

10168W001_seqlisting

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

<160> 366

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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
50     55     60
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Arg Lys Thr Val Tyr
65     70     75     80
Leu Gln Met Asn Ser Leu Arg Gly Glu Asp Thr Ala Val Tyr Tyr Cys
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 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
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 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
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 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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 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
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 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
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 Thr Leu Val Thr Val Ser Ser
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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
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Asp Asp Phe Ala Ala Tyr Tyr Cys Gln Gln Tyr Asn Asp Tyr Ser Tyr
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Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
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 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
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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
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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asn Thr Ile Phe
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Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
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ccaggggaagg gactggagtg ggtctcagct attagtgggtc gtggtgatag tacatactac 180
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ctgcaaatga 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
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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

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			85					90		95
Thr	Phe	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	
		100					105			

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 1 5

<210> 77
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<210> 78
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 <400> 78
 Ala Ala Ser
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<210> 79
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 <400> 79
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<210> 80
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10168w001_seqlisting

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<211> 363

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<220>

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tcctgtgcag cctctggatt cacctttaac agatatgcca tgacctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct ataagtggta gtggtagcag cacatactac 180
acagactccg tgaaggccg gttcaccatc tccagagaca attccaagaa ttcggtggat 240
ctgcaaatgc acagcctgag agtcgaagac acggccatat attattgtgc gagagggact 300
acagtcacta cggggtacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 360
tca 363

<210> 82

<211> 121

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<400> 82

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Arg Ser Gly Gly
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

<210> 83

<211> 24

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<211> 24

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<400> 85

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<210> 86

<211> 8

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<213> Artificial Sequence

<220>

<223> synthetic

<400> 86

Ile Ser Gly Ser Gly Ser Ser Thr
1 5

<210> 87

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 87

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Ala Arg Gly Thr Thr Val Thr Thr Gly Tyr Gly Met Asp Val
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<210> 89

<211> 321

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 89

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ttcacttgcc aggcgagtca ggacattacc aattctttaa attggtatca acagaaacct 120

10168w001_seqlisting

gggagagccc ctaagctcct gatctacgat gcacgtatt tgaaggcagg ggtcccatca 180
 agattcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240
 gaagatatgg caacatatta ctgtcaacaa tatgatgatc tcccatcac ttttggccag 300
 gggaccaagc tggagatcaa a 321

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

<220>
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<400> 90
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 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
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 <213> Artificial Sequence

<220>
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<400> 91
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<210> 92
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 <212> PRT
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<220>
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<400> 92
 Gln Asp Ile Thr Asn Ser
 1 5

<210> 93
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 <213> Artificial Sequence

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<400> 93
 gatgcatcg 9

<210> 94
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<400> 94

Asp Ala Ser

1

<210> 95

<211> 27

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<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

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<211> 360

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 97

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ccaggaagg 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
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<210> 98

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 98

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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
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10168w001_seqlisting

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
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<220>
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<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
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<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
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10168w001_seqlisting

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<400> 104
 Ala Arg Glu Gly Asn Val Asp Thr Thr Met Ile Phe Asp Tyr
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<210> 105
 <211> 321
 <212> DNA
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<220>
 <223> synthetic

<400> 105
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 gggaaagccc ctaaactcct gatctatgct gcatccagtt tacaaagtgg ggtcccatcg 180
 aggttcgccg gccgtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtctacaa gatttcaatt acccgtggac gttcggccaa 300
 gggaccaag 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
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 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
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18

<210> 108
 <211> 6

<212> PRT
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<400> 108
 Gln Gly Ile Arg Asn Asp
 1 5

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

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 <223> synthetic

<400> 109
 gctgcatcc

9

<210> 110
 <211> 3
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<400> 110
 Ala Ala Ser
 1

<210> 111
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<220>
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<400> 111
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27

<210> 112
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<220>
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<400> 112
 Leu Gln Asp Phe Asn Tyr Pro Trp Thr
 1 5

<210> 113
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 <212> DNA
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<220>
 <223> synthetic

<400> 113

10168w001_seqlisting

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gggaaagccc ctaaactcct gatctatgct gcatccagtt tacaaagtgg ggtcccacg 180
aggttcgccg gccgtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcatcaa gatttcaatt acccgtggac gttcggccaa 300
gggaccaagg tggaatcaa a                                     321

