

728242_ST25 (1)
SEQUENCE LISTING

<110> THE UNITED STATES OF AMERICA, AS REPRESENTED BY THE
SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES

<120> ANTI-KRAS-G12D T CELL RECEPTORS

<130> 728242

<150> US 62/369,883

<151> 2016-08-02

<160> 70

<170> PatentIn version 3.5

<210> 1

<211> 189

<212> PRT

<213> Homo sapiens

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Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val

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100

105

110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
 115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
 130 135 140

Ser Ala Lys Thr Arg Gln Arg Val Glu Asp Ala Phe Tyr Thr Leu Val
 145 150 155 160

Arg Glu Ile Arg Gln Tyr Arg Leu Lys Lys Ile Ser Lys Glu Glu Lys
 165 170 175

Thr Pro Gly Cys Val Lys Ile Lys Lys Cys Ile Ile Met
 180 185

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Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
 1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
 20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
 35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
 50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
 65 70 75 80

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Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Asp Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Lys His Lys Glu Lys Met Ser Lys Asp Gly Lys Lys
165 170 175

Lys Lys Lys Lys Ser Lys Thr Lys Cys Val Ile Met
180 185

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Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

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Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Arg Val Glu Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Gln Tyr Arg Leu Lys Lys Ile Ser Lys Glu Glu Lys
165 170 175

Thr Pro Gly Cys Val Lys Ile Lys Lys Cys Ile Ile Met
180 185

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Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10 15

728242_ST25 (1)

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Asp Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Lys His Lys Glu Lys Met Ser Lys Asp Gly Lys Lys
165 170 175

Lys Lys Lys Lys Ser Lys Thr Lys Cys Val Ile Met
180 185

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Gly Ala Gly Gly Val Gly Lys Ser Ala Leu
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Gly Ala Asp Gly Val Gly Lys Ser Ala Leu
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<213> Homo sapiens

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Gly Ala Gly Gly Val Gly Lys Ser Ala
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<211> 9

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<400> 8

Gly Ala Asp Gly Val Gly Lys Ser Ala
1 5

<210> 9

<211> 7

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Asn Ile Ala Thr Asn Asp Tyr

728242_ST25 (1)

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Gly Tyr Lys Thr Lys
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Cys Leu Val Gly Asp Met Asp Gln Ala Gly Thr Ala Leu Ile Phe
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Ser Gly His Asp Thr
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Tyr Tyr Glu Glu Glu Glu
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<400> 14

Cys Ala Ser Ser Leu Gly Glu Gly Arg Val Asp Gly Tyr Thr Phe
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<210> 15
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Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
 1 5 10 15

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
 20 25 30

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
 35 40 45

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
 50 55 60

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

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
 85 90 95

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Asp Met Asp Gln
 100 105 110

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

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Ser

<210> 16
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Met Gly Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
 1 5 10 15

Gly Leu Val Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
 20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His
 35 40 45

Asp Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
 50 55 60

Ile Phe Gln Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro
 65 70 75 80

Asp Arg Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
 85 90 95

Val Asn Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
 100 105 110

Ser Leu Gly Glu Gly Arg Val Asp Gly Tyr Thr Phe Gly Ser Gly Thr
 115 120 125

Arg Leu Thr Val Val
 130

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<210> 17
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<400> 17

Asn Ile Ala Thr Asn Asp Tyr
 1 5

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<400> 18

Gly Tyr Lys Thr Lys
 1 5

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<400> 19

Cys Leu Val Gly Asp Met Asp Gln Ala Gly Thr Ala Leu Ile Phe
 1 5 10 15

<210> 20
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<400> 20

Ser Gly His Asp Thr
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728242_ST25 (1)

<400> 21

Tyr Tyr Glu Glu Glu Glu
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<211> 15

<212> PRT

<213> Homo sapiens

<400> 22

Cys Ala Ser Ser Leu Gly Arg Ala Ser Asn Gln Pro Gln His Phe
1 5 10 15

<210> 23

<211> 129

<212> PRT

<213> Homo sapiens

<400> 23

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
1 5 10 15

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
20 25 30

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
35 40 45

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
50 55 60

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

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
85 90 95

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Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Asp Met Asp Gln
 100 105 110

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

Ser

<210> 24
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 <212> PRT
 <213> Homo sapiens

