	Glu	Asn	Ile	Val	Ile	Gln	Val	Tyr	Gly	Tyr	Thr	Glu
		35					40					45			
Ala	Phe	Asp	Ala	Thr	Ile	Ser	Ile	Lys	Ser	Tyr	Pro	Asp	Lys	Lys	Phe
	50					55					60				
Ser	Tyr	Ser	Ser	Gly	His	Val	His	Leu	Ser	Ser	Glu	Asn	Lys	Phe	Gln
65					70					75					80
Asn	Ser	Ala	Ile	Leu	Thr	Ile	Gln	Pro	Lys	Gln	Leu	Pro	Gly	Gly	Gln
			85						90					95	
Asn	Pro	Val	Ser	Tyr	Val	Tyr	Leu	Glu	Val	Val	Ser	Lys	His	Phe	Ser
			100					105					110		
Lys	Ser	Lys	Arg	Met	Pro	Ile	Thr	Tyr	Asp	Asn	Gly	Phe	Leu	Phe	Ile
		115					120					125			
His	Thr	Asp	Lys	Pro	Val	Tyr	Thr	Pro	Asp	Gln	Ser	Val	Lys	Val	Arg
	130					135					140				
Val	Tyr	Ser	Leu	Asn	Asp	Asp	Leu	Lys	Pro	Ala	Lys	Arg	Glu	Thr	Val
145					150					155					160
Leu	Thr	Phe	Ile	Asp	Pro	Glu	Gly	Ser	Glu	Val	Asp	Met	Val	Glu	Glu
			165						170					175	
Ile	Asp	His	Ile	Gly	Ile	Ile	Ser	Phe	Pro	Asp	Phe	Lys	Ile	Pro	Ser
		180						185					190		
Asn	Pro	Arg	Tyr	Gly	Met	Trp	Thr	Ile	Lys	Ala	Lys	Tyr	Lys	Glu	Asp
	195					200						205			
Phe	Ser	Thr	Thr	Gly	Thr	Ala	Tyr	Phe	Glu	Val	Lys	Glu	Tyr	Val	Leu
	210					215					220				
Pro	His	Phe	Ser	Val	Ser	Ile	Glu	Pro	Glu	Tyr	Asn	Phe	Ile	Gly	Tyr
225					230					235					240
Lys	Asn	Phe	Lys	Asn	Phe	Glu	Ile	Thr	Ile	Lys	Ala	Arg	Tyr	Phe	Tyr
			245						250					255	
Asn	Lys	Val	Val	Thr	Glu	Ala	Asp	Val	Tyr	Ile	Thr	Phe	Gly	Ile	Arg
		260					265						270		
Glu	Asp	Leu	Lys	Asp	Asp	Gln	Lys	Glu	Met	Met	Gln	Thr	Ala	Met	Gln
		275					280						285		

