

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> Anti-C5 Antibodies and Uses Thereof

<130> 10168WO01

<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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ctgcaaatga acagcctgag aggcgaggac acggctgttt attactgtgc gagagatgcc 300
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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
 85 90 95
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aggttcagcg gcagtggatc tgggacagag ttactctca ccatcagcag cctgcagcct 240
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 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Lys Ala Ser Ser Leu Asp Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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 Thr Phe Gly Leu Gly Thr Lys Leu Glu Ile Lys
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 20 25 30
 Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Tyr Ile Ser Ser Ser Gly Asn Thr Ile Lys Tyr Ala Asp Ser Met
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Phe
 65 70 75 80
 Val Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Tyr Lys Ser Ser Ser Asp Tyr Phe Asp His Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
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Ala Arg Tyr Lys Ser Ser Ser Asp Tyr Phe Asp His
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ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgc catcccagcc 180
agggtcagtg gcagtggggc tgggacagac ttactctca ccatcagcag cctagagcct 240
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Tyr

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile

35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Ala Ile Pro Ala Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro

65 70 75 80

Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln Ser Gly Asn Trp Pro Leu

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Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

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Gln Ser Val Arg Ser Tyr

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Gln Gln Ser Gly Asn Trp Pro Leu Thr

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ccaggcaagg ggctggagtg ggtggcagtt atctgggatg atggaaataa taaatattat 180
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Ser Leu Arg Leu Ser Cys Gly Ala Ser Gly Phe Thr Phe Ser Thr Tyr
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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
85 90 95
Ala Arg Asp Ser Glu Val Ala Pro Val Gly Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

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Gly Phe Thr Phe Ser Thr Tyr Gly
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24

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Ile Trp Asp Asp Gly Asn Asn Lys

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aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg cagcttatta ctgccaacag tataatgatt attcgtacac ttttgccag 300
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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Asp Asp Phe Ala Ala Tyr Tyr Cys Gln Gln Tyr Asn Asp Tyr Ser Tyr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

100 105

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

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Ile Arg Asn Lys Ala Asn Ala Tyr Asn Thr
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Val Arg Val Trp Asn Tyr Ala Tyr Phe Ala Met Asp Val
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ggggaagccc ctaacctcct gatctccgct gcatccagtt tacacagtgg ggtcccttca 180
aggttcagtg gcagtgggct tgggacagat ttcactctca ccatcggcag tctgcagcct 240
gaagattttg cgacttacta ctgtcaacag acgtacaata ccatattcac ttccggccct 300
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Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Asn Ile Gly Ile Phe
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Asn Leu Leu Ile
35 40 45
Ser Ala Ala Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Gly Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asn Thr Ile Phe
85 90 95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

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Gln Gln Thr Tyr Asn Thr Ile Phe Thr

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gcagactccg tgaagggccg gctcaccatc tccagagaca attccaagaa cacgctgtat 240
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20 25 30
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35 40 45
Ser Ala Ile Ser Gly Arg Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Leu Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Val Lys Glu Gly Glu Gln Leu Val Tyr Trp Tyr Phe Asp Leu Trp Gly
100 105 110
Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

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<400> 70
Ile Ser Gly Arg Gly Asp Ser Thr
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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttt caactactt ctgtcaacag agttacacta ccccgctcac ttcggcgga 300
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Asn Phe
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35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ser Thr Tyr Phe Cys Gln Gln Ser Tyr Thr Thr Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

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1 5

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ccagggaagg ggctggagtg ggtctcagct ataagtggta gtggtagcag cacatactac 180
acagactccg tgaaaggccg gttcaccatc tccagagaca attccaagaa ttcggtggat 240
ctgcaaatgc acagcctgag agtcgaagac acggccatat attattgtgc gagagggact 300
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<400> 82

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Arg Tyr

20 25 30

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Ser Ser Thr Tyr Tyr Thr Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Val Asp

65 70 75 80

Leu Gln Met His Ser Leu Arg Val Glu Asp Thr Ala Ile Tyr Tyr Cys

85 90 95

Ala Arg Gly Thr Thr Val Thr Thr Gly Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

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<210> 86
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<400> 86
Ile Ser Gly Ser Gly Ser Ser Thr
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Ala Arg Gly Thr Thr Val Thr Thr Gly Tyr Gly Met Asp Val
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gggagagccc ctaagctcct gatctacgat gcatcgtatt tgaaggcagg ggtcccatca 180
agattcagtg gaagtggatc tgggacagat ttactttca ccatcagcag cctgcagcct 240
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gggaccaagc tggagatcaa a 321

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<212> PRT
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<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

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

<210> 93
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Asp Ala Ser
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<210> 95
<211> 27
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Gln Gln Tyr Asp Asp Leu Pro Tyr Thr

