

2015-08-05 32896-226065PCT_ST25.txt
SEQUENCE LISTING

<110> MEMORIAL SLOAN KETTERING CANCER CENTER
ROTOLO, Jimmy
KOLESNICK, Richard

<120> ANTI-CERAMIDE ANTIBODIES

<130> 32896-226065PCT

<150> US 62/034,453

<151> 2014-08-07

<160> 45

<170> PatentIn version 3.5

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<211> 10

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<223> Synthetic: heavy chain variable region CDR1 of the anti-ceramide antibody

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Gly Tyr Thr Phe Thr Asp His Thr Ile His
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<223> Synthetic: heavy chain variable region CDR2

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Tyr Asn Tyr Pro Arg Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

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<223> Synthetic: heavy chain variable region CDR3

<400> 3

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

<210> 4

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<400> 4

Arg Ala Ser Lys Ser Ile Ser Lys Tyr Leu Ala
1 5 10

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Ser Gly Ser Thr Leu Gln Ser
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<400> 6

Gln Gln His Asn Glu Tyr Pro Trp Thr
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<210> 7

<211> 119

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<223> Synthetic: heavy chain variable region sequence

<400> 7

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

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Asn Pro Arg Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Gly
50 55 60

Lys Ala Thr Leu Thr Asp Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
65 70 75 80

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

Lys Gly Phe Ile Thr Thr Val Val Pro Ser Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ala
 115

<210> 8
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<400> 8

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

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
 20 25 30

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

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile 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 Met Tyr Tyr Cys Gln Gln His Asn Glu Tyr Pro Trp
 85 90 95

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

<210> 9
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<400> 9

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn
 1 5 10

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<400> 10

Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
1 5 10 15

Gly

<210> 11

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<400> 11

Arg Cys Tyr Tyr Gly Leu Tyr Phe Asp Val
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<210> 12

<211> 11

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<223> Synthetic: light chain variable region CDR1

<400> 12

Lys Ala Ser Gln Asp Ile Asn Arg Tyr Leu Ser
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<210> 13

<211> 7

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<400> 13

Arg Ala Asn Arg Leu Val Asp
1 5

<210> 14

<211> 9

<212> PRT

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<400> 14

Leu Gln Tyr Asp Glu Phe Pro Tyr Thr
1 5

<210> 15
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Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30

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

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Thr Arg Arg Cys Tyr Tyr Gly Leu Tyr Phe Asp Val Trp Gly Thr Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser
 115

<210> 16
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<220>
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Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Arg Tyr Ala Ser Leu Gly
 1 5 10 15

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

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

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

Gly Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Tyr Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro
85 90 95

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

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<400> 17

Gly Tyr Thr Phe Thr Ser Tyr Trp Met His
1 5 10

<210> 18
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<223> Synthetic: heavy chain variable region CDR2

<400> 18

Tyr Ile Asn Pro Ser Ser Gly Tyr Thr Lys Tyr Asn Gln Phe Lys Asp
1 5 10 15

<210> 19
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<213> Artificial Sequence

<220>
<223> Synthetic: heavy chain variable region CDR3

<400> 19

Gly Gly Tyr Tyr Gly Phe Ala Tyr
1 5

<210> 20
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: light chain variable region CDR1

<400> 20

Ser Ala Ser Ser Ser Val Ser Tyr Met Tyr

1

5

10

<210> 21

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Synthetic: light chain variable region CDR2

<400> 21

Leu Thr Ser Asn Leu Ala Ser

1

5

<210> 22

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: light chain variable region CDR3

<400> 22

Gln Gln Trp Ser Ser Asn Pro Leu Thr

1

5

<210> 23

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: heavy chain variable region sequence

<400> 23

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

1

5

10

15

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

20

25

30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

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

50

55

60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Ser Ser Leu Thr Tyr Glu Asp Ser Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Gly Gly Tyr Tyr Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu

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105

110

Val Thr Val Ser Ala
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<220>
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<400> 24

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Arg Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

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

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

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<400> 25

Gly Phe Ser Leu Thr Gly Tyr Gly Val His
1 5 10

<210> 26
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<220>
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<400> 26

Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile Ser
 1 5 10 15

<210> 27
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 <212> PRT
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<220>
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<400> 27

Asn Tyr Gly Tyr Asp Tyr Ala Met Asp Tyr
 1 5 10

<210> 28
 <211> 11
 <212> PRT
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<220>
 <223> Synthetic: light chain variable region CDR1

<400> 28

Arg Ala Ser Gln Ser Ile Gly Thr Ser Ile His
 1 5 10

<210> 29
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: light chain variable region CDR2

<400> 29

Tyr Ala Ser Glu Ser Ile Ser
 1 5

<210> 30
 <211> 9
 <212> PRT
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<220>
 <223> Synthetic: light chain variable region CDR3

<400> 30

Gln Gln Ser Asn Ser Trp Pro Phe Thr
 1 5

<210> 31
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: heavy chain variable region sequence

<400> 31

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

<210> 32

<211> 107

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic: light chain variable region sequence

<400> 32

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

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

<210> 33
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 <212> PRT
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<220>
 <223> Synthetic: heavy chain variable region CDR1 of the anti-ceramide antibody

<400> 33

Gly Tyr Thr Phe Thr Asn Tyr Trp Met His
 1 5 10

<210> 34
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: heavy chain variable region CDR2

<400> 34

Ala Ile Tyr Pro Gly Asp Ser Asp Thr Ser Tyr Asn Gln Lys Phe Lys
 1 5 10 15

Gly

<210> 35
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: heavy chain variable region CDR3

<400> 35

Gly Leu Tyr Tyr Gly Tyr Asp
 1 5

<210> 36
 <211> 16
 <212> PRT
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<220>
 <223> Synthetic: light chain variable region CDR1

<400> 36

Lys Ser Ser Gln Ser Leu Ile Asp Ser Asp Gly Lys Thr Phe Leu Asn
 1 5 10 15

<210> 37
 <211> 7
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: light chain variable region CDR2

<400> 37

Leu Val Ser Lys Leu Asp Ser
1 5

<210> 38

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: said light chain variable region CDR3

<400> 38

Trp Gln Gly Thr His Phe Pro Tyr Thr
1 5

<210> 39

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: heavy chain variable region sequence comprising the sequence

<400> 39

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

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

Lys Gly Lys Ala Lys Leu Thr Ala Val Thr Ser Thr Ser Thr Ala Phe
65 70 75 80

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

Thr Gly Leu Tyr Tyr Gly Tyr Asp Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser
115

<210> 40
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 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic: light chain variable region sequence

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

<210> 41
 <211> 109
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 <213> Homo sapiens

<220>
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 <223> human V gene 1-46

<400> 41
 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 Thr Ser Tyr
 20 25 30
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105

<210> 42
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: VL 2A2

<400> 42

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Ile Asp Ser
20 25 30

Asp Gly Lys Thr Phe Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

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

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

Arg

<210> 43
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human V gene A1

<400> 43

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
 20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45

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

Thr His Trp Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110

<210> 44
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic: Humanized 2A2 Heavy chain sequence

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 tgcaaggctt ctggctacac ctttaccaac tactggatgc actgggtaag acaggcgcct 180
 ggacaggggtc tggaatggat gggcgctatt taccctggag atagtgatac tagctacaac 240
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<210> 45
 <211> 463
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: Humanized 2A2 Heavy chain sequence

<400> 45

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

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asn Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Met Gly Ala Ile Tyr Pro Gly Asp Ser Asp Thr Ser Tyr Asn
 65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
 85 90 95

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Leu Tyr Tyr Gly Tyr Asp Trp Gly Gln Gly Thr
 115 120 125

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 130 135 140

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 145 150 155 160

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 165 170 175

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 180 185 190
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 195 200 205
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 210 215 220
 Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 225 230 235 240
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 245 250 255
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 260 265 270
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 275 280 285
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 290 295 300
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 305 310 315 320
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 325 330 335
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 340 345 350
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 355 360 365
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 370 375 380
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 385 390 395 400
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 405 410 415
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 420 425 430
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 435 440 445

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
450 455 460