

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.
Orengo, Jamie M.
Murphy, Andrew J.
Badithe, Ashok T.
Kamat, Vishal
Liu, Yashu

<120> HUMAN ANTIBODIES TO BET V 1 AND METHODS OF USE THEREOF

<130> 10301W001

<140> TBD

<141> 2018-05-31

<150> 62/513,872

<151> 2017-06-01

<150> 62/571,696

<151> 2017-10-12

<150> 62/662,165

<151> 2018-04-24

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<170> PatentIn version 3.5

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gtggagtctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctactgtat 240

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Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Met Ser Ser Met Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asn Ile Lys Gln Asp Gly Thr Glu Lys Asn Tyr Val Glu 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 Ile Asn Ser Leu Arg Gly Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Tyr Ser Ser Ser Ser Gly Tyr Tyr Tyr Tyr Gly Leu
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Asn Lys Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Ser Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Ala
85 90 95

Leu His Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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atagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctactgtat 240
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 20 25 30

Asp Met Asn Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Ile
 35 40 45

Ser Tyr Ile Ser Tyr Ser Asp His Asn Ile Tyr Tyr Ile 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 Ile Tyr Tyr Cys
 85 90 95

Ala Arg Glu Ala Leu Ala Ser Ser Ser Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
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Gly Phe Thr Phe Ser Asn Tyr Asp

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Ile Ser Tyr Ser Asp His Asn Ile

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Ala Arg Glu Ala Leu Ala Ser Ser Ser Phe Asp Tyr
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20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Thr Gly Ala Thr Gly Val 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 Leu Tyr Tyr Cys Gln Gln Tyr Asn Lys Trp Pro Arg
85 90 95

Thr Ile Gly Gln Gly Thr Lys Val Glu Ile Lys
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Ser Ala Ser
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Gln Gln Tyr Asn Lys Trp Pro Arg Thr
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Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Asn Val
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Val Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Ser Ser Met Leu His Phe Gln His Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
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Gly Tyr Thr Phe Thr Asn Tyr Gly
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Ile Ser Ala Tyr Asn Gly Asn Thr
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gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

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

Lys

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Trp Ala Ser
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Gln Gln Tyr Ser Ser Ala Pro Tyr Thr
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tccctgaagc tgaggtctgt gaccgccgcg gacacggctg tgtattactg tgcgaaattg 300
gagtggctgc gcttggactt ctggggccag ggaaccacgg tcaccgtctc ctca 354

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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Asn Tyr Trp Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ile Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Lys Asp Gln Phe
65 70 75 80

Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Lys Leu Glu Trp Leu Arg Leu Asp Phe Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
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Gly Gly Ser Ile Ser Ser Ser Asn Tyr Trp
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Ala Lys Leu Glu Trp Leu Arg Leu Asp Phe
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aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
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gggacacgac tggagattaa a 321

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Val 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 Thr Tyr Tyr Cys Gln Gln Ala Lys Ser Phe Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

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Gln Gly Ile Ser Ser Trp
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Ala Ala Ser
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ccaggcaagg ggctggagtg ggtgggagtt atatggtctg atggaagtga taaaaagtat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
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<400> 66

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Val Ile Trp Ser Asp Gly Ser Asp Lys Lys 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	Leu	Met	Asn	Ser	Leu	Arg	Asp	Asp	Asp	Thr	Ala	Val	Tyr	His	Cys
			85					90						95	
Ala	Arg	Glu	Gly	Gly	Phe	Leu	Tyr	Ser	Ser	Ser	Ser	His	Phe	Asp	Tyr
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Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser					
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Ile Trp Ser Asp Gly Ser Asp Lys
1 5

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Ala Arg Glu Gly Gly Phe Leu Tyr Ser Ser Ser Ser His Phe Asp Tyr
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gggaaagccc ctaaactcct gatctttgct gcatccagtt tacaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caatttatta ctgtctacaa gattacaagt acccattcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

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<400> 74

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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Thr 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

Phe 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 Ile Tyr Tyr Cys Leu Gln Asp Tyr Lys Tyr Pro Phe
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

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Gln Gly Ile Arg Asn Asp
1 5

<210> 77
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9

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Ala Ala Ser
1

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27

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Leu Gln Asp Tyr Lys Tyr Pro Phe Thr
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ccaggcaagg ggctggagtg ggtggcagtt atatcagatg atggaagtta taaattctat 180
gcagactcca tgaagggccg attcaccatc tctagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatcgg 300
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<400> 82

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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Asp Asp Gly Ser Tyr Lys Phe Tyr Ala Asp Ser Met
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 Lys Asp Arg Gly Arg Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<400> 83
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<400> 84

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 85
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24

<210> 86
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Ile Ser Asp Asp Gly Ser Tyr Lys
1 5

<210> 87
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Ala Lys Asp Arg Gly Arg Ser Gly Trp Tyr Tyr Phe Asp Tyr
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 aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
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 gggaccaagg tggaaatcaa a 321

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<400> 90

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ser Tyr Ser Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 91
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<400> 91
cagagtatta gtagctgg

18

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<400> 92

Gln Ser Ile Ser Ser Trp
1 5

<210> 93
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<400> 93
aaggcgtct

9

<210> 94
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<400> 94

Lys Ala Ser
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<210> 95
<211> 27
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<400> 95
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27

<210> 96
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<400> 96

Gln Gln Tyr Asp Ser Tyr Ser Arg Thr
1 5

<210> 97
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<400> 97
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ccagggaagg gtctggagtg ggtttcattc attagtata gtagtagtaa catatactac 180
gcagactctg tgaagggccg attcaccatc tccagagaca atgccaagaa gtcactgtat 240
cttcaaataa ccagcctgag ggccgaggac acggctgttt attactgtgc gagagaagcc 300
attggcagca cctcctttga caactggggc cagggaaccc tggtcaccgt ctcctca 357