1 5

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<400> 97

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ccagggaagg gactggagtg gattggctat atctattaca gtgggagttc caactacaac 180
ccctccctca agagtcgagc caccatttca gtagacacgt ccaagaacca gttctccctg 240
aagctgagtt ctgtgaccgc tgcggacacg gccgtatatt actgtgcgag agaagggaac 300
gtggatacaa ctatgatatt tgactactgg ggccaggga cctgggtcac cgtctcctca 360

<210> 98

<211> 120

<212> PRT

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<220>

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<400> 98

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Val Ser Ser Ser

20 25 30

Tyr Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Tyr Ile Tyr Ser Gly Ser Ser Asn Tyr Asn Pro Ser Leu Lys

50 55 60

Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

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

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<210> 100
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Gly Asp Ser Val Ser Ser Ser Tyr
1 5

<210> 101
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<400> 101
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<210> 102
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<400> 102
Ile Tyr Tyr Ser Gly Ser Ser
1 5

<210> 103
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<212> DNA
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<400> 103
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<210> 104
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<400> 104
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1 5 10

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<400> 105
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gggaaagccc ctaaactcct gatctatgct gcatccagtt taaaagtgg ggtcccatcg 180
aggttcgccg gccgtggatc tggcacagat ttactctca ccatcagcag cctgcagcct 240
gaagatttg caacttatta ctgtctaca gatttcaatt acccgtggac gtcggccaa 300
gggaccaagg tggaatcaa a 321

<210> 106
<211> 107
<212> PRT
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<220>
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<400> 106
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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
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<400> 107
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<210> 108
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<400> 108
 Gln Gly Ile Arg Asn Asp
 1 5

<210> 109
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<400> 109
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<210> 110
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<400> 110

Ala Ala Ser
1

<210> 111
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ctacaagatt tcaattaccc gtggacg 27

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Leu Gln Asp Phe Asn Tyr Pro Trp Thr
1 5

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<400> 113
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gggaaagccc ctaaactcct gatctatgct gcatccagtt tacaaagtgg ggtcccatcg 180
aggttcgccg gccgtggatc tggcacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caactatta ctgtcatcaa gatttcaatt acccgtggac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

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<400> 114
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1 5 10 15

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

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<400> 115
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<210> 116
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<400> 116
 Gln Gly Ile Arg Asn Asp
 1 5

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<400> 117
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<400> 118
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<400> 119
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<400> 120
His Gln Asp Phe Asn Tyr Pro Trp Thr
1 5

<210> 121
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<400> 121
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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 actgtgcgag agaacataac 300
gtggatacaa ctatgatatt tgactactgg ggccaggga cctggtcac cgtctcctca 360

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<400> 122

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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 His Asn Val Asp Thr Thr Met Ile Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 123

<211> 24

<212> DNA

<213> Artificial Sequence

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<400> 123

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<210> 124

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<400> 124

Gly Asp Ser Val Ser Ser Ser Tyr
1 5

<210> 125

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atctattaca gtgggagttc c 21

<210> 126
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Ile Tyr Tyr Ser Gly Ser Ser
1 5

<210> 127
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<400> 127
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<210> 128
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<400> 128
Ala Arg Glu His Asn Val Asp Thr Thr Met Ile Phe Asp Tyr
1 5 10

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gggaaagccc ctaaactcct gatctatgct gcatccagtt taaaaagtgg ggtcccatcg 180
agggtcgccg gccgtggatc tggcacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacaa gatttcaatt acccgtggca ctgcggccaa 300
gggaccaagg tggaaatcaa a 321

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<212> PRT
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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
His Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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ccagggaagg gactggagtg gattggctat atctattaca gtgggagttc caactacaac 180
ccctccctca agagtcgagc caccattca gtagacacgt ccaagaacca gttctccctg 240
aagctgagtt ctgtgaccgc tgcggacacg gccgtatatt actgtgcgag agaagggaac 300
gtggatacaa ctatgataca tgactactgg ggccaggga cctggtcac cgtctectca 360

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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

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Ile Tyr Tyr Ser Gly Ser Ser
1 5

<210> 143
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<210> 144
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ccagggaagg gactggagtg gattggctat atctattaca gtgggagttc caactacaac 180
ccctccctca agagtcgagc caccatttca gtagacacgt ccaagaacca gttctccctg 240
aagctgagtt ctgtgaccgc tgcggacacg gccgtatatt actgtgagag agaagggaac 300
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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 His 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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ggtgactccg tcagtagttc ctac

24

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Gly Asp Ser Val Ser Ser Ser Tyr
1 5

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Ile Tyr Tyr Ser Gly Ser Ser
1 5

<210> 151
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<400> 151
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<210> 152
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<400> 152
Ala Arg Glu Gly Asn Val Asp His Thr Met Ile Phe Asp Tyr
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<210> 153
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<400> 153