<400> 24

Met Gly Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
 1 5 10 15

Gly Leu Val Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
 20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His
 35 40 45

Asp Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
 50 55 60

Ile Phe Gln Tyr Tyr Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro
 65 70 75 80

Asp Arg Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
 85 90 95

Val Asn Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
 100 105 110

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Ser Leu Gly Arg Ala Ser Asn Gln Pro Gln His Phe Gly Asp Gly Thr
 115 120 125

Arg Leu Ser Ile Leu
 130

<210> 25
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Asn Ile Ala Thr Asn Asp Tyr
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 <212> PRT
 <213> Homo sapiens

<400> 26

Gly Tyr Lys Thr Lys
 1 5

<210> 27
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 27

Cys Leu Val Gly Asp Arg Asp Gln Ala Gly Thr Ala Leu Ile Phe
 1 5 10 15

<210> 28
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Ser Gly His Asp Thr
1 5

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<211> 6
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<400> 29

Tyr Tyr Glu Glu Glu Glu
1 5

<210> 30
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<213> Homo sapiens

<400> 30

Cys Ala Ser Ser Phe Gly Gln Ser Ser Thr Tyr Gly Tyr Thr Phe
1 5 10 15

<210> 31
<211> 129
<212> PRT
<213> Homo sapiens

<400> 31

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
1 5 10 15

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
20 25 30

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
35 40 45

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
50 55 60

728242_ST25 (1)

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

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
85 90 95

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Asp Arg Asp Gln
100 105 110

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

Ser

<210> 32
<211> 133
<212> PRT
<213> Homo sapiens

<400> 32

Met Gly Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Leu Val Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His
35 40 45

Asp Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
50 55 60

Ile Phe Gln Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro
65 70 75 80

728242_ST25 (1)

Asp Arg Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
85 90 95

Val Asn Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Ser Phe Gly Gln Ser Ser Thr Tyr Gly Tyr Thr Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Val
130

<210> 33
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<400> 33

Asp Arg Gly Ser Gln Ser
1 5

<210> 34
<211> 6
<212> PRT
<213> Homo sapiens

<400> 34

Ile Tyr Ser Asn Gly Asp
1 5

<210> 35
<211> 13
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<213> Homo sapiens

<400> 35

Cys Ala Ala Ala Met Asp Ser Ser Tyr Lys Leu Ile Phe
1 5 10

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<210> 36
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<400> 36

Trp Ser His Ser Tyr
 1 5

<210> 37
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 <212> PRT
 <213> Homo sapiens

<400> 37

Ser Ala Ala Ala Asp Ile
 1 5

<210> 38
 <211> 12
 <212> PRT
 <213> Homo sapiens

<400> 38

Cys Ala Ser Ser Asp Pro Gly Thr Glu Ala Phe Phe
 1 5 10

<210> 39
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 39

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

Trp Val Trp Ser Gln Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu
 20 25 30

728242_ST25 (1)

Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp
35 40 45

Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser
50 55 60

Pro Glu Leu Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly
65 70 75 80

Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu
85 90 95

Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Ala
100 105 110

Ala Met Asp Ser Ser Tyr Lys Leu Ile Phe Gly Ser Gly Thr Arg Leu
115 120 125

Leu Val Arg Pro
130

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<212> PRT
<213> Homo sapiens

<400> 40

Met Gly Thr Arg Leu Phe Phe Tyr Val Ala Leu Cys Leu Leu Trp Ala
1 5 10 15

Gly His Arg Asp Ala Gly Ile Thr Gln Ser Pro Arg Tyr Lys Ile Thr
20 25 30

Glu Thr Gly Arg Gln Val Thr Leu Met Cys His Gln Thr Trp Ser His
35 40 45

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Ser Tyr Met Phe Trp Tyr Arg Gln Asp Leu Gly His Gly Leu Arg Leu
50 55 60

Ile Tyr Tyr Ser Ala Ala Ala Asp Ile Thr Asp Lys Gly Glu Val Pro
65 70 75 80

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

Leu Glu Ser Ala Thr Arg Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

Ser Asp Pro Gly Thr Glu Ala Phe Phe Gly Gln Gly Thr Arg Leu Thr
115 120 125

Val Val
130

<210> 41
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<213> Homo sapiens

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<223> Xaa can be any naturally occurring amino acid