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

<220>
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<400> 98

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Gly
1 5 10 15

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

20

25

30

Glu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Phe Ile Ser Asp Ser Ser Ser Asn Ile Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser 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 Ala Ile Gly Ser Thr Ser Phe Asp Asn Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 99
 <211> 24
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<400> 99
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24

<210> 100
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<400> 100

Gly Phe Thr Phe Ser Ser Tyr Glu
 1 5

<210> 101
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<212> DNA
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<400> 101
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24

<210> 102
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<400> 102

Ile Ser Asp Ser Ser Ser Asn Ile
1 5

<210> 103
<211> 36
<212> DNA
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<400> 103
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36

<210> 104
<211> 12
<212> PRT
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<220>
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<400> 104

Ala Arg Glu Ala Ile Gly Ser Thr Ser Phe Asp Asn
1 5 10

<210> 105
<211> 321
<212> DNA
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<220>

<223> synthetic

<400> 105

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ggccaggctc ccaggcgcct catctatagt gcatccacca gggccactgg tatcccagcc      180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct      240
gaagattttg caatttatta ctgtcatcaa tataataact ggcctctcac tttcggcgga      300
gggaccaagg tggagatcaa a                                              321
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<210> 106

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 106

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1           5           10           15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
          20           25           30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Arg Leu Ile
          35           40           45

Tyr Ser 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 Ile Tyr Tyr Cys His Gln Tyr Asn Asn Trp Pro Leu
          85           90           95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105
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18

<210> 108
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<400> 108

Gln Ser Val Ser Ser Ser
1 5

<210> 109
<211> 9
<212> DNA
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<400> 109
agtgcattcc

9

<210> 110
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<400> 110

Ser Ala Ser
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<210> 111
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<400> 111

catcaatata ataactggcc tctcact

27

<210> 112

<211> 9

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His Gln Tyr Asn Asn Trp Pro Leu Thr

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<210> 113

<211> 357

<212> DNA

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<400> 113

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tcctgtgcag cctctggggtt caccgtcagt agcaactcca tgagctgggt ccgccaggct 120

ccaggggagg ggctggagtg ggtctcagtt attttttagcg gtggtatcac atactactca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagaac tgaggacacg gccgtatatt actgtgcgcg tcattctaac 300

tggaactttg atgcttttga tatctggggc caagggacaa tggtcaccgt ctcttca 357

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<211> 119

<212> PRT

<213> Artificial Sequence

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<400> 114

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 Thr Val Ser Ser Asn
20 25 30

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Phe Ser Gly Gly Ile Thr Tyr Tyr Ser Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg His Ser Asn Trp Asn Phe Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

<210> 115
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<212> DNA
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<400> 115
gggttcaccg tcagtagcaa ctcc

24

<210> 116
<211> 8
<212> PRT
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<220>
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<400> 116

Gly Phe Thr Val Ser Ser Asn Ser

1

5

<210> 117
<211> 21
<212> DNA
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<400> 117
atttttagcg gtggtatcac a

21

<210> 118
<211> 7
<212> PRT
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<400> 118

Ile Phe Ser Gly Gly Ile Thr
1 5

<210> 119
<211> 39
<212> DNA
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<400> 119
gcgcgtcatt ctaactggaa ctttgatgct tttgatatc

39

<210> 120
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<400> 120

Ala Arg His Ser Asn Trp Asn Phe Asp Ala Phe Asp Ile
1 5 10

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

<220>
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<400> 121
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 gggaaagccc ctaacctcct gatctatgct acatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg gaacttacta ttgtcaacag agttacagta tcccgtacac ttttggccag 300
 gggaccaagc tggagatcaa a 321

<210> 122
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 122

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 Phe Asp Thr Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
 35 40 45

Tyr Ala Thr 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 Gly Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ile Pro Tyr
 85 90 95

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

<210> 123
<211> 18
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<220>
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<400> 123
cagagctttg acacctat

18

<210> 124
<211> 6
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<220>
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<400> 124

Gln Ser Phe Asp Thr Tyr
1 5

<210> 125
<211> 9
<212> DNA
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<220>
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<400> 125
gctacatcc

9

<210> 126
<211> 3
<212> PRT
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<220>
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<400> 126

Ala Thr Ser
1

<210> 127
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<400> 127
 caacagagtt acagtatccc gtacact

27

<210> 128
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Gln Gln Ser Tyr Ser Ile Pro Tyr Thr
 1 5

<210> 129
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 <212> DNA
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<220>
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 cctggacaag ggcttgagt gatgggattg atcaacccta atactggtgg cacaaacttt 180
 gcacagaaat ttcagggcag ggtcaccatg accagggact cgtcaatcag cgcagcctac 240
 atggaactga gcaggctgag atctgacgac acggccgtgt attactgtgc gagacaacac 300
 tggaaccgtt attttgacaa ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 130
 <211> 118
 <212> PRT
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg 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 Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Leu Ile Asn Pro Asn Thr Gly Gly Thr Asn Phe Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Ser Ser Ile Ser Ala Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln His Trp Asn Arg Tyr Phe Asp Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 131

<211> 24

<212> DNA

<213> Artificial Sequence

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<400> 131

ggatacacct tcaccggcta ctat

24

<210> 132

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

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<400> 132

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

<210> 133

<211> 24

<212> DNA

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<223> synthetic

<400> 133

atcaacccta atactggtgg caca

24

<210> 134

<211> 8

<212> PRT

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Ile Asn Pro Asn Thr Gly Gly Thr
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<210> 135

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<212> DNA

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<400> 135

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 gggaaagccc ctaaactcct gatccaagag gcgtccagta tagaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctta tcgtcagcag cctgcagcct 240
 gatgattttg caacttatta ctgccaacag tataatagtt attcgtggac gttcggccac 300
 gggaccaagg tggaaatcaa a 321