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ccagggaagg gactagagtg gatttcatac attggtagta gtggaatac ctttactac 180
gcagactctg tgaagggccg gttcaccatt tccagagaca acgccaaca tttactgtat 240
ctgcaaataa ccagcctgag agccgaggac acggccgtgt attactgtgc gagagaagaa 300
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<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 tcaagtactc 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

attgtagta 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 ttgagtgcc 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

10

<213> Artificial Sequence

<223> synthetic

gacatccagt tgaccagtc tccatcttc ctgtctgcat ctgtaggaga cagagtacc 60
atcacttgct gggccagtc gggcattagc agttatttag cctgggtatca gcaaaaacca 120
ggtaaagccc ctaaactct gatccatact gcatccactt tgcaaaagg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttactctca caatcagcaa cctgcagcct 240
gaagattttg caactatta ctgtcaacag cttaatagtt acccattcac ttctggcct 300
gggaccaaag tggatatcaa a 321

<213> Artificial Sequence

<223> synthetic

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

<213> Artificial Sequence

<223> synthetic

cagggcata gcagttat

<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>
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<400> 165
actgcatcc 9

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

<220>
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<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>
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<400> 168

Gln Gln Leu Asn Ser Tyr Pro Phe Thr

1 5

<210> 169

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 169

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tcctgtgcag cctctggatt caccttcggt ggccatgccca tgcactgggt cgcaggct 120
ccaggcaagg ggctggagtg gctggcagtt atatcatctg atggcagtaa taaacagtat 180
gcagattctg tgaagggccg attcaccatc tccagggaca atcccaagaa cacgctgtat 240
ctgcaaatga acagtctgag agttggggac acggctattt attactgtgc gaaagagggtg 300
gcacctcgtt attattatta cggctctggac gtctggggcc aagggaccac ggtcaccgtc 360
tcctca 366

<210> 170

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 170

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

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 171

ggattcacct tcggtggcca tgcc

24

<210> 172

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 172

Gly Phe Thr Phe Gly Gly His Ala

1 5

<210> 173

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 173

atatcatctg atggcagtaa taaa

24

<210> 174

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 174

Ile Ser Ser Asp Gly Ser Asn Lys

1 5

<210> 175

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 175

gcgaaagagg tggcacctcg ttattattat tacggtctgg acgtc

45

<210> 176

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

<220>
<223> synthetic

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

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

<220>
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<400> 177
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60
atcacttgcc gggcgagtca ggacattagc aatttttag cctggtatca gcagaaacca 120
gggaagggtc ctaaactcct gatctatact gcattccatt tacaatcagg ggtcccatct 180
cggttcagtg gcagtggatc tgggacagat ttcactctca ccgtcagcag cctacagcct 240
gaagatgtg caacttatta ctgtcaaaag tatgccggcg ccctcacttt cggccctggg 300
accaaagtg atataaaa 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

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tcctgtgcag cctctggatt cacgtttaga agctatgccca tgagctgggt ccgccaggct 120
ccagggaagg ggccggagtg ggtctcaggt ataggtggta atggtgttac cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgttt 240
ctgcaaatga atagcctgag agccgaggac acggccgtat attattgtgt gcaggggggt 300
ttaggtggtt attttacagg ctactggggc cagggaaccc tggtcaccgt ctctca 357

<210> 186

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 186

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

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

<220>
<223> synthetic

<400> 187
ggattcacgt ttagaagcta tgcc 24

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 189
ataggtggta atggtgttac caca 24

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

<220>
<223> synthetic

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

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

<220>

<223> synthetic

<400> 191

gtgcaggggg gtttaggtgg ttattttaca ggctac 36

<210> 192

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 192

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

<210> 193

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 193

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

<210> 194

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 194

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

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

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

<220>
<223> synthetic

<400> 195
cagagtatta gtacctat 18

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 197
gatgcatcc 9

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

<220>
<223> synthetic

<400> 198
Asp Ala Ser
1

<210> 199

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

<220>
<223> synthetic

<400> 199
caacagagtt acagtgcgcc gctcact 27

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 202
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Leu Ile Trp Leu Asp Gly Ser Asn Asp Tyr Tyr Ala Asp Ser Val

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

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

<220>
 <223> synthetic

<400> 203
 ggattcacct tcagtggta tggc 24

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

<220>
 <223> synthetic

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

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

<220>
 <223> synthetic

<400> 205
 atatggcttg atggaagtaa tgac 24

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

<220>
 <223> synthetic

<400> 206

Ile Trp Leu Asp Gly Ser Asn Asp
1 5

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

<220>
<223> synthetic

<400> 207
gcgagagatg gcccgggtgc tgctataccc gactac 36

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 209
gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggccagtc gagtattagt aggtggttgg cctggtatca gctgaaacca 120
gggaaagccc ctaagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
agggtcagcg gcagtggatc tgggacagac ttactctca ccatcagcag cctgcaacct 240
gatgattttg caactatta ctgccaacag tataatactt attcgtacac ttttgccag 300
gggaccaagc tggagatcaa a 321