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

<220>
 <223> synthetic

<400> 114
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 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>
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<400> 116
 Gln Gly Ile Arg Asn Asp
 1 5

<210> 117
 <211> 9
 <212> DNA
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<220>
 <223> synthetic

<400> 117
 gctgcatcc 9

<210> 118

10168w001_seqlisting

<211> 3
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<220>
<223> synthetic

<400> 118
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1

<210> 119
<211> 27
<212> DNA
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<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 actgtgcgag agaacataac 300
gtggatacaa ctatgatatt tgactactgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 122
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 122
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1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Val Ser Ser
20 25 30
Tyr Trp Thr Trp Ile Arg Gln Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

10168w001_seqlisting

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								

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<220>
 <223> synthetic

<400> 123
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<210> 124
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<400> 124
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 1 5

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

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<400> 125
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<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

10168W001_seqlisting

<400> 127
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<210> 128
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<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>
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<400> 129
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gggaaagccc ctaaactcct gatctatgct gcatccagtt tacaaagtgg ggtcccatcg 180
aggttcgccg gccgtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacaa gatttcaatt acccgtggca cttcggccaa 300
gggaccaagg tggaatcaa a 321

<210> 130
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<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
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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>
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<400> 133
 gctgcatcc

9

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

<220>
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<400> 134
 Ala Ala Ser
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<210> 135
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<220>
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<400> 135
 ctacaagatt tcaattaccc gtggcac

27

<210> 136
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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
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<220>
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ccagggaagg gactggagtg gattggctat atctattaca gtgggagttc caactacaac 180
ccctccctca agagtcgagc caccatttca gtagacacgt ccaagaacca gttctccctg 240
aagctgagtt ctgtgaccgc tgcggacacg gccgtatatt actgtgagag agaagggaa 300
gtggatacaa ctatgataca tgactactgg ggccagggaa ccctggtcac cgtctcctca 360

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

<220>
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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 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
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<212> PRT
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<220>
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<400> 140
Gly Asp Ser Val Ser Ser Ser Tyr
1 5

<210> 141
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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10168w001_seqlisting

<400> 141
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<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>
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<400> 144
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1 5 10

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

<220>
<223> synthetic

<400> 145
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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
gtggatcaca ctatgatatt tgactactgg ggccagggaa ccctgggtcac cgtctcctca 360

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

<220>
<223> synthetic

<400> 146
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

10168w001_seqlisting

1	Thr	Leu	Ser	Leu	5	Thr	Cys	Thr	Val	10	Ser	Gly	Asp	Ser	Val	15	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
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 147
 ggtgactccg tcagtagttc ctac

24

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

<220>
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<400> 148
 Gly Asp Ser Val Ser Ser Ser Tyr
 1 5

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

<220>
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<400> 149
 atctattaca gtgggagttc c

21

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

<220>
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<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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tcctgtgcag	cctctggatt	caccttcagt	gactcctaca	tgtcctggat	ccgtcaggct	120
ccaggggaagg	gactagagtg	gatttcatac	attggtagta	gtggaatac	cttttactac	180
gcagactctg	tgaagggccg	gttcaccatt	tccagagaca	acgccaacaa	tttactgtat	240
ctgcaaataa	ccagcctgag	agccgaggac	acggccgtgt	attactgtgc	gagagaagaa	300
ggcgattttt	ggagtgccgt	tgactcctgg	ggccagggaa	ccctggtcac	cgtctcctca	360

<210> 154

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 154

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										

<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

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<210> 161
 <211> 321
 <212> DNA
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<220>
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<400> 161
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 ggtaaagccc ctaaactcct gatccatact gcattccactt 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
caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcggt ggccatgcca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg gctggcagtt atatcatctg atggcagtaa taaacagtat 180
gcagattctg tgaagggccg attcaccatc tccagggaca atcccaagaa cacgctgtat 240
ctgcaaatga acagtctgag agttggggac acggctattt attactgtgc gaaagagggtg 300
gcacctcggt attattatta cggctctggac gtctggggcc aaggggaccac ggtcaccgtc 360
tcctca

<210> 170
<211> 122
<212> PRT
<213> Artificial Sequence

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<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
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

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Gly Phe Thr Phe Gly Gly His Ala
 1          5

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<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

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Ile Ser Ser Asp Gly Ser Asn Lys
 1          5