Asn	Thr	Met	Leu	Ile	Asn	Gly	Ile	Ala	Gln	Val	Thr	Phe	Asp	Ser	Glu
290						295					300				
Thr	Ala	Val	Lys	Glu	Leu	Ser	Tyr	Tyr	Ser	Leu	Glu	Asp	Leu	Asn	Asn
305					310					315					320
Lys	Tyr	Leu	Tyr	Ile	Ala	Val	Thr	Val	Ile	Glu	Ser	Thr	Gly	Gly	Phe
				325					330					335	
Ser	Glu	Glu	Ala	Glu	Ile	Pro	Gly	Ile	Lys	Tyr	Val	Leu	Ser	Pro	Tyr
			340					345					350		
Lys	Leu	Asn	Leu	Val	Ala	Thr	Pro	Leu	Phe	Leu	Lys	Pro	Gly	Ile	Pro
		355					360					365			
Tyr	Pro	Ile	Lys	Val	Gln	Val	Lys	Asp	Ser	Leu	Asp	Gln	Leu	Val	Gly
	370					375					380				
Gly	Val	Pro	Val	Thr	Leu	Asn	Ala	Gln	Thr	Ile	Asp	Val	Asn	Gln	Glu
385					390					395					400
Thr	Ser	Asp	Leu	Asp	Pro	Ser	Lys	Ser	Val	Thr	Arg	Val	Asp	Asp	Gly
				405					410					415	
Val	Ala	Ser	Phe	Val	Leu	Asn	Leu	Pro	Ser	Gly	Val	Thr	Val	Leu	Glu
			420					425					430		
Phe	Asn	Val	Lys	Thr	Asp	Ala	Pro	Asp	Leu	Pro	Glu	Glu	Asn	Gln	Ala
		435				440						445			
Arg	Glu	Gly	Tyr	Arg	Ala	Ile	Ala	Tyr	Ser	Ser	Leu	Ser	Gln	Ser	Tyr
	450					455					460				
Leu	Tyr	Ile	Asp	Trp	Thr	Asp	Asn	His	Lys	Ala	Leu	Leu	Val	Gly	Glu
465					470					475					480
His	Leu	Asn	Ile	Ile	Val	Thr	Pro	Lys	Ser	Pro	Tyr	Ile	Asp	Lys	Ile
				485					490					495	
Thr	His	Tyr	Asn	Tyr	Leu	Ile	Leu	Ser	Lys	Gly	Lys	Ile	Ile	His	Phe
			500					505					510		
Gly	Thr	Arg	Glu	Lys	Phe	Ser	Asp	Ala	Ser	Tyr	Gln	Ser	Ile	Asn	Ile
		515					520					525			
Pro	Val	Thr	Gln	Asn	Met	Val	Pro	Ser	Ser	Arg	Leu	Leu	Val	Tyr	Tyr
	530					535					540				
Ile	Val	Thr	Gly	Glu	Gln	Thr	Ala	Glu	Leu	Val	Ser	Asp	Ser	Val	Trp
545					550					555					560
Leu	Asn	Ile	Glu	Glu	Lys	Cys	Gly	Asn	Gln	Leu	Gln	Val	His	Leu	Ser
				565					570					575	
Pro	Asp	Ala	Asp	Ala	Tyr	Ser	Pro	Gly	Gln	Thr	Val	Ser	Leu	Asn	Met
			580					585					590		
Ala	Thr	Gly	Met	Asp	Ser	Trp	Val	Ala	Leu	Ala	Ala	Val	Asp	Ser	Ala
		595					600					605			
Val	Tyr	Gly	Val	Gln	Arg	Gly	Ala	Lys	Lys	Pro	Leu	Glu	Arg	Val	Phe
	610					615					620				
Gln	Phe	Leu	Glu	Lys	Ser	Asp	Leu	Gly	Cys	Gly	Ala	Gly	Gly	Gly	Leu
625					630					635					640
Asn	Asn	Ala	Asn	Val	Phe	His	Leu	Ala	Gly	Leu	Thr	Phe	Leu	Thr	Asn
				645					650					655	
Ala	Asn	Ala	Asp	Asp	Ser	Gln	Glu	Asn	Asp	Glu	Pro	Cys	Lys	Glu	Ile
			660					665					670		
Leu	Arg	Pro	Arg	Arg	Thr	Leu	Gln	Lys	Lys	Ile	Glu	Glu	Ile	Ala	Ala
		675					680					685			
Lys	Tyr	Lys	His	Ser	Val	Val	Lys	Lys	Cys	Cys	Tyr	Asp	Gly	Ala	Cys
	690					695					700				
Val	Asn	Asn	Asp	Glu	Thr	Cys	Glu	Gln	Arg	Ala	Ala	Arg	Ile	Ser	Leu
705					710					715					720
Gly	Pro	Arg	Cys	Ile	Lys	Ala	Phe	Thr	Glu	Cys	Cys	Val	Val	Ala	Ser

Ile Lys Ala Asp Asn Phe Leu Leu Glu Asn Thr Leu Pro Ala Gln Ser
 1170 1175 1180
 Thr Phe Thr Leu Ala Ile Ser Ala Tyr Ala Leu Ser Leu Gly Asp Lys
 1185 1190 1195 1200
 Thr His Pro Gln Phe Arg Ser Ile Val Ser Ala Leu Lys Arg Glu Ala
 1205 1210 1215
 Leu Val Lys Gly Asn Pro Pro Ile Tyr Arg Phe Trp Lys Asp Asn Leu
 1220 1225 1230
 Gln His Lys Asp Ser Ser Val Pro Asn Thr Gly Thr Ala Arg Met Val
 1235 1240 1245
 Glu Thr Thr Ala Tyr Ala Leu Leu Thr Ser Leu Asn Leu Lys Asp Ile
 1250 1255 1260
 Asn Tyr Val Asn Pro Val Ile Lys Trp Leu Ser Glu Glu Gln Arg Tyr
 1265 1270 1275 1280
 Gly Gly Gly Phe Tyr Ser Thr Gln Asp Thr Ile Asn Ala Ile Glu Gly
 1285 1290 1295
 Leu Thr Glu Tyr Ser Leu Leu Val Lys Gln Leu Arg Leu Ser Met Asp
 1300 1305 1310
 Ile Asp Val Ser Tyr Lys His Lys Gly Ala Leu His Asn Tyr Lys Met
 1315 1320 1325
 Thr Asp Lys Asn Phe Leu Gly Arg Pro Val Glu Val Leu Leu Asn Asp
 1330 1335 1340
 Asp Leu Ile Val Ser Thr Gly Phe Gly Ser Gly Leu Ala Thr Val His
 1345 1350 1355 1360
 Val Thr Thr Val Val His Lys Thr Ser Thr Ser Glu Glu Val Cys Ser
 1365 1370 1375
 Phe Tyr Leu Lys Ile Asp Thr Gln Asp Ile Glu Ala Ser His Tyr Arg
 1380 1385 1390
 Gly Tyr Gly Asn Ser Asp Tyr Lys Arg Ile Val Ala Cys Ala Ser Tyr
 1395 1400 1405
 Lys Pro Ser Arg Glu Glu Ser Ser Ser Gly Ser Ser His Ala Val Met
 1410 1415 1420
 Asp Ile Ser Leu Pro Thr Gly Ile Ser Ala Asn Glu Glu Asp Leu Lys
 1425 1430 1435 1440
 Ala Leu Val Glu Gly Val Asp Gln Leu Phe Thr Asp Tyr Gln Ile Lys
 1445 1450 1455
 Asp Gly His Val Ile Leu Gln Leu Asn Ser Ile Pro Ser Ser Asp Phe
 1460 1465 1470
 Leu Cys Val Arg Phe Arg Ile Phe Glu Leu Phe Glu Val Gly Phe Leu
 1475 1480 1485
 Ser Pro Ala Thr Phe Thr Val Tyr Glu Tyr His Arg Pro Asp Lys Gln
 1490 1495 1500
 Cys Thr Met Phe Tyr Ser Thr Ser Asn Ile Lys Ile Gln Lys Val Cys
 1505 1510 1515 1520
 Glu Gly Ala Ala Cys Lys Cys Val Glu Ala Asp Cys Gly Gln Met Gln
 1525 1530 1535
 Glu Glu Leu Asp Leu Thr Ile Ser Ala Glu Thr Arg Lys Gln Thr Ala
 1540 1545 1550
 Cys Lys Pro Glu Ile Ala Tyr Ala Tyr Lys Val Ser Ile Thr Ser Ile
 1555 1560 1565
 Thr Val Glu Asn Val Phe Val Lys Tyr Lys Ala Thr Leu Leu Asp Ile
 1570 1575 1580
 Tyr Lys Thr Gly Glu Ala Val Ala Glu Lys Asp Ser Glu Ile Thr Phe
 1585 1590 1595 1600
 Ile Lys Lys Val Thr Cys Thr Asn Ala Glu Leu Val Lys Gly Arg Gln