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Xaa Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
1 5 10 15

Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
20 25 30

Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
35 40 45

728242_ST25 (1)

Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
50 55 60

Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65 70 75 80

Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
85 90 95

Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
100 105 110

Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
115 120 125

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
130 135 140

<210> 42
<211> 177
<212> PRT
<213> Homo sapiens

<400> 42

Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
1 5 10 15

Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
20 25 30

Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
35 40 45

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys
50 55 60

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Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
65 70 75 80

Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
85 90 95

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
100 105 110

Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
115 120 125

Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu Ser
130 135 140

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
145 150 155 160

Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
165 170 175

Phe

<210> 43

<211> 179

<212> PRT

<213> Homo sapiens

<400> 43

Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
1 5 10 15

Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
20 25 30

Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn

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35

40

45

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys
 50 55 60

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
 65 70 75 80

Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
 85 90 95

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
 100 105 110

Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
 115 120 125

Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser
 130 135 140

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
 145 150 155 160

Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
 165 170 175

Ser Arg Gly

<210> 44

<211> 137

<212> PRT

<213> Mus musculus

<400> 44

Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg
 1 5 10 15

728242_ST25 (1)

Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile
20 25 30

Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr
35 40 45

Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala
50 55 60

Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr
65 70 75 80

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

Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser
100 105 110

Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu
115 120 125

Leu Met Thr Leu Arg Leu Trp Ser Ser
130 135

<210> 45
<211> 173
<212> PRT
<213> Mus musculus

<400> 45

Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
1 5 10 15

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

728242_ST25 (1)

Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
35 40 45

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala Tyr Lys
50 55 60

Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
65 70 75 80

Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe
85 90 95

His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro
100 105 110

Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly
115 120 125

Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu
130 135 140

Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser
145 150 155 160

Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser
165 170

<210> 46
<211> 137
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<213> Artificial Sequence

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<223> Synthetic

<220>
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728242_ST25 (1)

<222> (48)..(48)

<223> Xaa is Thr or Cys

<220>

<221> MISC_FEATURE

<222> (112)..(112)

<223> Xaa is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp

<220>

<221> MISC_FEATURE

<222> (114)..(114)

<223> Xaa is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp

<220>

<221> MISC_FEATURE

<222> (115)..(115)

<223> Xaa is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp

<400> 46

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

Asn	Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp	Lys	Xaa
		35					40					45			

Val	Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala	Ile	Ala
	50					55					60				

Trp	Ser	Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys	Glu	Thr
65					70					75				80	

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

Glu	Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Xaa
			100					105					110		

728242_ST25 (1)

Val Xaa Xaa Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu
 115 120 125

Leu Met Thr Leu Arg Leu Trp Ser Ser
 130 135

<210> 47
 <211> 173
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (57)..(57)
 <223> Xaa is Ser or Cys

<400> 47

Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
 1 5 10 15

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

Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
 35 40 45

Gly Lys Glu Val His Ser Gly Val Xaa Thr Asp Pro Gln Ala Tyr Lys
 50 55 60

Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
 65 70 75 80

Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe
 85 90 95

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His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro
100 105 110

Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly
115 120 125

Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu
130 135 140

Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser
145 150 155 160

Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser
165 170

<210> 48
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 48

Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg
1 5 10 15

Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile
20 25 30

Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Cys
35 40 45

Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala
50 55 60

Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr
65 70 75 80

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

Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Leu
100 105 110

Val Ile Val Leu Arg Ile Leu Leu Lys Val Ala Gly Phe Asn Leu
115 120 125

Leu Met Thr Leu Arg Leu Trp Ser Ser
130 135

<210> 49
<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 49

Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
1 5 10 15

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

Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
35 40 45

Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Ala Tyr Lys
50 55 60

Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
65 70 75 80

728242_ST25 (1)

Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe
85 90 95

His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro
100 105 110

Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly
115 120 125

Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu
130 135 140

Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser
145 150 155 160

Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser
165 170

<210> 50

<211> 266

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 50

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
1 5 10 15

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
20 25 30

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
35 40 45

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
50 55 60

728242_ST25 (1)