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

<220>
 <223> synthetic

<400> 175
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<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 cctgggtatca gcagaaacca 120
 gggaagggtc ctaaactcct gatctatact gcattccactt 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
 ccaggggaagg ggccggagtg ggtctcaggt ataggtggta atggtgttac cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgttt 240
 ctgcaaatga atagcctgag agccgaggac acggccgtat attatttgtgt gcaggggggt 300
 ttagtggtt attttacagg ctactggggc caggaaccc 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
 115

<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

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<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
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 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 ccccgcctac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> 194
 <211> 107

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<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>
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<400> 195
cagagtatta gtacctat

18

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

<220>
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<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 acagtgcctt 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
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 tcctgtgcag cgtctggatt caccttcagt gggttatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcactt atatggcttg atggaagtaa tgactactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgttatat 240
 ctgcaaataa acagactgag agccgaggac acggctgtgt attactgtgc gagagatggc 300
 ccggttgctg ctataccca ctactggggc cagggaaccc tggtcaccgt ctctctca 357

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

<220>
 <223> synthetic

<400> 202
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 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
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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>
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<400> 207
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36

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

<220>
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<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
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atcacttgcc gggccagtc gagtattagt aggtggttgg cctgggtatca gctgaaacca 120
gggaaagccc ctaagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagac ttcactctca ccatcagcag cctgcaacct 240
gatgattttg caacttatta ctgccaacag tataatactt attcgtacac ttttggccag 300
gggaccaagc tggagatcaa a 321

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

<220>
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<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
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 tcctgtgcag cctctggatt cacctttgat gaatatggca tgacttgggt ccgccaagtt 120
 ccagggaagg ggctggagtg ggtctctggt attacttgga atggtgggtt cacagattat 180
 acagactctg tgaagggccg attcaccagc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agccgaggac acggccttgt attactgtgc gagagatgga 300
 tatagcagct cgtggggggc ttatgatata tggggccaag ggacaatggt caccgtctct 360
 tca 363

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<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

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<400> 219
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24

<210> 220
 <211> 8
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<220>
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<400> 220
 Gly Phe Thr Phe Asp Glu Tyr Gly
 1 5

<210> 221
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 <212> DNA
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<220>
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<400> 221
 attacttgga atggtggttt caca

24

<210> 222
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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

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<400> 223

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42

<210> 224

<211> 14

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Ala Arg Asp Gly Tyr Ser Ser Ser Trp Gly Ala Tyr Asp Ile
1 5 10

<210> 225

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 225

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atcacttgcc	gggcaagtca	gagcattagc	acctatTTaa	attgggtatca	gcagaaacca	120
gggaaagccc	ctaagctcct	gatctatgct	gcatccagtt	tgcaaagtgg	ggtcccatta	180
aggttcagtg	gcagtgatc	tgggactgat	ttcactctca	ccatcagcag	tctgcaacct	240
gaagattttg	caagttatTT	ctgtcaacag	agttacagta	ccccgtacac	ttttggccag	300
gggaccaagc	tgagatcaa	a				321

<210> 226

<211> 107

<212> PRT

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<220>

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<400> 226

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
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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			

10168w001_seqlisting
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

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 <211> 18
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<400> 227
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<210> 228
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<220>
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<400> 228
 Gln Ser Ile Ser Thr Tyr
 1 5

<210> 229
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 <212> DNA
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<220>
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<400> 229
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<210> 230
 <211> 3
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<220>
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<400> 230
 Ala Ala Ser
 1

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

<220>
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<400> 231
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<210> 232
 <211> 9
 <212> PRT
 <213> Artificial Sequence

10168w001_seqlisting

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<400> 232

Gln Gln Ser Tyr Ser Thr Pro Tyr Thr
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<210> 233

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 233

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tcctgtgcag cctctggatt cacctttaat gattatgcca tgcactgggt ccgtcaagct 120
ccaggggaagg gtctggagtg ggtctctctt attagtggag atggtggtaa cacatactat 180
gcagactctg tgaagggccg actcaccatc tccagagaca acagcaaaaa ctccctgtat 240
ctgcaaatga acagtctgag aacagaggac accgccttat attactgtgc aaaagataag 300
ggctggaact tcggttactt cgatctcttg ggccgtggca ccctggtcac tgtctcctca 360

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<211> 120

<212> PRT

<213> Artificial Sequence

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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>