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

<220>
<223> synthetic

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

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

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

<220>
 <223> synthetic

<400> 211
 cagagtatta gtaggtgg 18

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

<220>
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<400> 212
 Gln Ser Ile Ser Arg Trp
 1 5

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

<220>
 <223> synthetic

<400> 213
 aaggcgtct 9

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

<220>

<223> synthetic

<400> 214

Lys Ala Ser

1

<210> 215

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 215

caacagtata atacttattc gtacact

27

<210> 216

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 216

Gln Gln Tyr Asn Thr Tyr Ser Tyr Thr

1

5

<210> 217

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 217

gaggtgcagc tggaggagtc tgggggaggt gtggtacggc ctgggggggc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gaatatggca tgactgggt cgcgaagtt 120
ccagggaagg ggctggagtg ggtctctggt attacttga atggtggtt 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

<210> 218

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

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

<210> 219
 <211> 24
 <212> DNA
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<220>
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<400> 219
 ggattcacct ttgatgaata tggc 24

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

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

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

<220>
 <223> synthetic

<400> 221
 attacttgga atggtggttt caca 24

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 223
gcgagagatg gatatagcag ctctgtggggg gcttatgata ta 42

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

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

<210> 225
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
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<400> 225
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atcacttgcc gggcaagtca gagcattagc acctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcacccagtt tgcaaagtgg ggtcccatta 180
aggttcagtg gcagtggatc tgggactgat ttcacttca ccatcagcag tctgcaacct 240
gaagattttg caagttattt ctgtcaacag agttacagta ccccgtaac ttttgccag 300
gggaccaagc tggagatcaa a 321

<210> 226
<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 226

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

<210> 227

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 227

cagagcatta gcacctat 18

<210> 228

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 228

Gln Ser Ile Ser Thr Tyr
1 5

<210> 229

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 229

gctgcatcc

9

<210> 230

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 230

Ala Ala Ser

1

<210> 231

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 231

caacagagtt acagtacccc gtacact

27

<210> 232

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 232

Gln Gln Ser Tyr Ser Thr Pro Tyr Thr

1

5

<210> 233

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 233

gaagtgcagc tgggtggagtc tgggggaggc gtggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttaat gattatgcca tgcactgggt cgtcaagct 120
ccagggaagg gtctggagtg ggtctctctt attagtggag atggtggtaa cacatactat 180
gcagactctg tgaagggccg actcaccatc tcagagaca acagcaaaaa ctccctgtat 240
ctgcaaatga acagtctgag aacagaggac accgccttat attactgtgc aaaagataag 300
ggctggaact tcggttactt cgatctctgg ggccgtggca ccctgggtcac tgtctctca 360

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

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

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

<220>
<223> synthetic

<400> 235
ggattcacct ttaatgatta tgcc 24

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

<220>
<223> synthetic

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

<210> 237
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 237
attagtggag atggtggtaa caca 24

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 239
gcaaaagata agggctggaa cttcggttac ttcgatctc 39

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

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

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

<220>
<223> synthetic

<400> 241

gacatccaga tgaccagtc tccatctcc ctgtctacat ctgtgggaga cagagtcacc 60
 atcacttgcc gggcaagtca gaacattgac acctatttaa attggtatca gcagaaacca 120
 gggaaagccc ctaaactct gatctatgat gcatccagtt tacaaagtgg ggtcccatca 180
 cggttcagtg gcagcggatc tgggacagat ttactctca ccatcaccag tctgcaacct 240
 gaagattttg ccacttacta ctgtcaacag aatgacaata ttcttaccct tctcactttc 300
 ggcggaggga ccaaggtgga gatcaaa 327

<210> 242

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 242

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

<210> 243

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 243

cagaacattg acacctat 18

<210> 244

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 244

Gln Asn Ile Asp Thr Tyr
 1 5

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

<220>
<223> synthetic

<400> 245
gatgcatcc 9

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

<220>
<223> synthetic

<400> 246
Asp Ala Ser
1

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

<220>
<223> synthetic

<400> 247
caacagaatg acaatattct tcaccctctc act 33

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

<220>
<223> synthetic

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

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

<220>

<223> synthetic

<400> 249

gaggtgcagc tgggtggagtc tgggggaggc ttggccaac cggggggggtc cctgagactc 60
tcctgtgcag cctctggatt ccactcta atagattgga tggactgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtggccaac ataaagcaag atggaagtga ggaaaactat 180
gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctactttat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatcga 300
agcacctcgt gggccctta ctggtcttc gatctctggg gccgtggcac cctggtcact 360
gtctctca 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
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Arg Ser Trp 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

