

SEQUENCE LISTING

<110> MEDIMMUNE LIMITED

<120> ANTIBODIES TO ALPHA-SYNUCLEIN AND USES THEREOF

<130> 1848081-0002-091-WO1

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<150> 62/344,746

<151> 2016-06-02

<160> 61

<170> PatentIn version 3.5

<210> 1

<211> 140

<212> PRT

<213> Homo sapiens

<400> 1

Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val
1 5 10 15

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys
20 25 30

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
35 40 45

Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr
50 55 60

Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys
65 70 75 80

Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys
85 90 95

Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile
100 105 110

Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro
115 120 125

Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
130 135 140

<210> 2

<211> 122

<212> PRT

<213> Homo sapiens

<400> 2

Glu Val Gln Leu Leu 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 Ser Ser Tyr
20 25 30

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

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

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

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

<210> 3

<211> 115

<212> PRT

<213> Homo sapiens

<400> 3

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

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

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

Leu Leu Arg Tyr Lys Ser Asp Ala Asp Lys His Gln Gly Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile
65 70 75 80

Leu Phe Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
85 90 95

Met Val Trp His Ser Gly Ala Trp Val Phe Gly Gly Gly Thr Lys Leu
100 105 110

Thr Val Leu
115

<210> 4
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<213> Homo sapiens

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<222> (1)..(122)

<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 4

Glu Val Gln Leu Leu 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 Ser Ser Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Gly Gly Ala Asn His Val Lys Tyr Tyr Tyr Gly Met Asp Val Trp
100 105 110

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

<210> 5
<211> 5
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<213> Homo sapiens

<400> 5
Ser Tyr Ala Met Ser
1 5

<210> 6
<211> 17
<212> PRT
<213> Homo sapiens

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<223> /replace="Ala"

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<222> (4)..(4)
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<220>
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<220>
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<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 6
Ser Ile Ser His Leu Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 7
<211> 13
<212> PRT
<213> Homo sapiens

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<220>
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<220>
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<222> (1)..(13)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 7
Gly Ala Asn His Val Lys Tyr Tyr Tyr Gly Met Asp Val
1 5 10

<210> 8
<211> 114
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<222> (29)..(29)
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<222> (82)..(82)
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<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 8

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

Ser Ala Ser Leu Thr Cys Thr Leu Arg Ser Gly Ala Pro Leu Pro Lys
20 25 30

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

Leu Leu Arg Tyr Lys Ser Asp Ala Asp Lys His Gln Gly Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile
65 70 75 80

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

Val Trp Asp His Gly Val Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
100 105 110

Val Leu

<210> 9

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (7)..(7)

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<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
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<400> 9
Thr Leu Arg Ser Gly Ala Pro Leu Pro Lys Tyr Arg Ile Tyr
1 5 10

<210> 10
<211> 11
<212> PRT
<213> Homo sapiens

<400> 10
Tyr Lys Ser Asp Ala Asp Lys His Gln Gly Ser
1 5 10

<210> 11
<211> 9
<212> PRT
<213> Homo sapiens

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<220>
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<222> (9)..(9)

<223> /replace="Tyr"

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<221> MISC_FEATURE

<222> (1)..(9)

<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 11

Met Val Trp Asp His Gly Val Trp Val

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<210> 12

<211> 452

<212> PRT

<213> Homo sapiens

<400> 12

Glu Val Gln Leu Leu 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 Ser Ser Tyr

20 25 30

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

35 40 45

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

50 55 60

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

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro

115 120 125

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

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

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

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

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

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

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu
225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 13
<211> 366
<212> DNA
<213> Homo sapiens

<220>
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gag gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc agc tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc 144
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

tca tcc att tcc cac ctt ggt ggt agc aca tac tac gca gac tcc gtg 192

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

aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat tac tgt 288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg gga ggg gca aac cac ggg aag tac tac tac gga atg gac aag tgg 336
Ala Gly Gly Ala Asn His Gly Lys Tyr Tyr Tyr Gly Met Asp Lys Trp
100 105 110

ggc caa ggg acc acg gtc acc gtc tcc tca 366
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 14

<211> 122

<212> PRT

<213> Homo sapiens

<400> 14

Glu Val Gln Leu Leu 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 Ser Ser Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Gly Gly Ala Asn His Gly Lys Tyr Tyr Tyr Gly Met Asp Lys Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 15