<223> synthetic

<400> 235

ggattcacct ttaatgatta tgcc

24

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<213> Artificial Sequence

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Gly Phe Thr Phe Asn Asp Tyr Ala
1 5

<210> 237

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 237

attagtggag atggtggtaa caca

24

<210> 238

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

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<400> 238

Ile Ser Gly Asp Gly Asn Thr
1 5

<210> 239

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 239

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<210> 240

<211> 13

<212> PRT

<213> Artificial Sequence

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<400> 240

Ala Lys Asp Lys Gly Trp Asn Phe Gly Tyr Phe Asp Leu
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<210> 241

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

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<400> 241

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gggaaagccc ctaaactcct gatctatgat gcatccagtt tacaaagtgg ggtcccatca 180

10168w001_seqlisting

cggttcagtg gcagcggatc tgggacagat ttcactctca ccatcaccag tctgcaacct 240
gaagattttg ccacttacta ctgtcaacag aatgacaata ttcttcaccc tctcactttc 300
ggcggagga ccaaggtgga gatcaaa 327

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<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
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<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 243
cagaacattg acacctat 18

<210> 244
<211> 6
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<220>
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<400> 244
Gln Asn Ile Asp Thr Tyr
1 5

<210> 245
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<220>
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<400> 245
gatgcatcc 9

<210> 246
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10168w001_seqlisting

<220>
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<400> 246
Asp Ala Ser
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<210> 247
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<220>
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<400> 247
caacagaatg acaatattct tcaccctctc act 33

<210> 248
<211> 11
<212> PRT
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<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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ccagggaagg ggctggagtg ggtggccaac ataaagcaag atggaagtga ggaaaactat 180
gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactttat 240
ctgcaaataga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatcga 300
agcacctcgt gggctcccta ctggttcttc gatctctggg gccgtggcac cctggtcact 360
gtctcctca 369

<210> 250
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 250
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

10168w001_seqlisting

65	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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 <212> DNA
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<220>
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<400> 251
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<210> 252
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 252
 Gly Phe His Ser Asn Arg Tyr Trp
 1 5

<210> 253
 <211> 24
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<400> 253
 ataaagcaag atggaagtga ggaa 24

<210> 254
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<400> 254
 Ile Lys Gln Asp Gly Ser Glu Glu
 1 5

<210> 255
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 255
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10168w001_seqlisting

<210> 256
 <211> 16
 <212> PRT
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<220>
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<400> 256
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<210> 257
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
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 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
 caagggacac 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
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<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

gaagtgcagc tgggtggagtc tggggggaggc gtggtacagc ggggggagtc cctgagactc 60

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ccagggaagg gtctagagtg gatctctctt attagtgggt atggtgacac tacatgggat 180
ggagactctg tgaagggccg attcaccatc tccagagaca acaacgaaaa ctccctcttt 240
ctgcaaatga acgatctgag aactgaggac accgccatgt actactgtgc aagagatatg 300
gggtggaact tcitttcagtt gcaatactgg ggccaggga ccctggtcac cgtctctctca 360
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<211> 120
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<213> Artificial Sequence

<220>
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 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
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<213> Artificial Sequence

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<223> synthetic

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<210> 268
<211> 8
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Asp Phe Ile Phe Lys Asp Tyr Ala
 1          5
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<210> 269
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<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

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<400> 269
attagtgggtg atggtgacac taca 24
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 <212> PRT
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<220>
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<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 tggggtggaa cttctttcag ttgcaatac 39

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

<220>
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<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
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 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 accctgggtca ccgtctcctc 360
 a 361

<210> 274
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 274
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 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ile Arg Gly
 20 25 30

10168w001_seqlisting

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								

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 <212> DNA
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<210> 276
 <211> 10
 <212> PRT
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<220>
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<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>
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<400> 277
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<210> 278
 <211> 7
 <212> PRT
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<220>
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<400> 278
 Ser Tyr Tyr Ser Gly Thr Ala
 1 5

<210> 279
 <211> 36
 <212> DNA
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<400> 279

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36

<210> 280

<211> 12

<212> PRT

<213> Artificial Sequence

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<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

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<223> synthetic

<400> 281

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ccgggacagg	cccctagact	gctgatctac	ggggcaagtt	ccagggccac	cggaatcccc	180
gaccggttca	gtggaagcgg	aagcgggaacc	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>