<210> 138
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 <212> PRT
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<220>
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<400> 138

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 Val Gly Asn Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Gln Glu Ala Ser Ser Ile Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Ile Val Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Trp
85 90 95

Thr Phe Gly His Gly Thr Lys Val Glu Ile Lys
100 105

<210> 139
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<212> DNA
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<400> 139
cagagtgttg gtaactgg

18

<210> 140
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<212> PRT
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<220>
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<400> 140

Gln Ser Val Gly Asn Trp
1 5

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

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<400> 141
gaggcgtcc

9

<210> 142
<211> 3
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<220>
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<400> 142

Glu Ala Ser
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<210> 143

<211> 27

<212> DNA

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<400> 143

caacagtata atagttattc gtggacg

27

<210> 144

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<212> PRT

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Gln Gln Tyr Asn Ser Tyr Ser Trp Thr
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<212> DNA

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<400> 145

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acctgctctg tctctggtgg ctccatcact aattacttct ggacctggat ccggcagtcc 120

ccagggaagg gactggaatg gattgggtat atctattaca gtggggggcac caactataac 180

ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca attctccctg 240

aatatgaatt ctgtgaccgc tgcggacacg gccgtctatt actgtgcggg gagctactac 300

tacggtgtgg acgtctgggg ccaagggacc acggtcaccg tctcctca 348

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 1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile Thr Asn Tyr
 20 25 30

Phe Trp Thr Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

Asn Met Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Gly Ser Tyr Tyr Tyr Gly Val Asp Val Trp Gly Gln Gly Thr Thr Val
 100 105 110

Thr Val Ser Ser
 115

<210> 147
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<400> 147

ggtggctcca tcactaatta cttc

24

<210> 148

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

<220>
<223> synthetic

<400> 148

Gly Gly Ser Ile Thr Asn Tyr Phe
1 5

<210> 149
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<213> Artificial Sequence

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<400> 150

Ile Tyr Tyr Ser Gly Gly Thr
1 5

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gcggggagct actactacgg tgtggacgtc

30

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Ala Gly Ser Tyr Tyr Tyr Gly Val Asp Val
1 5 10

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<211> 321

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ggccaggctc ccagactcct catctatgat gcatccaaca ggcccactgg catcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcaacag cctagagtct 240
gaagattttg cagtttatct ctgtcagcag cgtaacaact ggccattcac tttcggccct 300
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Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Lys Ser Phe
20 25 30

Leu Ala Trp Tyr Arg Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Pro Thr Gly Ile Pro Ala Arg Phe Ser Gly
Page 50

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Arg Asn Asn Trp Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 155
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cagagtatta aaagcttc

18

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<400> 156

Gln Ser Ile Lys Ser Phe
1 5

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<400> 157
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9

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Asp Ala Ser
1

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27

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<400> 160

Gln Gln Arg Asn Asn Trp Pro Phe Thr
1 5

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ccaggaaagg ggctagagtg gatttcactc attagtagta gtggtagtgc catatattac 180
tcagactctg tgaagggccg attcaccata tccagggaca atgccaggaa atcactgtat 240

ctgcaagtga acagcctgag agccgaggac acggccgtat attactgtgc gagagatcgg 300
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 <212> PRT
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<400> 162

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 Tyr
 20 25 30

Tyr Met Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Ser Leu Ile Ser Ser Ser Gly Ser Ala Ile Tyr Tyr Ser Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Lys Ser Leu Tyr
 65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Gly Glu Trp Ala Leu Gly Ala Tyr Tyr Tyr Gly Leu
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 163
 <211> 24
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<400> 163
ggattcacct tcagtgacta ctac

24

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<211> 8
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<220>
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<400> 164

Gly Phe Thr Phe Ser Asp Tyr Tyr
1 5

<210> 165
<211> 24
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<220>
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<400> 165
attagtagta gtggtagtgc cata

24

<210> 166
<211> 8
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<220>
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<400> 166

Ile Ser Ser Ser Gly Ser Ala Ile
1 5

<210> 167
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<400> 167

gcgagagatc ggggggagtg gggcctcgga gcctactact acggtttgga cgtc

54

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<400> 168

Ala	Arg	Asp	Arg	Gly	Glu	Trp	Ala	Leu	Gly	Ala	Tyr	Tyr	Tyr	Gly	Leu
1				5					10					15	

Asp Val

<210> 169
<211> 336
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<400> 169

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tacctgcaga	agtcagggca	gtctccacag	ctcctgatct	atttgggttc	taatcgggcc	180
tccgggggtcc	ctgacagggt	cagtggcagt	ggatcaggca	cagattttac	actgaaaatc	240
agcagaatgg	aggctgagga	tgttgggggt	tattactgca	tgcaagctct	acaaactccg	300
tacacttttg	gccaggggac	caagctggag	atcaaaa			336

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<220>
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<400> 170

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Pro	Gly
1				5					10					15	

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ser Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Met Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 171
<211> 33
<212> DNA
<213> Artificial Sequence

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<400> 171
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33

<210> 172
<211> 11
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<220>
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<400> 172

Gln Ser Leu Leu His Ser Asp Gly Tyr Asn Tyr
1 5 10

<210> 173
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<213> Artificial Sequence

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<223> synthetic

<400> 173

ttgggttct

9

<210> 174

<211> 3

<212> PRT

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<223> synthetic

<400> 174

Leu Gly Ser

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<210> 175

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 175

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<210> 176

<211> 9

<212> PRT

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<220>

<223> synthetic

<400> 176

Met Gln Ala Leu Gln Thr Pro Tyr Thr

1

5

<210> 177

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

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cagcagccag ggaagggcct ggaatggatt gggtacattt cttatagagg gacaacctac      180
tacaacccga ccctcgagag tcgtgttagc atttcagtag acacgtttaa gaatcaattc      240
tccctgatgt tgcactccgt gactgtcgcg gacacggccg tgtattattg tgcgaaagta      300
ctccaagggc tcgtcagatt cagggactac ggtttcgacg tctggggcca agggaccacg      360
gtcaccgtct cctca                                          375
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<211> 125