				1605					1610					1615					
Tyr	Leu	Ile	Met	Gly	Lys	Glu	Ala	Leu	Gln	Ile	Lys	Tyr	Asn	Phe	Ser				
				1620					1625					1630					
Phe	Arg	Tyr	Ile	Tyr	Pro	Leu	Asp	Ser	Leu	Thr	Trp	Ile	Glu	Tyr	Trp				
				1635					1640					1645					
Pro	Arg	Asp	Thr	Thr	Cys	Ser	Ser	Cys	Gln	Ala	Phe	Leu	Ala	Asn	Leu				
				1650					1655					1660					
Asp	Glu	Phe	Ala	Glu	Asp	Ile	Phe	Leu	Asn	Gly	Cys								
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<220>
 <223> human C5 peptide aa591-599

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<210> 361
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 361
 Trp Glu Val His Leu Val Pro Arg Arg Lys Gln Leu Gln Phe Ala Leu
 1 5 10 15
 Pro Asp Ser Leu
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<210> 362
 <211> 121
 <212> PRT
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<220>
 <223> HCVR of M1M17628N

<400> 362
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 Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Arg Asp
 20 25 30
 Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Asp Tyr Met
 35 40 45
 Gly Tyr Ile Ser Tyr Ser Gly Gly Thr Tyr Tyr Asn Pro Ser Leu Lys

50					55					60					
Ser	Arg	Phe	Ser	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Tyr	Leu
65					70					75					80
Gln	Leu	Asn	Ser	Val	Thr	Phe	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	Ala
				85					90					95	
Arg	Gly	Val	Ser	Tyr	Tyr	Gly	Ser	Thr	Tyr	Tyr	Phe	Asp	Tyr	Trp	Gly
			100					105					110		
Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser							
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 <212> PRT
 <213> Artificial Sequence

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<400> 363															
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Asp	Thr	Ile	Thr	Ile	Thr	Cys	His	Ala	Ser	Gln	Asn	Ile	His	Val	Trp
			20					25				30			
Leu	Asn	Trp	Tyr	Gln	Gln	Thr	Pro	Gly	Asn	Ile	Pro	Lys	Leu	Leu	Ile
		35				40					45				
Tyr	Lys	Ala	Ser	Asn	Leu	His	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Ala
	50					55				60					
Ser	Gly	Ser	Gly	Thr	Gly	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser
65					70				75					80	
Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Gly	Gln	Ser	Tyr	Pro	Leu
				85				90					95		
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys					
		100						105							

<210> 364
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IRBP peptide

<400> 364															
Gly	Pro	Thr	His	Leu	Phe	Gln	Pro	Ser	Leu	Val	Leu	Asp	Met	Ala	Lys
1				5					10					15	
Val	Leu	Leu	Asp												
			20												

<210> 365
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>

<223> HCVR of M1M17627N

<400> 365

Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			20					25					30		
Trp	Ile	His	Trp	Met	Arg	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Arg	Ile	His	Pro	Ser	Asp	Ser	Asp	Thr	Asn	Tyr	Asn	Gln	Lys	Phe
	50					55					60				
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	Ser	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Ile	Leu	Pro	Pro	Pro	Pro	Tyr	Tyr	Tyr	Ala	Asn	Tyr	Gly	Gly	Gly
		100					105						110		
Thr	Met	Asp	Tyr	Trp	Gly	Arg	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	
		115					120					125			

<210> 366

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> LCVR of M1M17627N

<400> 366

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