<210> 251

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 251

ggattccact ctaatagata ttgg 24

<210> 252

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 252

Gly Phe His Ser Asn Arg Tyr Trp

1 5

<210> 253

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 253

ataaagcaag atggaagtga ggaa

24

<210> 254

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 254

Ile Lys Gln Asp Gly Ser Glu Glu

1 5

<210> 255

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 255

gcgagagatc gaagcacctc gtgggtccct tactggttct tcgatctc

48

<210> 256

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 256

Ala Arg Asp Arg Ser Thr Ser Trp Val Pro Tyr Trp Phe Phe Asp Leu

1 5 10 15

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

<220>
<223> synthetic

<400> 257
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgta 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

1

<210> 263

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 263

caacagagtt acagtacccc tccgatcacc

30

<210> 264

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 264

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr

1 5 10

<210> 265
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 265
gaagtgcagc tggaggagtc tgggggaggc gtgtacagc ggggggagtc cctgagactc 60
tcctgttcag cctctgactt catctttaa gattatgcca tgtactgggt ccgtcaaatt 120
ccagggaagg gtctagagtg gatctctctt attagtgggt atggtgacac tacatgggtat 180
ggagactctg tgaagggccg attcaccatc tccagagaca acaacgaaaa ctccctcttt 240
ctgcaaatga acgatctgag aactgaggac accgccatgt actactgtgc aagagatatg 300
gggtggaact tcttcagtt gcaatactgg ggccaggga ccctggtcac cgtctctca 360

<210> 266
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 266
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Arg Gly Glu
1 5 10 15
Ser Leu Arg Leu Ser Cys Ser Ala Ser Asp Phe Ile Phe Lys Asp Tyr
20 25 30
Ala Met Tyr Trp Val Arg Gln Ile Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Ser Leu Ile Ser Gly Asp Gly Asp Thr Thr Trp Tyr Gly Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Asn Glu Asn Ser Leu Phe
65 70 75 80
Leu Gln Met Asn Asp Leu Arg Thr Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Asp Met Gly Trp Asn Phe Phe Gln Leu Gln Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 267
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 267
gacttcattct ttaaagatta tgcc 24

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 269
attagtgggtg atgggtgacac taca 24

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 271
gcaagagata tgggggtggaa cttctttcag ttgcaatac 39

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

<220>

<223> synthetic

<400> 272

Ala Arg Asp Met Gly Trp Asn Phe Phe Gln Leu Gln Tyr

1 5 10

<210> 273

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 273

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

<210> 274

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 274

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

<210> 275

<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 275
ggtggctcca tcacagagg tagtacctac 30

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 277
agttattaca gtgggaccgc c 21

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 279

acaagagaaa taggagtggc tggctctttt gacatc

36

<210> 280

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 280

Thr Arg Glu Ile Gly Val Ala Gly Leu Phe Asp Ile

1 5 10

<210> 281

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 281

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

<210> 282

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 282

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

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

<220>
<223> synthetic

<400> 283
agagcaagtc agtcagtctc tagctcttat ctcgcc 36

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 285
ggggcaagtt ccagggccac c 21

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

<220>
<223> synthetic

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

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

<220>

<223> synthetic

<400> 287

caacagtacg gaagcagccc gtggacg

27

<210> 288

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 288

Gln Gln Tyr Gly Ser Ser Pro Trp Thr

1 5

<210> 289

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 289

caggagcagt tgggtcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgtaagg ctctggata caccttcacc ggctactata tacattgggt ggcacaggcc 120
cctggactag ggcttgaatg gatgggatgg atcaacccta acagtgggtg caaaaatat 180
gcacagaagt tcagggcag ggtcaccatg accagggaca cgtccatcaa tacagcctac 240
atggagctga aaagactgaa atctgacgac tcggccgtat attactgtgc gagagacgcc 300
cctcccatg atgttttga tatctggggc caaggacat tggtcaccgt ctcttca 357

<210> 290

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 290

Gln Glu Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr

20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met

35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe

50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr

65 70 75 80

Met Glu Leu Lys Arg Leu Lys Ser Asp Asp Ser Ala Val Tyr Tyr Cys

85 90 95

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

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

<220>
<223> synthetic

<400> 291
ggatacacct tcaccggcta ctat 24

<210> 292
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 292
Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

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

<220>
<223> synthetic

<400> 293
atcaacccta acagtgtgg 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 tgatgtttt 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 ctaagcgct gatctatgct gcatccagtt tgcaaattgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagatttg caactatta ctgtctacag cataatagtt acccgctcac ttctggcgga 300
gggaccaagg tggagatcaa a 321