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<400> 178

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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 Ala
          20              25             30
```

```
Asp His Tyr Trp Ser Trp Ile Arg Gln Gln Pro Gly Lys Gly Leu Glu
          35              40             45
```

```
Trp Ile Gly Tyr Ile Ser Tyr Arg Gly Thr Thr Tyr Tyr Asn Pro Thr
          50              55             60
```

```
Leu Glu Ser Arg Val Ser Ile Ser Val Asp Thr Phe Lys Asn Gln Phe
65              70             75             80
```

```
Ser Leu Met Leu His Ser Val Thr Val Ala Asp Thr Ala Val Tyr Tyr
          85              90             95
```

```
Cys Ala Lys Val Leu Gln Gly Leu Val Arg Phe Arg Asp Tyr Gly Phe
          100             105            110
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Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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30

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<400> 180

Gly Gly Ser Ile Ser Ser Ala Asp His Tyr
1 5 10

<210> 181
<211> 21
<212> DNA
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<220>
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<400> 181
atttcttata gagggacaac c

21

<210> 182
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<400> 182

Ile Ser Tyr Arg Gly Thr Thr
1 5

<210> 183
<211> 51
<212> DNA
<213> Artificial Sequence

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<400> 183
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<211> 17
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<400> 184

Ala	Lys	Val	Leu	Gln	Gly	Leu	Val	Arg	Phe	Arg	Asp	Tyr	Gly	Phe	Asp
1			5					10						15	

Val

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gggaaatccc ctaaactcct gatctatgat gcttttactt tacacactgg ggtcccatca 180
aggtttagcg gcagtggatc tgggacagaa ttcacttca caatcagcag cctgcagcct 240
gaggattttg caacttttta ctgtcaacac ctttatagtt ttccattcac tttcggccct 300
gggaccaaag tggatatcaa a 321

<210> 186

<211> 107
<212> PRT
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<400> 186

Asp Ile Gln Leu Thr Gln Ser Pro Pro Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Asp Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Asn Pro Gly Lys Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Phe Thr Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Phe Tyr Cys Gln His Leu Tyr Ser Phe Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

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18

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<400> 188

Gln Asp Ile Ser Ser Tyr
1 5

<210> 189

<211> 9

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 189

gatgctttt

9

<210> 190

<211> 3

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<400> 190

Asp Ala Phe
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<210> 191

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 191

caacaccttt atagttttcc attcact

27

<210> 192

<211> 9

<212> PRT

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<223> synthetic

<400> 192

Gln His Leu Tyr Ser Phe Pro Phe Thr
1 5

<210> 193
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ccaggggagg gcctggagt ggtcgcagcc atttatcgga atagtgattc catagactat 180
gcggactctg tgaagggccg attcaccatt tccagagaca acgccaagaa ctccctatat 240
ctgcaaata acagtctgaa aactgaggac acggcgttgt attactgtgc aaaagatgag 300
ggatttttgg agtactttga ctcttggggc cagggaaccc tggtcaccgt ctctca 357

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<400> 194

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 Thr Phe Arg Asn Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Val
35 40 45

Ala Ala Ile Tyr Arg Asn Ser Asp Ser Ile Asp Tyr Ala 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 Lys Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Glu Gly Phe Leu Glu Tyr Phe Asp Ser Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

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ggattcacct ttaggaatta tgcc

24

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<400> 196

Gly Phe Thr Phe Arg Asn Tyr Ala
1 5

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atttatcgga atagtgattc cata

24

<210> 198
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<400> 198

Ile Tyr Arg Asn Ser Asp Ser Ile
1 5

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<400> 200

Ala Lys Asp Glu Gly Phe Leu Glu Tyr Phe Asp Ser
1 5 10

<210> 201

<211> 324

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<400> 201

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cctggccagg ctcccaggct cctcatctac ggtgtatcca gcaggttcat tggcatccca 180

gacaggttca gtggcggtgg gtctgggaca gacttcactc tcaccatcac cagactggag 240

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caagggacca aggtggaaat caaa

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

Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Val Ser Ser Arg Phe Ile Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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cagagtgtta gcagcagctt c

21

<210> 204

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<400> 204

Gln Ser Val Ser Ser Ser Phe
1 5

<210> 205
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ggtgtatcc

9

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Gly Val Ser
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27

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Gln Gln Tyr Gly Arg Ser Pro Trp Thr
1 5

<210> 209

<211> 366

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<400> 209

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ccaggcaagg gactggaatg ggtggcagtt atatcatatg atggagatga taaatactat 180
ggagactccg tgaagggccg attcaccatt tccagagaca attccaagac catggtgtat 240
ctgcacatga acagcctgag aactgaggac acggctgtgt attattgtgc gaaagatgga 300
tatagtctct acgggaagga ctactttgac tattggggcc aggggaaccct ggtcaccgtc 360
tcctca 366

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<211> 122

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<400> 210

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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Asp Asp Lys Tyr Tyr Gly Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Thr Met Val Tyr
65 70 75 80

Leu His Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Tyr Ser Leu Tyr Gly Lys Asp Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<211> 8
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<213> Artificial Sequence

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Gly Phe Thr Phe Ser Arg Tyr Ala
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atatcatatg atggagatga taaa

24

<210> 214
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Ile Ser Tyr Asp Gly Asp Asp Lys
1 5

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45

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<400> 216

Ala Lys Asp Gly Tyr Ser Leu Tyr Gly Lys Asp Tyr Phe Asp Tyr
1 5 10 15

<210> 217
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60

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cctgaccagg ctcccagact cctcatctat ggtgcgtcca gcagggccac tggcatccca	180
gacaggttca gtggcagtga gtctgggaca gactttactc tcaccatcag cagactggag	240
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caagggacca aggtggaaat caaa	324