<211> 17

<212> PRT

<213> Homo sapiens

<400> 15

Ser Ile Ser His Leu Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 16

<211> 13

<212> PRT

<213> Homo sapiens

<400> 16

Gly Ala Asn His Gly Lys Tyr Tyr Tyr Gly Met Asp Lys

1 5 10

<210> 17

<211> 221

<212> PRT

<213> Homo sapiens

<400> 17

Gln Ala Val Leu Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly Ala

1 5 10 15

Ser Ala Ser Leu Thr Cys Thr Leu Arg Ser Gly Ala Pro Leu Pro Lys

20 25 30

Tyr Arg Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr

35 40 45

Leu Leu Arg Tyr Lys Ser Asp Ala Asp Lys His Gln Gly Ser Gly Val

50 55 60

Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile

65 70 75 80

Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys

85 90 95

Met Val Trp Asp His Gly Val Trp Tyr Phe Gly Gly Gly Thr Lys Leu
100 105 110

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

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
145 150 155 160

Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215 220

<210> 18
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caggctgtgc tgactcagcc ggcttcctc tctgcgtctc ctggagcatc agccagtctc 60
acctgcacct tgcgcagtgg ggcgcccctg ccgaagtata ggatatactg gtatcagcag 120
aagccagggga gtcctcccca gtatctcctg aggtacaaat cagacgcaga taaacaccag 180
ggctctggag tccccagccg cttttctgga tccaaagatg cttcggccaa tgcagggatt 240
ttactcatct ctgggctcca gtctgaggat gaggctgact attattgtat ggtttgggac 300
cacggcgtct ggtatttcgg cggagggacc aagctgaccg tccta 345

<210> 19
<211> 115

<212> PRT

<213> Homo sapiens

<400> 19

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

Ser Ala Ser Leu Thr Cys Thr Leu Arg Ser Gly Ala Pro Leu Pro Lys
20 25 30

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

Leu Leu Arg Tyr Lys Ser Asp Ala Asp Lys His Gln Gly Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile
65 70 75 80

Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
85 90 95

Met Val Trp Asp His Gly Val Trp Tyr Phe Gly Gly Gly Thr Lys Leu
100 105 110

Thr Val Leu
115

<210> 20

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<212> PRT

<213> Homo sapiens

<400> 20

Thr Leu Arg Ser Gly Ala Pro Leu Pro Lys Tyr Arg Ile Tyr
1 5 10

<210> 21

<211> 9

<212> PRT

<213> Homo sapiens

<400> 21

Met Val Trp Asp His Gly Val Trp Tyr
1 5

<210> 22

<211> 452

<212> PRT

<213> Homo sapiens

<400> 22

Glu Val Gln Leu Leu 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 Ser Ser Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Gly Gly Ala Arg Arg Gly Arg Ile Tyr Tyr Gly Met Asp Lys Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

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

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

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

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

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

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

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu
225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 23
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<212> DNA
<213> Homo sapiens

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ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gggaggggca 300
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tcctca 366

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<213> Homo sapiens

<400> 24
Glu Val Gln Leu Leu 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 Ser Ser Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Gly Gly Ala Arg Arg Gly Arg Ile Tyr Tyr Gly Met Asp Lys Trp
 100 105 110

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

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<400> 25
Ser Tyr Ala Met Ser
1 5

<210> 26
<211> 17
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<400> 26
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 27
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<400> 27
Gly Ala Arg Arg Gly Arg Ile Tyr Tyr Gly Met Asp Lys
1 5 10

<210> 28
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<400> 28

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

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

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

Leu Leu Arg Tyr Lys Ser Asp Ala Asp Lys His Gln Gly Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile
65 70 75 80

Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
85 90 95

Met Val Trp Ser Ser Gly Ala Trp Tyr Phe Gly Gly Gly Thr Lys Leu
100 105 110

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

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
145 150 155 160

Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser

210 215 220

<210> 29

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<212> DNA

<213> Homo sapiens

<400> 29

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aagccaggga gtcctcccca gtatctctg aggtacaaat cagacgcaga taaacaccag 180

ggctctggag tcccagccg cttttctgga tccaaagatg cttcggccaa tgcagggatt 240

ttactcatct ctgggtcca gtctgaggat gaggtgact attattgtat ggtttgggcc 300

agcggcgctt ggtacttcgg cggagggacc aagctgaccg tccta 345

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<400> 30

Gln Ala Val Leu Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly Ala

1 5 10 15

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

20 25 30

Tyr Arg Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr

35 40 45

Leu Leu Arg Tyr Lys Ser Asp Ala Asp Lys His Gln Gly Ser Gly Val

50 55 60

Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile

65 70 75 80

Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys

85 90 95

Met Val Trp Ser Ser Gly Ala Trp Tyr Phe Gly Gly Gly Thr Lys Leu

100 105 110

Thr Val Leu
115

<210> 31
<211> 14
<212> PRT
<213> Homo sapiens

<400> 31
Thr Leu Arg Ser Ser Gly Asp Phe Ser Arg Tyr Arg Ile Tyr
1 5 10

<210> 32
<211> 11
<212> PRT
<213> Homo sapiens

<400> 32
Tyr Lys Ser Asp Ala Asp Lys His Gln Gly Ser
1 5 10

<210> 33
<211> 9
<212> PRT
<213> Homo sapiens

<400> 33
Met Val Trp Ser Ser Gly Ala Trp Tyr
1 5

<210> 34
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)..(1)
<223> /replace="Val"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="Leu"