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<400> 283

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36

<210> 284
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<220>
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<400> 284
 Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
 1 5 10

<210> 285
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 <212> DNA
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<400> 285
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21

<210> 286
 <211> 7
 <212> PRT
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<400> 286
 Gly Ala Ser Ser Arg Ala Thr
 1 5

<210> 287
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 <212> DNA
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<400> 287
 caacagtacg gaagcagccc gtggacg

27

<210> 288
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 <212> PRT
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<400> 288
 Gln Gln Tyr Gly Ser Ser Pro Trp Thr
 1 5

<210> 289
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 <212> DNA
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<400> 289

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cctggactag ggcttgaatg gatgggatgg atcaacccta acagtgggtgg cacaaaatat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcaa tacagcctac 240
atggagctga aaagactgaa atctgacgac tcggccgtat attactgtgc gagagacgcc 300
cctcccatg atgtttttga tatctggggc caaggacat tggtcaccgt ctcttca 357
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<210> 290

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 290

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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
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<210> 291

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 291

ggatacacct tcaccggcta ctat

24

<210> 292

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 292

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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 acagtgggtgg 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	gctggtatca	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

10168w001_seqlisting

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>
 <223> synthetic

<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

10168W001_seqlisting

<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

caggtgcagc	tgcaagagtc	gggcccagga	ctggtgaagc	cttcacagac	cctgtccctc	60
acctgcactg	tctctggtgg	ctccatcagt	agtggtgctt	accactggag	ctggatccgc	120
cagcaccag	ggaagggcct	agagtggatt	ggatacatct	attacaatgg	ggacacctac	180
tataatccgt	ccctcaagag	tcgctgtacc	atttcagtgg	acacgtctaa	gaaccaattc	240
ttcctgaagg	tgacctctgt	gactgccgcg	gacacggcca	tgtattactg	tgcgggagaa	300
aagcagctga	ctgcttttga	tatctggggc	caagggacat	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>

<223> synthetic

<400> 307

ggtggctcca 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

10168W001_seqlisting

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 313
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ataacttgcc gggcgagtc ggacattaat aattttttta 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
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<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
gagggtgcagt tgggtggagtc tggggggaggt gtgggttcggc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatggca tgacctgggt ccgccaagct 120
ccagggaagg ggctggagtg ggtctctgggt attaattgga atggcgatag cacagagtat 180
tcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agccgaggac acggccttct atcactgtgc gagagagaat 300
aactggaact tctactttga ctactggggc cagggaaccc tggtcaccgt ctctctca 357

<210> 322
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 322

10168w001_seqlisting

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

10168W001_seqlisting

<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 gggccagtca gagggttagc 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>
<223> synthetic

<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
 1

 <210> 335
 <211> 27
 <212> DNA
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 <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

10168W001_seqlisting

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

<220>
<223> synthetic

<400> 337
caggtccacc tggtagagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggct 60
tcctgcaagg tttccgaaa caccctcact gaattatcca tgcactgggt gcgacaggct 120
cctggaaaag ggcttgagtg gatgggaggt tttgatcctg aagatgggtga cacaatctac 180
tcacagaagt tccagggcag agtcaccttg accgaggaca catctacaga cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgttc aacagtgggg 300
ggacctacct ctgactgctg gggccagga accctgggtca 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

10168w001_seqlisting

<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 tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120
gggaaagccc ctaaggctct gatcttcgat gcatccaatt tagaaccagg ggtcccatca 180
aggttcagtg gaagtggatc tgggacagat ttactttca ccatcatcag cctgcagcct 240
gaagatattg caacatatta ctgtcaacaa tatgataatc tcccgatcac cttcggccag 300
gggacacgac tggacattaa a 321

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

<220>

10168w001_seqlisting

<223> synthetic

<400> 346

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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

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<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

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Gln Asp Ile Ser Asn Tyr
 1           5

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<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

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Asp Ala Ser
 1

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<210> 351

10168w001_seqlisting

<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>
<223> synthetic

<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 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

10168w001_seqlisting

Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
290	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

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	Arg	Thr	Val	Ala	Ala
			100					105					110		
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
		115					120					125			
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
	130					135					140				
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
145					150					155					160
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
				165					170					175	
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr
			180					185					190		
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser
		195					200					205			
Phe	Asn	Arg	Gly	Glu	Cys										
	210														