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

<220>
<223> synthetic

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

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

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

<220>
<223> synthetic

<400> 299
cagggcatta gaaatgat 18

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

<220>
<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

<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 agtgggtgctt accactggag ctggatccgc 120
cagcaccag ggaagggcct agagtggatt ggatacatct attacaatgg ggacacctac 180
tataatccgt ccctcaagag tcgcggtacc attcagtgg acacgtctaa gaaccaatc 240
ttctgaagg tgacctctgt gactgccgcg gacacggcca tgtattactg tgcgggagaa 300
aagcagctga ctgcttttga tatctggggc caaggacat tggtcaccgt ctcttca 357

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

<220>
<223> synthetic

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

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

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

<220>
<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 tgctttgat atc 33

<210> 312

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 312

Ala Gly Glu Lys Gln Leu Thr Ala Phe Asp Ile

1 5 10

<210> 313

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 313

gtcatccaga tgaccagtc tccatcctcc ctgtctgcat ctgttgaga cagagtcacc 60
ataacttggc gggcgagtca ggacattaat aatttttaa attggtatca acagaaatta 120
gggaaagccc ctactcct gatctccgat gcatccaatt tgcagacagg agtcccgta 180
aggttcagtg gaagtggatc tgggacagat ttactttca ccatcagcag cctgcagcct 240
gaagatattg ctgcatatta ctgtcaacaa tatgatcatt tccgtatac tttggccag 300
gggaccagac tggagaacaa t 321

<210> 314

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 314

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

<210> 315

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 315

caggacatta ataatttt 18

<210> 316

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 316

Gln Asp Ile Asn Asn Phe
1 5

<210> 317

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 317

gatgcatcc 9

<210> 318

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 318

Asp Ala Ser

1

<210> 319

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 319

caacaatatg atcatttccc gtatact

27

<210> 320

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 320

Gln Gln Tyr Asp His Phe Pro Tyr Thr

1

5

<210> 321

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 321

gaggtgcagt tggaggagtc tgggggaggt gtggttcggc ctgggggggc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatggca tgacctgggt ccgccaagct 120
ccaggggaagg ggctggagtg ggtctctggt attaattgga atggcgatag cacagagtat 180
tcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agccgaggac acggccttct atcactgtgc gagagagaat 300
aactggaact tctacttga ctactggggc cagggaaccc tggtcaccgt ctctca 357

<210> 322

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 322

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

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

20 25 30

Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Gly Ile Asn Trp Asn Gly Asp Ser Thr Glu Tyr Ser Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Phe Tyr His Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 323

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 323

ggattcacct ttgatgatta tggc

24

<210> 324

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 324

Gly Phe Thr Phe Asp Asp Tyr Gly

1 5

<210> 325

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 325

attaattgga atggcgatag caca

24

<210> 326

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 326

Ile Asn Trp Asn Gly Asp Ser Thr

1 5

<210> 327

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 327

gcgagagaga ataactggaa cttctacttt gactac

36

<210> 328

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 328

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

1 5 10

<210> 329

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 329

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctcgagggga aagagccacc 60

ctctcctgta gggccagtc gagtgtagc agcaactag cctggtacca gcagaaactt 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtggtgc tgggacagag ttactctca ccatcagcag cctgcagtct 240

gaagatttg cagtttatta ttgtcagcag tataataact ggccgtggac gtcggccaa 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

<213> Artificial Sequence

<220>

<223> synthetic

<400> 335

cagcagtata ataactggcc gtggacg

27

<210> 336

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 336

Gln Gln Tyr Asn Asn Trp Pro Trp Thr

1

5

<210> 337

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 337

cagggtccacc tggtagagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggct 60
tcctgcaagg ttccggaaa caccctcact gaattatcca tgcactgggt gcgacaggct 120
cctggaaaag ggcttgagtg gatgggaggt ttgatcctg aagatgggtga cacaatctac 180
tcacagaagt tccagggcag agtcaccttg accgaggaca catctacaga cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgttc aacagtgggg 300
ggacctacct ctgactgctg gggccagggg accctgggtca ccgtctctc a 351

<210> 338

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 338

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

<210> 339

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 339

ggaaacaccc tcactgaatt atcc 24

<210> 340

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 340

Gly Asn Thr Leu Thr Glu Leu Ser
1 5

<210> 341

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

<220>
<223> synthetic

<400> 341
tttgatcctg aagatgggtga caca 24

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 343
tcaacagtgg ggggacctac ctctgactgc 30

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

<220>
<223> synthetic

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

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

<220>
<223> synthetic

<400> 345

gacatccaga tgaccagtc tccatctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc aggcgagtca ggacattagc aactatttaa attggatca gcagaaacca 120
gggaaagccc ctaaggctct gatcttcgat gcatccaatt tagaaccagg ggtcccatca 180
aggttcagtg gaagtggatc tgggacagat ttactttca ccatcatcag cctgcagcct 240
gaagatattg caacatatta ctgtcaacaa tatgataatc tcccgatcac ctcggccag 300
gggacacgac tggacattaa a 321