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

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
85 90 95

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Asp Met Asp Gln
100 105 110

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

Ser Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro
130 135 140

Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln
145 150 155 160

Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys
165 170 175

Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile
180 185 190

Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu
195 200 205

Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu
210 215 220

Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu
225 230 235 240

Leu Val Ile Val Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn
245 250 255

728242_ST25 (1)

Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 51
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 51

Met Gly Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Leu Val Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His
35 40 45

Asp Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
50 55 60

Ile Phe Gln Tyr Tyr Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro
65 70 75 80

Asp Arg Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
85 90 95

Val Asn Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Ser Leu Gly Glu Gly Arg Val Asp Gly Tyr Thr Phe Gly Ser Gly Thr
115 120 125

728242_ST25 (1)

Arg Leu Thr Val Val Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val
 130 135 140

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
 145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
 165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp
 180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
 195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
 210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
 225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
 245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu
 260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
 275 280 285

Ala Val Leu Val Ser Thr Leu Val Val Met Ala Met Val Lys Arg Lys
 290 295 300

Asn Ser
 305

728242_ST25 (1)

<210> 52
 <211> 266
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 52

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
 1 5 10 15

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
 20 25 30

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
 35 40 45

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
 50 55 60

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

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
 85 90 95

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Asp Met Asp Gln
 100 105 110

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

Ser Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro
 130 135 140

Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln
 145 150 155 160

728242_ST25 (1)

Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys
165 170 175

Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile
180 185 190

Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu
195 200 205

Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu
210 215 220

Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu
225 230 235 240

Leu Val Ile Val Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn
245 250 255

Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 53
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 53

Met Gly Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Leu Val Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
20 25 30

728242_ST25 (1)

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His
 35 40 45

Asp Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
 50 55 60

Ile Phe Gln Tyr Tyr Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro
 65 70 75 80

Asp Arg Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
 85 90 95

Val Asn Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
 100 105 110

Ser Leu Gly Arg Ala Ser Asn Gln Pro Gln His Phe Gly Asp Gly Thr
 115 120 125

Arg Leu Ser Ile Leu Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val
 130 135 140

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
 145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
 165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp
 180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
 195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
 210 215 220

728242_ST25 (1)

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Thr Leu Val Val Met Ala Met Val Lys Arg Lys
290 295 300

Asn Ser
305

<210> 54
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 54

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
1 5 10 15

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
20 25 30

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
35 40 45

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
50 55 60

728242_ST25 (1)

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

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
85 90 95

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Asp Arg Asp Gln
100 105 110

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

Ser Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro
130 135 140

Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln
145 150 155 160

Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys
165 170 175

Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile
180 185 190

Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu
195 200 205

Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu
210 215 220

Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu
225 230 235 240

Leu Val Ile Val Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn
245 250 255

728242_ST25 (1)

Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 55
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 55

Met Gly Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Leu Val Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His
35 40 45

Asp Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
50 55 60

Ile Phe Gln Tyr Tyr Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro
65 70 75 80

Asp Arg Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
85 90 95

Val Asn Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Ser Phe Gly Gln Ser Ser Thr Tyr Gly Tyr Thr Phe Gly Ser Gly Thr
115 120 125

728242_ST25 (1)

Arg Leu Thr Val Val Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val
 130 135 140

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
 145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
 165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp
 180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
 195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
 210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
 225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
 245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu
 260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
 275 280 285

Ala Val Leu Val Ser Thr Leu Val Val Met Ala Met Val Lys Arg Lys
 290 295 300

Asn Ser
 305

728242_ST25 (1)

<210> 56
 <211> 269
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 56

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

Trp Val Trp Ser Gln Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu
 20 25 30

Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp
 35 40 45

Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser
 50 55 60

Pro Glu Leu Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly
 65 70 75 80

Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu
 85 90 95

Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Ala
 100 105 110

Ala Met Asp Ser Ser Tyr Lys Leu Ile Phe Gly Ser Gly Thr Arg Leu
 115 120 125

Leu Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu
 130 135 140

Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe
 145 150 155 160

728242_ST25 (1)

Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile
 165 170 175

Thr Asp Lys Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn
 180 185 190

Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile
 195 200 205

Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp
 210 215 220

Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe
 225 230 235 240

Gln Asn Leu Leu Val Ile Val Leu Arg Ile Leu Leu Leu Lys Val Ala
 245 250 255

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 260 265

<210> 57
 <211> 303
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 57

Met Gly Thr Arg Leu Phe Phe Tyr Val Ala Leu Cys Leu Leu Trp Ala
 1 5 10 15

Gly His Arg Asp Ala Gly Ile Thr Gln Ser Pro Arg Tyr Lys Ile Thr
 20 25 30

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Glu Thr Gly Arg Gln Val Thr Leu Met Cys His Gln Thr Trp Ser His
 35 40 45

Ser Tyr Met Phe Trp Tyr Arg Gln Asp Leu Gly His Gly Leu Arg Leu
 50 55 60

Ile Tyr Tyr Ser Ala Ala Ala Asp Ile Thr Asp Lys Gly Glu Val Pro
 65 70 75 80

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

Leu Glu Ser Ala Thr Arg Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
 100 105 110

Ser Asp Pro Gly Thr Glu Ala Phe Phe Gly Gln Gly Thr Arg Leu Thr
 115 120 125

Val Val Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe
 130 135 140

Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val
 145 150 155 160

Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp
 165 170 175

Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Ala
 180 185 190

Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val
 195 200 205

Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val
 210 215 220

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Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro
225 230 235 240

Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp
245 250 255

Cys Gly Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr
260 265 270

Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu
275 280 285

Val Ser Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser
290 295 300

<210> 58
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 58

Arg Ala Lys Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
1 5 10 15

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
20 25

<210> 59
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 59

gccacagcac tgttgctctt gaagtcc

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<210> 60
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 60
 caggcagtat ctggagtcac tgag

24

<210> 61
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 61

Met	Thr	Glu	Tyr	Lys	Leu	Val	Val	Val	Gly	Ala	Gly	Gly	Val	Gly	Lys
1				5					10					15	

Ser	Ala	Leu	Thr	Ile	Gln	Leu	Ile
							20

<210> 62
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 62

Met	Thr	Glu	Tyr	Lys	Leu	Val	Val	Val	Gly	Ala	Asp	Gly	Val	Gly	Lys
1				5					10					15	

Ser	Ala	Leu	Thr	Ile	Gln	Leu	Ile
							20

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<210> 63
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 63
 atgaggcaag tggcgagagt gatcgtgttc ctgaccctga gtactttgag ccttgctaag 60
 accacccagc ccatctccat ggactcatat gaaggacaag aagtgaacat aacctgtagc 120
 cacaacaaca ttgtacaaa tgattatatc acgtggtacc aacagtttcc cagccaagga 180
 ccacgattta ttattcaagg atacaagaca aaagttacaa acgaagtggc ctccctgttt 240
 atccctgccg acagaaagtc cagcactctg agcctgcccc gggtttccct gagcgacact 300
 gctgtgtact actgcctcgt gggtgacatg gaccaggcag gaactgctct gatctttggg 360
 aagggaacca ccttatcagt gagttcca 388

<210> 64
 <211> 400
 <212> DNA
 <213> Homo sapiens

<400> 64
 atgggccccg ggctcctctg ctgggcactg ctttgtctcc tgggagcagg cttagtggac 60
 gctggagtca cccaaagtcc cacacacctg atcaaaacga gaggacagca agtgactctg 120
 agatgctctc ctaagtctgg gcatgacact gtgtcctggg accaacaggc cctgggtcag 180
 gggccccagt ttatctttca gtattatgag gaggaagaga gacagagagg caacttcctt 240
 gatcgattct caggtcacca gttccctaac tatagctctg agctgaatgt gaacgccttg 300
 ttgctggggg actcggccct ctatctctgt gccagcagct tgggtgaggg aagagtggac 360
 ggctacacct tcggttcggg gaccaggtta accgtttag 400

<210> 65
 <211> 387
 <212> DNA
 <213> Artificial Sequence

728242_ST25 (1)

<220>

<223> Synthetic

<400> 65

atgcgccagg tggctcgcgt aatcgtgttt ctgactctga gcactctgtc actcgccaag	60
acgacccagc ccatttcaat ggactcatat gaaggtcagg aggtgaatat cacatgctcc	120
cacaataaca ttgctacaaa cgattacatt acatgggtatc aacagtttcc ctctcaaggg	180
cctcgattca taatacaagg gtataagacc aaagttacga atgaggtcgc atccctcttt	240
attcccgccg accggaagag ttctactctt tccctgccta gggtagacct gagtgatact	300
gctgtttact actgcctggg tggagacatg gaccaggcgg gaactgccct catattcggc	360
aagggcacga cactctctgt gtcattct	387