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<220>
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<400> 218

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Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Thr	Asn	Ser
			20					25					30		

Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	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	Glu	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	Val	Arg	Ser	Pro
				85					90					95	

Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys
			100					105			

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21

<210> 220
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<400> 220

Gln Ser Ile Thr Asn Ser Tyr
1 5

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

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<400> 221
ggtgCGTCC

9

<210> 222
<211> 3
<212> PRT
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<400> 222

Gly Ala Ser
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<400> 223

cagcagtatg ttaggtcacc gtggacg

27

<210> 224
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 224

Gln Gln Tyr Val Arg Ser Pro Trp Thr
1 5

<210> 225
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 225

caggtgcagc tacagcagtg gggcgcagga ctgttgaagc cctcggagac cctgtccctc	60
acctgcgttg tctatggtga gtctttcggg aattaccatt ggaattggat ccgccagtcc	120
ccaggggaagc ggctggagtg gattggggaa atcaatcaaa atggacacac caattacaac	180
ccgtccctca agagtcgagt caccatatca gtggacacgt ccaagatcca attttcctg	240
agactgaact ctgtgaccgc cgcggacacg gctgtgtatt tctgtgagag aggccataac	300
tacgtaaatt cctacttcgg tttggacgtc tggggccaag ggaccacggt caccgtctcc	360
tca	363

<210> 226
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 226

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Val Val Tyr Gly Glu Ser Phe Gly Asn Tyr
20 25 30

His Trp Asn Trp Ile Arg Gln Ser Pro Gly Lys Arg Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Gln Asn Gly His Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Ile Gln Phe Ser Leu
65 70 75 80

Arg Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
85 90 95

Arg Gly His Asn Tyr Val Asn Ser Tyr Phe Gly Leu Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 227
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 227
ggtgagtctt tcgtaatta ccat

24

<210> 228
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 228

Gly Glu Ser Phe Gly Asn Tyr His
1 5

<210> 229

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

<220>
<223> synthetic

<400> 229
atcaatcaaa atggacacac c

21

<210> 230
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 230

Ile Asn Gln Asn Gly His Thr
1 5

<210> 231
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 231
gcgagaggcc ataactacgt aaattcctac ttcggtttgg acgtc

45

<210> 232
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 232

Ala Arg Gly His Asn Tyr Val Asn Ser Tyr Phe Gly Leu Asp Val
1 5 10 15

<210> 233
<211> 321
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 233

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gaaattgtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc      60
ctctcctgca ggaccagtca gagtgtgaagc atcagcttag cctggtacca gcggaaacct      120
ggccaggctc ccaggctcct catctttggt tcatccacca gggccactgg tgtcccagcc      180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct      240
gaagattttg cagtttatta ctgtcagcag tataataact ggccgtacac ttttggccag      300
gggaccaagc tggagatcaa a                                              321
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<210> 234