<210> 355
 <211> 1676
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human C5

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<400> 355

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Met Gly Leu Leu Gly Ile Leu Cys Phe Leu Ile Phe Leu Gly Lys Thr
 1      5      10      15
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

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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
				725					730					735	
Gln	Leu	Arg	Ala	Asn	Ile	Ser	His	Lys	Asp	Met	Gln	Leu	Gly	Arg	Leu
			740					745					750		
His	Met	Lys	Thr	Leu	Leu	Pro	Val	Ser	Lys	Pro	Glu	Ile	Arg	Ser	Tyr
		755					760					765			
Phe	Pro	Glu	Ser	Trp	Leu	Trp	Glu	Val	His	Leu	Val	Pro	Arg	Arg	Lys
	770					775					780				
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
				805					810					815	
Ala	Lys	Val	Phe	Lys	Asp	Val	Phe	Leu	Glu	Met	Asn	Ile	Pro	Tyr	Ser
			820					825					830		
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
	850					855					860				
Ile	Cys	Thr	Ser	Glu	Ser	Pro	Val	Ile	Asp	His	Gln	Gly	Thr	Lys	Ser
865					870					875					880
Ser	Lys	Cys	Val	Arg	Gln	Lys	Val	Glu	Gly	Ser	Ser	Ser	His	Leu	Val
				885					890					895	
Thr	Phe	Thr	Val	Leu	Pro	Leu	Glu	Ile	Gly	Leu	His	Asn	Ile	Asn	Phe
			900					905					910		
Ser	Leu	Glu	Thr	Trp	Phe	Gly	Lys	Glu	Ile	Leu	Val	Lys	Thr	Leu	Arg
		915					920					925			
Val	Val	Pro	Glu	Gly	Val	Lys	Arg	Glu	Ser	Tyr	Ser	Gly	Val	Thr	Leu
	930					935					940				
Asp	Pro	Arg	Gly	Ile	Tyr	Gly	Thr	Ile	Ser	Arg	Arg	Lys	Glu	Phe	Pro
945					950					955					960
Tyr	Arg	Ile	Pro	Leu	Asp	Leu	Val	Pro	Lys	Thr	Glu	Ile	Lys	Arg	Ile
				965					970					975	
Leu	Ser	Val	Lys	Gly	Leu	Leu	Val	Gly	Glu	Ile	Leu	Ser	Ala	Val	Leu
			980					985					990		
Ser	Gln	Glu	Gly	Ile	Asn	Ile	Leu	Thr	His	Leu	Pro	Lys	Gly	Ser	Ala
		995					1000					1005			
Glu	Ala	Glu	Leu	Met	Ser	Val	Val	Pro	Val	Phe	Tyr	Val	Phe	His	Tyr
	1010					1015					1020				
Leu	Glu	Thr	Gly	Asn	His	Trp	Asn	Ile	Phe	His	Ser	Asp	Pro	Leu	Ile
1025					1030					1035					1040
Glu	Lys	Gln	Lys	Leu	Lys	Lys	Lys	Leu	Lys	Glu	Gly	Met	Leu	Ser	Ile
				1045					1050					1055	
Met	Ser	Tyr	Arg	Asn	Ala	Asp	Tyr	Ser	Tyr	Ser	Val	Trp	Lys	Gly	Gly
			1060					1065					1070		

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Ser Ala Ser Thr Trp Leu Thr Ala Phe Ala Leu Arg Val Leu Gly Gln
 1075 1080 1085
 Val Asn Lys Tyr Val Glu Gln Asn Gln Asn Ser Ile Cys Asn Ser Leu
 1090 1095 1100
 Leu Trp Leu Val Glu Asn Tyr Gln Leu Asp Asn Gly Ser Phe Lys Glu
 1105 1110 1115 1120
 Asn Ser Gln Tyr Gln Pro Ile Lys Leu Gln Gly Thr Leu Pro Val Glu
 1125 1130 1135
 Ala Arg Glu Asn Ser Leu Tyr Leu Thr Ala Phe Thr Val Ile Gly Ile
 1140 1145 1150
 Arg Lys Ala Phe Asp Ile Cys Pro Leu Val Lys Ile Asp Thr Ala Leu
 1155 1160 1165
 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

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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
 1665 1670 1675