<210> 66

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 66

atggggccag gcctgctttg ctgggcgctg ctgtgcctcc tgggtgccgg tttggtggac	60
gctggtgtaa ctgagtcctc aacacatctg atcaagacac gcggccagca gggtacactg	120
cgctgttcac ccaagagtgg gcacgataca gtttcctggg accagcaagc tctgggtcaa	180
ggacctcagt ttatattcca atattacgaa gaggaggagc gccagcgcgg aaatttccca	240
gacagattct ccgggcacca gtttcccaac tactcatctg agctgaacgt taacgccctg	300
ctgctgggag actccgctct ctacctgtgc gcatctagcc tcgggagggc tagtaaccag	360
ccccagcact tcggcgacgg aaccaggctg tctattctg	399

<210> 67

<211> 388

<212> DNA

<213> Homo sapiens

728242_ST25 (1)

<400> 67
 atgaggcaag tggcgagagt gatcgtgttc ctgaccctga gtactttgag ccttgctaag 60
 accacccagc ccatctccat ggactcatat gaaggacaag aagtgaacat aacctgtagc 120
 cacaacaaca ttgctacaaa tgattatatc acgtgggtacc aacagtttcc cagccaagga 180
 ccacgattta ttattcaagg atacaagaca aaagttacaa acgaagtggc ctccctgttt 240
 atccctgccg acagaaagtc cagcactctg agcctgcccc gggtttccct gagcgacact 300
 gctgtgtact actgcctcgt ggggtgacagg gaccaggcag gaactgctct gatctttggg 360
 aagggaacca ccttatcagt gagttcca 388

<210> 68
 <211> 400
 <212> DNA
 <213> Homo sapiens

<400> 68
 atgggccccg ggctcctctg ctgggcactg ctttgtctcc tgggagcagg cttagtggac 60
 gctggagtca cccaaagtcc cacacacctg atcaaaacga gaggacagca agtgactctg 120
 agatgctctc ctaagtctgg gcatgacact gtgtcctggg accaacaggc cctggggtcag 180
 gggccccagt ttatctttca gtattatgag gaggaagaga gacagagagg caacttcctt 240
 gatcgattct caggtcacca gttccctaac tatagctctg agctgaatgt gaacgccttg 300
 ttgctggggg actcggccct ctatctctgt gccagcagct ttggacagtc aagcacatat 360
 ggctacacct tcggttcggg gaccagggtta accgtttag 400

<210> 69
 <211> 397
 <212> DNA
 <213> Homo sapiens

<400> 69
 atgaaatcct tgagagtttt actagtgatc ctgtggcttc agttgagctg ggtttggagc 60
 caacagaagg aggtggagca gaattctgga cccctcagtg ttccagaggg agccattgcc 120

728242_ST25 (1)

tctctcaact gcacttacag tgaccgaggt tcccagtcct tcttctggta cagacaatat	180
tctgggaaaa gccctgagtt gataatgttc atatactcca atggtgacaa agaagatgga	240
aggtttacag cacagctcaa taaagccagc cagtatgttt ctctgctcat cagagactcc	300
cagcccagtg attcagccac ctacctctgt gccgcggcga tggatagcag ctataaattg	360
atcttcggga gtgggaccag actgctggtc aggcctg	397

<210> 70
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 70	
atgggcacca ggctcttctt ctatgtggcc ctttgtctgc tgtgggcagg acacagggat	60
gctggaatca cccagagccc aagatacaag atcacagaga caggaaggca ggtgaccttg	120
atgtgtcacc agacttggag ccacagctat atgttctggt atcgacaaga cctgggacat	180
gggctgaggc tgatctatta ctcagcagct gctgatatta cagataaagg agaagtcccc	240
gatggctatg ttgtctccag atccaagaca gagaatttcc ccctcactct ggagtcagct	300
acccgctccc agacatctgt gtatttctgc gccagcagtg accccggcac tgaagctttc	360
tttggacaag gcaccagact cacagttgta g	391