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 234

```
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1           5           10           15
```

```
Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Gln Ser Val Ser Ile Ser
          20           25           30
```

```
Leu Ala Trp Tyr Gln Arg Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
          35           40           45
```

```
Phe Gly Ser Ser Thr Arg Ala Thr Gly Val 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 Tyr
          85           90           95
```

```
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
          100          105
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<210> 235
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 235
cagagtgtaa gcatcagc

18

<210> 236
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 236

Gln Ser Val Ser Ile Ser
1 5

<210> 237
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 237
ggttcatcc

9

<210> 238
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 238

Gly Ser Ser
1

<210> 239
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 239
cagcagtata ataactggcc gtacact

27

<210> 240
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 240

Gln Gln Tyr Asn Asn Trp Pro Tyr Thr
1 5

<210> 241
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 241
caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcgcc gccactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaacactt acactgggtg cacaaactat 180
gggcagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcac cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgttt attactgtgc gcgagatcgg 300
cggaactgga acttcgtctt tgaatattgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 242
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 242

Gln Val 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 Ala Ala His
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Gly Thr Asn Tyr Gly Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Thr Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Arg Asn Trp Asn Phe Val Phe Glu Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 243
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 243
 ggatacacct tcgccgccca ctat

24

<210> 244
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 244

Gly Tyr Thr Phe Ala Ala His Tyr
1 5

<210> 245
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 245
atcaacactt acactggtgg caca

24

<210> 246
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 246

Ile Asn Thr Tyr Thr Gly Gly Thr
1 5

<210> 247
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 247
gcgcgagatc ggcggaactg gaacttcgtc tttgaatat

39

<210> 248
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 248

Ala Arg Asp Arg Arg Asn Trp Asn Phe Val Phe Glu Tyr
1 5 10

<210> 249
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 249
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcagttgcc gggcaagtca gaacattaag aactatttaa attggtatca gcagaaacca 120
gggaaagccc ctaaactcct gatctatgaa gcatctaatt tgcaaagtgg ggcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctggaacct 240
gaagattttg caacttacta ctgtcaacag agtttttagta ttccgtggac gttcggccaa 300
gggaccaagg tggaatcaa a 321

<210> 250
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 250

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 Ser Cys Arg Ala Ser Gln Asn Ile Lys Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Glu Ala Ser Asn Leu Gln Ser Gly Ala Pro Ser 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 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ile Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 251
cagaacatta agaactat

18

<210> 252
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 252

Gln Asn Ile Lys Asn Tyr
1 5

<210> 253
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 253
gaagcatct

9

<210> 254
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 254

Glu Ala Ser

1

<210> 255
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 255
caacagagtt ttagtattcc gtggacg 27

<210> 256
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 256

Gln Gln Ser Phe Ser Ile Pro Trp Thr
1 5

<210> 257
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 257
caggtgcagc tgggtgcagtc tggggctgaa gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacg gcctactatt tacactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggattg ctcaaccctt atactggtgg ctcatactat 180
acacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcga cacagcctac 240
atggaactga acagtctgag atctgacgac acggccatct attactgtgc gagagataag 300
aggagctact acatccccta tgcttttgaa atctggggcc aagggacaat ggtcaccgtc 360
tcttca 366

<210> 258
<211> 122

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 258

Gln Val 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 Ile Ala Tyr
20 25 30

Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Leu Leu Asn Pro Tyr Thr Gly Gly Ser Tyr Tyr Thr Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asp Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Arg Ser Asp Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Asp Lys Arg Ser Tyr Tyr Ile Pro Tyr Ala Phe Glu Ile Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 259
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 259
ggatacacct tcatcgacct ctat

24

<210> 260
<211> 8
<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 260

Gly Tyr Thr Phe Ile Ala Tyr Tyr
1 5

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 261

ctcaaccctt atactggtgg ctca

24

<210> 262

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 262

Leu Asn Pro Tyr Thr Gly Gly Ser
1 5

<210> 263

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 263

gcgagagata agaggagcta ctacatccct tatgcttttg aaatc

45

<210> 264

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 264

Ala	Arg	Asp	Lys	Arg	Ser	Tyr	Tyr	Ile	Pro	Tyr	Ala	Phe	Glu	Ile
1				5					10				15	

<210> 265

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 265

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

<210> 266

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 266

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> 267
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 267
cagagcatta gcagctat

18

<210> 268
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 268

Gln Ser Ile Ser Ser Tyr
1 5

<210> 269
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 269
gctgcatcc

9

<210> 270
<211> 3
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 270

Ala Ala Ser

1

<210> 271

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 271

caacagagtt acagtacccc tccgatcacc

30

<210> 272

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 272

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr

1

5

10

<210> 273

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 273

gaggtgcagc tgggtggagtc tgggggaggc ttggttcagc ctggggtgtc cctgagactc 60

tcctgtgtag cctctggatt cacctttagc aattatgaca taacctggat ccgccagatt 120

ccagggaagg ggctggagtg ggtctcaaga atcagtggta gtggtggaag tacatatttc 180

gcagactccg tgaagggtcg gttcatcatc tccagagaca attccaaaaa tacggtgtat 240

atgcaaatga acagtttgag agccgaagac tcggccgtat attactgtgc gagaagagat 300

tccgtcttat ttagtatgaa cagttggctc gaccctggg gccagggaac cctggtcacc 360
gtctcctca 369

<210> 274
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 274

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Val
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Asp Ile Thr Trp Ile Arg Gln Ile Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Ser Gly Ser Gly Gly Ser Thr Tyr Phe Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65 70 75 80

Met Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Asp Ser Val Leu Phe Ser Met Asn Ser Trp Leu Asp Pro
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 275
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 275
ggattcacct ttagcaatta tgac

24

<210> 276
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 276

Gly Phe Thr Phe Ser Asn Tyr Asp
1 5

<210> 277
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 277
atcagtggta gtggtggaag taca

24

<210> 278
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 278

Ile Ser Gly Ser Gly Gly Ser Thr
1 5

<210> 279
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 279
gcgagaagag attccgtctt atttagtatg aacagttggc tcgacccc

48

<210> 280
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 280

Ala	Arg	Arg	Asp	Ser	Val	Leu	Phe	Ser	Met	Asn	Ser	Trp	Leu	Asp	Pro
1				5					10				15		

<210> 281
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 281

gagggtgcagc	tggtgcagtc	tggagcagag	gtgaaaaagc	ccggggagtc	tctgaagatc	60
tcctgttcgg	gatctggata	caggtttacc	aactactgga	tcgcctgggt	gcgccagatg	120
cccgggaaag	gcctggagtg	gatgggtctc	attcatcctg	atgactctga	tattagatac	180
agcccgtcct	tccaaggcca	ggtcaccttt	tcagtcgaca	agtccatcaa	caccgcctac	240
ctgcagtgga	gcagcctgaa	ggcctcggac	accgccatgt	attactgtac	gcgacaagac	300
ggaatactat	ggtctcataa	tgcctgggtc	gaccctggg	gccaggggaa	cctgggtcacc	360
gtctcctca						369

<210> 282
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 282

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1				5					10					15	

Ser	Leu	Lys	Ile	Ser	Cys	Ser	Gly	Ser	Gly	Tyr	Arg	Phe	Thr	Asn	Tyr
			20					25						30	

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Leu Ile His Pro Asp Asp Ser Asp Ile Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Phe Ser Val Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

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

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 283
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 283
ggatacaggt ttaccaacta ctgg

24

<210> 284
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 284

Gly Tyr Arg Phe Thr Asn Tyr Trp
1 5

<210> 285
<211> 24
<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 285

attcatcctg atgactctga tatt

24

<210> 286

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 286

Ile His Pro Asp Asp Ser Asp Ile
1 5

<210> 287

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 287

acgcgacaag acggaatact atggtctcat aatgcctggt tcgacccc

48

<210> 288

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 288

Thr Arg Gln Asp Gly Ile Leu Trp Ser His Asn Ala Trp Phe Asp Pro
1 5 10 15

<210> 289

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 289

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tcctgcaagg cctctggata caccttcatt agttacaata tcttctgggt gcgacaggcc      120
actggtcagg gccttgattg gatgggatgg atgaaccctt tcagaaataa cgcaggttat      180
gcacagaagt ttcagggcag agtcaccgtg acctgggaca cctccatcag cacagcctac      240
atggaactgt ccagcctgag ctctgaggac acggccatat attactgtgc gagagaacat      300
ggcagtagct ggggcttctt tgactactgg ggccagggaa ccctgggtcac cgtctcctca      360
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<210> 290

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 290

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Gln Val 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 Ile Ser Tyr
              20             25             30
```

```
Asn Ile Phe Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Asp Trp Met
35              40             45
```

```
Gly Trp Met Asn Pro Phe Arg Asn Asn Ala Gly Tyr Ala Gln Lys Phe
50              55             60
```

```
Gln Gly Arg Val Thr Val Thr Trp Asp Thr Ser Ile Ser Thr Ala Tyr
65              70             75             80
```

```
Met Glu Leu Ser Ser Leu Ser Ser Glu Asp Thr Ala Ile Tyr Tyr Cys
85              90             95
```

```
Ala Arg Glu His Gly Ser Ser Trp Gly Phe Phe Asp Tyr Trp Gly Gln
100             105            110
```

```
Gly Thr Leu Val Thr Val Ser Ser
```