<210> 356

<211> 1686

<212> PRT

<213> Artificial Sequence

<220>

<223> hC5 R885H

aa 1-1658: hC5 (aa 19-1676 of NM_001735.2 with
R885H change)

aa 1659-1686: myc-myc-hexahistidine tag

<400> 356

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
 355 360 365

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Pro	Val	Thr	Leu	Asn	Ala	Gln	Thr	Ile	Asp	Val	Asn	Gln	Glu	Thr	Ser
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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
			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	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
				485					490					495	
Arg	Glu	Lys	Phe	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	Ala	Tyr	Ser	Pro	Gly	Gln	Thr	Val	Ser	Leu	Asn	Met	Ala	Thr
				565					570					575	
Gly	Met	Asp	Ser	Trp	Val	Ala	Leu	Ala	Ala	Val	Asp	Ser	Ala	Val	Tyr
			580					585					590		
Gly	Val	Gln	Arg	Gly	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	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
		675					680					685			
Asn	Asp	Glu	Thr	Cys	Glu	Gln	Arg	Ala	Ala	Arg	Ile	Ser	Leu	Gly	Pro
	690					695					700				
Arg	Cys	Ile	Lys	Ala	Phe	Thr	Glu	Cys	Cys	Val	Val	Ala	Ser	Gln	Leu
705					710					715					720
Arg	Ala	Asn	Ile	Ser	His	Lys	Asp	Met	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		
Glu	Ser	Trp	Leu	Trp	Glu	Val	His	Leu	Val	Pro	Arg	Arg	Lys	Gln	Leu
		755					760					765			
Gln	Phe	Ala	Leu	Pro	Asp	Ser	Leu	Thr	Thr	Trp	Glu	Ile	Gln	Gly	Val
	770					775					780				
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
			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	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		

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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
				1285					1290					1295	
Val	Ser	Tyr	Lys	His	Lys	Gly	Ala	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			
Ile	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	Ser	Ser	Ser	Ser	Gly	Ser	Ser	His	Ala	Val	Met	Asp	Ile
		1395					1400					1405			
Ser	Leu	Pro	Thr	Gly	Ile	Ser	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	

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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 Ala Cys Lys Cys Val Glu Ala Asp Cys Gly Gln Met Gln Glu Glu
1505 1510 1515 1520
Leu Asp Leu Thr Ile Ser Ala Glu Thr Arg Lys Gln Thr Ala Cys Lys
1525 1530 1535
Pro Glu Ile Ala Tyr Ala Tyr Lys Val Ser Ile Thr Ser Ile Thr Val
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 Ser 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
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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> 357
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<212> PRT
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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
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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

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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
			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
		355					360					365			
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
			420					425					430		
Gly	Tyr	Arg	Ala	Ile	Ala	Tyr	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
				485					490					495	
Arg	Glu	Lys	Phe	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	Ala	Tyr	Ser	Pro	Gly	Gln	Thr	Val	Ser	Leu	Asn	Met	Ala	Thr
				565					570					575	
Gly	Met	Asp	Ser	Trp	Val	Ala	Leu	Ala	Val	Asp	Ser	Ala	Val	Tyr	
			580					585				590			
Gly	Val	Gln	Arg	Gly	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	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
		675					680					685			
Asn	Asp	Glu	Thr	Cys	Glu	Gln	Arg	Ala	Ala	Arg	Ile	Ser	Leu	Gly	Pro
	690					695					700				
Arg	Cys	Ile	Lys	Ala	Phe	Thr	Glu	Cys	Cys	Val	Val	Ala	Ser	Gln	Leu
705					710					715					720
Arg	Ala	Asn	Ile	Ser	His	Lys	Asp	Met	Gln	Leu	Gly	Arg	Leu	His	Met
				725					730					735	

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Lys	Thr	Leu	Leu	Pro	Val	Ser	Lys	Pro	Glu	Ile	Arg	Ser	Tyr	Phe	Pro
			740					745					750		
Glu	Ser	Trp	Leu	Trp	Glu	Val	His	Leu	Val	Pro	Arg	Arg	Lys	Gln	Leu
		755					760					765			
Gln	Phe	Ala	Leu	Pro	Asp	Ser	Leu	Thr	Thr	Trp	Glu	Ile	Gln	Gly	Val
	770					775					780				
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
			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
		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