<210> 346

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 346

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

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 347

caggacatta gcaactat 18

<210> 348

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 348

Gln Asp Ile Ser Asn Tyr
1 5

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

<220>
<223> synthetic

<400> 349
gatgcatcc

9

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

<220>
<223> synthetic

<400> 350
Asp Ala Ser
1

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

<220>
<223> synthetic

<400> 351
caacaatatg ataatctccc gatcacc

27

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

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

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

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

<220>
 <223> LC

<400> 354
 Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
 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

<400> 355

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
 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
 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
 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
1 5 10 15
Ala Ser Glu Asn Ile Val Ile Gln Val Tyr Gly Tyr Thr Glu Ala Phe
20 25 30
Asp Ala Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Lys Phe Ser Tyr
35 40 45
Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln Asn Ser
50 55 60
Ala 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
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 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
 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
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
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
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
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
His His His His His His		
1685		

<210> 357

<211> 1686

<212> PRT

<213> Artificial Sequence

<220>

<223> hC5 R885C

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

aa 1659-1686: myc-myc-hexahistidine tag

<400> 357

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

1 5 10 15

Ala Ser Glu Asn Ile Val Ile Gln Val Tyr Gly Tyr Thr Glu Ala Phe

20 25 30

Asp Ala Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Lys Phe Ser Tyr

35 40 45

Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln Asn Ser

50 55 60

Ala Val Leu Thr Ile Gln Pro Lys Gln Leu Pro Gly Gly Gln Asn Gln

65 70 75 80

Val Ser Tyr Val Tyr Leu Glu Val Val Ser Lys His Phe Ser Lys Ser

85 90 95

Lys Lys Ile Pro Ile Thr Tyr Asp Asn Gly Phe Leu Phe Ile His Thr

100 105 110

Asp Lys Pro Val Tyr Thr Pro Asp Gln Ser Val Lys Val Arg Val Tyr

115 120 125

Ser Leu Asn Asp Asp Leu Lys Pro Ala Lys Arg Glu Thr Val Leu Thr

130 135 140

Phe Ile Asp Pro Glu Gly Ser Glu Ile Asp Met Val Glu Glu Ile Asp

145 150 155 160

His Ile Gly Ile Ile Ser Phe Pro Asp Phe Lys Ile Pro Ser Asn Pro

165 170 175

Arg Tyr Gly Met Trp Thr Ile Gln Ala Lys Tyr Lys Glu Asp Phe Ser

180 185 190

Thr Thr Gly Thr Ala Phe Phe Glu Val Lys Glu Tyr Val Leu Pro His

195 200 205

Phe Ser Val Ser Val Glu Pro Glu Ser Asn Phe Ile Gly Tyr Lys Asn

210 215 220

Phe Lys Asn Phe Glu Ile Thr Ile Lys Ala Arg Tyr Phe Tyr Asn Lys

225 230 235 240

Val Val Thr Glu Ala Asp Val Tyr Ile Thr Phe Gly Ile Arg Glu Asp

245 250 255

Leu Lys Asp Asp Gln Lys Glu Met Met Gln Thr Ala Met Gln Asn Thr

260 265 270

Met Leu Ile Asn Gly Ile Ala Gln Val Thr Phe Asp Ser Glu Thr Ala

275 280 285

Val Lys Glu Leu Ser Tyr Tyr Ser Leu Glu Asp Leu Asn Asn Lys Tyr

290 295 300

Leu Tyr Ile Ala Val Thr Val Ile Glu Ser Thr Gly Gly Phe Ser Glu

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

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 Val Thr Thr Trp Glu Ile Gln Gly Val
 770 775 780
 Gly Ile Ser Asn Ser Gly Ile Cys Val Ala Asp Thr Ile 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 Val 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 Arg Gln Lys Val Glu Gly Ser Ser Asn His Leu Val Thr Phe