115

120

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

<220>
 <223> synthetic

<400> 291
 ggatacacct tcattagtta caat

24

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

<220>
 <223> synthetic

<400> 292

Gly Tyr Thr Phe Ile Ser Tyr Asn
 1 5

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

<220>
 <223> synthetic

<400> 293
 atgaaccct tcagaaataa cgca

24

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

<220>
 <223> synthetic

<400> 294

Met Asn Pro Phe Arg Asn Asn Ala
 1 5

<210> 295
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 295
 gcgagagaac atggcagtag ctggggcttc ttgactac 39

<210> 296
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 296
 Ala Arg Glu His Gly Ser Ser Trp Gly Phe Phe Asp Tyr
 1 5 10

<210> 297
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 297
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccttg gacgttcggc 300
 caagggacca aggtggaaat caaa 324

<210> 298
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 298

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> 299

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 299

cagagtgtta gcagcagcta c

21

<210> 300

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 300

Gln Ser Val Ser Ser Ser Tyr
1 5

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

<220>
<223> synthetic

<400> 301
ggtgcatcc

9

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

<220>
<223> synthetic

<400> 302

Gly Ala Ser
1

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

<220>
<223> synthetic

<400> 303
cagcagtatg gtagctcacc ttggacg

27

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

<220>
<223> synthetic

<400> 304

Gln Gln Tyr Gly Ser Ser Pro Trp Thr
1 5

<210> 305

<211> 483
<212> DNA
<213> Artificial Sequence

<220>
<223> Bet v1

<400> 305
atgggtgtgt ttaattatga gactgagacc acctctgtta tcccagcagc tcgactgttc 60
aaggccttta tccttgatgg cgataacctc tttccaaagg ttgcaccca agccattagc 120
agtgttgaaa acattgaagg aaatggaggg cctggaacca ttaagaagat cagctttccc 180
gaaggcctcc ctttcaagta cgtgaaggac agagttgatg aggtggacca cacaaacttc 240
aaatacaatt acagcgtgat cgagggcggt cccataggcg acacattgga gaagatctcc 300
aacgagataa agatagtggc aaccctgat ggaggatcca tcttgaagat cagcaacaag 360
taccacacca aaggtgacca tgaggtgaag gcagagcagg ttaaggcaag taaagaaatg 420
ggcgagacac ttttgagggc cgttgagagc tacctcttgg cacactccga tgcctacaac 480
taa 483

<210> 306
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> Bet v1 (M1-N160 of accession number CAB02159)

<400> 306

Met Gly Val Phe Asn Tyr Glu Thr Glu Thr Thr Ser Val Ile Pro Ala
1 5 10 15

Ala Arg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Asn Leu Phe Pro
20 25 30

Lys Val Ala Pro Gln Ala Ile Ser Ser Val Glu Asn Ile Glu Gly Asn
35 40 45

Gly Gly Pro Gly Thr Ile Lys Lys Ile Ser Phe Pro Glu Gly Leu Pro
50 55 60

Phe Lys Tyr Val Lys Asp Arg Val Asp Glu Val Asp His Thr Asn Phe
65 70 75 80

Lys Tyr Asn Tyr Ser Val Ile Glu Gly Gly Pro Ile Gly Asp Thr Leu
85 90 95

Glu Lys Ile Ser Asn Glu Ile Lys Ile Val Ala Thr Pro Asp Gly Gly
100 105 110

Ser Ile Leu Lys Ile Ser Asn Lys Tyr His Thr Lys Gly Asp His Glu
115 120 125

Val Lys Ala Glu Gln Val Lys Ala Ser Lys Glu Met Gly Glu Thr Leu
130 135 140

Leu Arg Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Ala Tyr Asn
145 150 155 160

<210> 307
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> AA 23-43 of Bet v1

<400> 307

Phe Ile Leu Asp Gly Asp Asn Leu Phe Pro Lys Val Ala Pro Gln Ala
1 5 10 15

Ile Ser Ser Val Glu
20

<210> 308
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> AA 44-56 of Bet v1

<400> 308

Asn Ile Glu Gly Asn Gly Gly Pro Gly Thr Ile Lys Lys
1 5 10

<210> 309

<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> AA 2-19 of Bet v1

<400> 309

Gly Val Phe Asn Tyr Glu Thr Glu Thr Thr Ser Val Ile Pro Ala Ala
1 5 10 15

Arg Leu

<210> 310
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> AA 57-70 of Bet v1

<400> 310

Ile Ser Phe Pro Glu Gly Leu Pro Phe Lys Tyr Val Lys Asp
1 5 10

<210> 311
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> AA 81-89 of Bet v1

<400> 311

Lys Tyr Asn Tyr Ser Val Ile Glu Gly
1 5

<210> 312
<211> 187
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant Bet v 1-MMH w S85A (1-159: Bet v1 (G2-N160 of accession number CAB02159) with Myc-Myc hexahistidine tag