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Glu Tyr Ser Leu Leu Val Lys Gln Leu Arg Leu Ser Met Asp Ile Asp
1285 1290 1295
Val Ser Tyr Lys His Lys Gly Ala 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
Ile 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 Ser 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 Ala Cys Lys Cys Val Glu Ala Asp Cys Gly Gln Met Gln Glu Glu
1505 1510 1515 1520
Leu Asp Leu Thr Ile Ser Ala Glu Thr Arg Lys Gln Thr Ala Cys Lys
1525 1530 1535
Pro Glu Ile Ala Tyr Ala Tyr Lys Val Ser Ile Thr Ser Ile Thr Val
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 Ser 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> 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

<400> 358

Gln Glu Gln Thr Tyr Val Ile Ser Ala Pro Lys Ile Phe Arg Val Gly
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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
					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		
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Gly	Met	Asp	Ser	Trp	Val	Ala	Leu	Thr	Ala	Val	Asp	Ser	Ala	Val	Tyr
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Arg	Gly	Ile	Tyr	Gly	Thr	Ile	Ser	Arg	Arg	Lys	Glu	Phe	Pro	Tyr	Arg
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 Ser Tyr Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln
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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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 His Thr Asp Lys Pro Val Tyr Thr Pro Asp Gln Ser Val Lys Val Arg
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 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
 195 200 205
 Phe Ser Thr Thr Gly Thr Ala Tyr Phe Glu Val Lys Glu Tyr Val Leu
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 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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 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
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 355 360 365
 Tyr Pro Ile Lys Val Gln Val Lys Asp Ser Leu Asp Gln Leu Val Gly
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Arg	Glu	Gly	Tyr	Arg	Ala	Ile	440	Ala	Tyr	Ser	Ser	Leu	Ser	Gln	Ser	Tyr		
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His	Leu	Asn	Ile	Ile	485	Val	Thr	Pro	Lys	490	Pro	Tyr	Ile	Asp	Lys	495	Ile	
Thr	His	Tyr	Asn	Tyr	Leu	Ile	Leu	Ser	505	Lys	Gly	Lys	Ile	Ile	His	Phe		
Gly	Thr	Arg	Glu	Lys	Phe	Ser	520	Ala	Ser	Tyr	Gln	Ser	Ile	Asn	Ile			
Pro	Val	Thr	Gln	Asn	Met	Val	535	Pro	Ser	Ser	Arg	Leu	Val	Tyr	Tyr			
Ile	Val	Thr	Gly	Glu	Gln	Thr	Ala	Glu	Leu	Val	Ser	Asp	Ser	Val	Trp			
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Pro	Asp	Ala	Asp	Ala	Tyr	Ser	Pro	Gly	585	Thr	Val	Ser	Leu	Asn	Met			
Ala	Thr	Gly	Met	Asp	Ser	Trp	Val	Ala	Leu	Ala	Ala	Val	Asp	Ser	Ala			
Val	Tyr	Gly	Val	Gln	Arg	Gly	615	Ala	Lys	Lys	Pro	Leu	Glu	Arg	Val	Phe		
Gln	Phe	Leu	Glu	Lys	Ser	630	Asp	Leu	Gly	Cys	Gly	Ala	Gly	Gly	Gly	Leu		
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Lys	Tyr	Lys	His	Ser	Val	Val	695	Lys	Lys	Cys	Cys	Tyr	Asp	Gly	Ala	Cys		
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Gln	Leu	Arg	Ala	Asn	Ile	Ser	His	Lys	Asp	Met	Gln	Leu	Gly	Arg	Leu			
His	Met	Lys	Thr	Leu	Leu	Pro	Val	Ser	Lys	Pro	Glu	Ile	Arg	Ser	Tyr			
Phe	Pro	Glu	Ser	Trp	Leu	Trp	Glu	Val	His	Leu	Val	Pro	Arg	Arg	Lys			
Gln	Leu	Gln	Phe	Ala	Leu	Pro	Asp	Ser	Leu	Thr	Thr	Trp	Glu	Ile	Gln			
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<210> 362
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HCVR of M1M17628N

<400> 362
 Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Ala Lys Pro Ser Gln
 1 5 10 15
 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

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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
 115 120

<210> 363
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LCVR of M1M17628N

<400> 363
 Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15
 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
 <211> 20
 <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

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			

<220>
<223> LCVR of M1M17627N

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