 865 870 875 880
 Thr Val Leu Pro Leu Glu Ile Gly Leu Gln Asn Ile Asn Phe Ser Leu
 885 890 895
 Glu Thr Ser Phe Gly Lys Glu Ile Leu Val Lys Ser Leu Arg Val Val
 900 905 910
 Pro Glu Gly Val Lys Arg Glu Ser Tyr Ser Gly Ile 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 Arg
 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
 Arg Asn Leu Glu Lys Lys Leu Lys Glu Gly Met Val 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 His
 1060 1065 1070
 Lys His 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 Asn Thr Ala Leu Ile Lys
 1140 1145 1150
 Ala Asp Thr 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 Ser Leu Gln His
 1205 1210 1215
 Lys Asp Ser Ser Val Pro Asn Thr Gly Thr Ala Arg Met Val Glu Thr
 1220 1225 1230
 Thr Ala Tyr Ala Leu Leu Thr Ser Leu Asn Leu Lys Asp Ile Asn Tyr
 1235 1240 1245
 Val Asn Pro Ile Ile Lys Trp Leu Ser Glu Glu Gln Arg Tyr Gly Gly
 1250 1255 1260
 Gly Phe Tyr Ser Thr Gln Asp Thr Ile Asn Ala Ile Glu Gly Leu Thr
 1265 1270 1275 1280
 Glu Tyr Ser Leu Leu Val Lys Gln Leu Arg Leu Asn Met Asp Ile Asp
 1285 1290 1295
 Val Ala Tyr Lys His Lys Gly Pro Leu His Asn Tyr Lys Met Thr Asp
 1300 1305 1310
 Lys Asn Phe Leu Gly Arg Pro Val Glu Val Leu Leu Asn Asp Asp Leu
 1315 1320 1325
 Val Val Ser Thr Gly Phe Gly Ser Gly Leu Ala Thr Val His Val Thr
 1330 1335 1340
 Thr Val Val His Lys Thr Ser Thr Ser Glu Glu Val Cys Ser Phe Tyr
 1345 1350 1355 1360
 Leu Lys Ile Asp Thr Gln Asp Ile Glu Ala Ser His Tyr Arg Gly Tyr
 1365 1370 1375
 Gly Asn Ser Asp Tyr Lys Arg Ile Val Ala Cys Ala Ser Tyr Lys Pro
 1380 1385 1390
 Ser Arg Glu Glu Ser Ser Ser Gly Ser Ser His Ala Val Met Asp Ile
 1395 1400 1405
 Ser Leu Pro Thr Gly Ile Asn Ala Asn Glu Glu Asp Leu Lys Ala Leu
 1410 1415 1420
 Val Glu Gly Val Asp Gln Leu Phe Thr Asp Tyr Gln Ile Lys Asp Gly
 1425 1430 1435 1440
 His Val Ile Leu Gln Leu Asn Ser Ile Pro Ser Ser Asp Phe Leu Cys
 1445 1450 1455
 Val Arg Phe Arg Ile Phe Glu Leu Phe Glu Val Gly Phe Leu Ser Pro
 1460 1465 1470
 Ala Thr Phe Thr Val Tyr Glu Tyr His Arg Pro Asp Lys Gln Cys Thr
 1475 1480 1485
 Met Phe Tyr Ser Thr Ser Asn Ile Lys Ile Gln Lys Val Cys Glu Gly
 1490 1495 1500
 Ala Thr Cys Lys Cys Ile Glu Ala Asp Cys Gly Gln Met Gln Lys Glu
 1505 1510 1515 1520
 Leu Asp Leu Thr Ile Ser Ala Glu Thr Arg Lys Gln Thr Ala Cys Asn
 1525 1530 1535
 Pro Glu Ile Ala Tyr Ala Tyr Lys Val Ile Ile Thr Ser Ile Thr Thr
 1540 1545 1550
 Glu Asn Val Phe Val Lys Tyr Lys Ala Thr Leu Leu Asp Ile Tyr Lys
 1555 1560 1565
 Thr Gly Glu Ala Val Ala Glu Lys Asp Ser Glu Ile Thr Phe Ile Lys
 1570 1575 1580
 Lys Val Thr Cys Thr Asn Ala Glu Leu Val Lys Gly Arg Gln Tyr Leu
 1585 1590 1595 1600
 Ile Met Gly Lys Glu Ala Leu Gln Ile Lys Tyr Asn Phe Thr Phe Arg
 1605 1610 1615
 Tyr Ile Tyr Pro Leu Asp Ser Leu Thr Trp Ile Glu Tyr Trp Pro Arg
 1620 1625 1630

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

<210> 359
 <211> 1676
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hC5 P01031

<400> 359
 Met Gly Leu Leu Gly Ile Leu Cys Phe Leu Ile Phe Leu Gly Lys Thr
 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
 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
 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
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> 360
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human C5 peptide aa591-599

<400> 360
 Asn Met Ala Thr Gly Met Asp Ser Trp
 1 5

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

<220>
 <223> human C5 peptide aa775-794

<400> 361
 Trp Glu Val His Leu Val Pro Arg Arg Lys Gln Leu Gln Phe Ala Leu
 1 5 10 15
 Pro Asp Ser Leu
 20

<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
 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 Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Ile Leu Pro Pro Pro Tyr Tyr Tyr Ala Asn Tyr Gly Gly Gly
100 105 110
Thr Met Asp Tyr Trp Gly Arg Gly Thr Ser Val Thr Val Ser Ser
115 120 125

<210> 366

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> LCVR of M1M17627N

<400> 366

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