<400> 312

Gly Val Phe Asn Tyr Glu Thr Glu Thr Thr Ser Val Ile Pro Ala Ala
 1 5 10 15

Arg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Asn Leu Phe Pro Lys
 20 25 30

Val Ala Pro Gln Ala Ile Ser Ser Val Glu Asn Ile Glu Gly Asn Gly
 35 40 45

Gly Pro Gly Thr Ile Lys Lys Ile Ser Phe Pro Glu Gly Leu Pro Phe
 50 55 60

Lys Tyr Val Lys Asp Arg Val Asp Glu Val Asp His Thr Asn Phe Lys
 65 70 75 80

Tyr Asn Tyr Ala Val Ile Glu Gly Gly Pro Ile Gly Asp Thr Leu Glu
 85 90 95

Lys Ile Ser Asn Glu Ile Lys Ile Val Ala Thr Pro Asp Gly Gly Ser
 100 105 110

Ile Leu Lys Ile Ser Asn Lys Tyr His Thr Lys Gly Asp His Glu Val
 115 120 125

Lys Ala Glu Gln Val Lys Ala Ser Lys Glu Met Gly Glu Thr Leu Leu
 130 135 140

Arg Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Ala Tyr Asn Glu
 145 150 155 160

Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Gly Glu Gln Lys Leu Ile
 165 170 175

Ser Glu Glu Asp Leu His His His His His His
 180 185

<210> 313
 <211> 413
 <212> PRT
 <213> Artificial Sequence

<220>

<223> hFceR1alpha-mFc

<400> 313

Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile
1 5 10 15

Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
20 25 30

Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu
35 40 45

Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly
50 55 60

Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu Ser Glu Pro Val Tyr
65 70 75 80

Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val
85 90 95

Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn
100 105 110

Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys
115 120 125

Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu
130 135 140

Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr
145 150 155 160

Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys Ala Pro Arg Glu Lys
165 170 175

Tyr Trp Leu Gln Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro
180 185 190

Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile
195 200 205

Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile
210 215 220

Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln
225 230 235 240

Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln
245 250 255

Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu
260 265 270

Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys
275 280 285

Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys
290 295 300

Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro
305 310 315 320

Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr
325 330 335

Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys
340 345 350

Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly
355 360 365

Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val
370 375 380

Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn
385 390 395 400

His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
405 410

<210> 314

<211> 160

<212> PRT
<213> Artificial Sequence

<220>

<223> Bet v 1 amino acid sequence from Uniprot: P15494

<400> 314

Met Gly Val Phe Asn Tyr Glu Thr Glu Thr Thr Ser Val Ile Pro Ala
1 5 10 15

Ala Arg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Asn Leu Phe Pro
20 25 30

Lys Val Ala Pro Gln Ala Ile Ser Ser Val Glu Asn Ile Glu Gly Asn
35 40 45

Gly Gly Pro Gly Thr Ile Lys Lys Ile Ser Phe Pro Glu Gly Phe Pro
50 55 60

Phe Lys Tyr Val Lys Asp Arg Val Asp Glu Val Asp His Thr Asn Phe
65 70 75 80

Lys Tyr Asn Tyr Ser Val Ile Glu Gly Gly Pro Ile Gly Asp Thr Leu
85 90 95

Glu Lys Ile Ser Asn Glu Ile Lys Ile Val Ala Thr Pro Asp Gly Gly
100 105 110

Ser Ile Leu Lys Ile Ser Asn Lys Tyr His Thr Lys Gly Asp His Glu
115 120 125

Val Lys Ala Glu Gln Val Lys Ala Ser Lys Glu Met Gly Glu Thr Leu
130 135 140

Leu Arg Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Ala Tyr Asn
145 150 155 160

<210> 315

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> AA 81-96 of Bet v1

<400> 315

Lys Tyr Asn Tyr Ser Val Ile Glu Gly Gly Pro Ile Gly Asp Thr Leu
1 5 10 15

<210> 316

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> H4H17038P2 HC

<400> 316

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Glu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Phe Ile Ser Asp Ser Ser Ser Asn Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser 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 Ala Ile Gly Ser Thr Ser Phe Asp Asn Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
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375

380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440 445

<210> 317
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H4H17038P2 LC

<400> 317

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val 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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Arg Leu Ile
 35 40 45

Tyr Ser 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 Ile Tyr Tyr Cys His Gln Tyr Asn Asn Trp Pro Leu
 85 90 95

Thr Phe Gly Gly 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> 318
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H16987P HC

<400> 318

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 Thr Val Ser Ser Asn
20 25 30

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Phe Ser Gly Gly Ile Thr Tyr Tyr Ser Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg His Ser Asn Trp Asn Phe Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 319
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H16987P LC

<400> 319

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 Phe Asp Thr Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
35 40 45

Tyr Ala Thr 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 Gly Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ile Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu 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> 320

<211> 443

<212> PRT
<213> Artificial Sequence

<220>
<223> H4H16992P HC

<400> 320

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 Ser Val Ser Gly Gly Ser Ile Thr Asn Tyr
20 25 30

Phe Trp Thr Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Asn Met Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Gly Ser Tyr Tyr Tyr Gly Val Asp Val Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210 215 220

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
245 250 255

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 321
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H16992P LC

<400> 321

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Lys Ser Phe
20 25 30

Leu Ala Trp Tyr Arg Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Pro Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Arg Asn Asn Trp Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp 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> 322
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H4H17082P2 HC

<400> 322

Gln Val 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 Ile Ser Tyr
 20 25 30

Asn Ile Phe Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Asp Trp Met
 35 40 45

Gly Trp Met Asn Pro Phe Arg Asn Asn Ala Gly Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Val Thr Trp Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Ser Ser Glu Asp Thr Ala Ile Tyr Tyr Cys
 85 90 95

Ala Arg Glu His Gly Ser Ser Trp Gly Phe 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> 323
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H17082P2 LC

<400> 323

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Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
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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 Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
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Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215