<220>
<221> VARIANT
<222> (75)..(75)
<223> /replace="Arg"

<220>

<221> MISC_FEATURE

<222> (1)..(123)

<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 34

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

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

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

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

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

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

Ala Arg Arg Ser Ser Leu Ala Ala Ala Asp Arg Gly Ala Phe Asp Ile
100 105 110

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

<210> 35

<211> 108

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (15)..(15)

<223> /replace="Gly" or "Ala"

<220>

<221> VARIANT

<222> (28)..(28)

<223> /replace="Arg"

<220>

<221> VARIANT

<222> (29)..(29)

<223> /replace="Arg" or "Thr"

<220>

<221> VARIANT

<222> (32)..(32)

<223> /replace="Thr"

<220>

<221> VARIANT

<222> (33)..(33)

<223> /replace="Ser"

<220>

<221> VARIANT

<222> (37)..(37)

<223> /replace="Gln"

<220>

<221> VARIANT

<222> (44)..(44)

<223> /replace="Ile"

<220>

<221> VARIANT

<222> (47)..(47)

<223> /replace="Ile"

<220>

<221> VARIANT

<222> (50)..(50)

<223> /replace="Glu"

<220>

<221> VARIANT

<222> (51)..(51)

<223> /replace="Asp"

<220>

<221> VARIANT

<222> (57)..(57)

<223> /replace="Ile"

<220>

<221> VARIANT

<222> (65)..(65)

<223> /replace="Arg"

<220>

<221> VARIANT

<222> (68)..(68)

<223> /replace="Thr"

<220>

<221> VARIANT

<222> (92)..(92)

<223> /replace="Asn"

<220>

<221> VARIANT

<222> (93)..(93)

<223> /replace="Thr"

<220>

<221> VARIANT

<222> (95)..(95)

<223> /replace="Lys" or "His"

<220>

<221> VARIANT

<222> (96)..(96)

<223> /replace="Pro"

<220>

<221> VARIANT

<222> (97)..(97)

<223> /replace="Trp"

<220>

<221> MISC_FEATURE

<222> (1)..(108)

<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 35

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

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

Asn Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Val Leu Val Met Tyr
35 40 45

Gly Lys Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 36
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (6)..(6)
<223> /replace="Arg"

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace="Arg" or "Thr"

<220>
<221> VARIANT
<222> (10)..(10)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="Ser"

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 36
Gln Gly Asp Ser Leu Thr Ser Tyr Tyr Ala Asn
1 5 10

<210> 37
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (2)..(2)

<223> /replace="Glu"

<220>

<221> VARIANT

<222> (3)..(3)

<223> /replace="Asp"

<220>

<221> MISC_FEATURE

<222> (1)..(7)

<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 37

Gly Lys Asn Asn Arg Pro Ser

1 5

<210> 38

<211> 11

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (5)..(5)

<223> /replace="Asn"

<220>

<221> VARIANT

<222> (6)..(6)

<223> /replace="Thr"

<220>

<221> VARIANT

<222> (8)..(8)

<223> /replace="Lys" or "His"

<220>

<221> VARIANT

<222> (9)..(9)

<223> /replace="Pro"

<220>

<221> VARIANT

<222> (10)..(10)

<223> /replace="Trp"

<220>

<221> MISC_FEATURE

<222> (1)..(11)

<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations"

for variant positions"

<400> 38

Asn Ser Arg Asp Ser Ser Gly Asn His Val Val

1 5 10

<210> 39

<211> 123

<212> PRT

<213> Homo sapiens

<400> 39

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

1 5 10 15

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

20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

Gly Arg Ile Ile Pro Ile Leu Gly Thr Ser Asn Tyr Ala Gln Lys Phe

50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr

65 70 75 80

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

85 90 95

Ala Arg Arg Ser Ser Leu Ala Ala Ala Asp Arg Gly Ala Phe Asp Ile

100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

115 120

<210> 40

<211> 5

<212> PRT

<213> Homo sapiens

<400> 40

Ser Tyr Ala Ile Ser

1 5

<210> 41
<211> 17
<212> PRT
<213> Homo sapiens

<400> 41
Arg Ile Ile Pro Ile Leu Gly Thr Ser Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 42
<211> 14
<212> PRT
<213> Homo sapiens

<400> 42
Arg Ser Ser Leu Ala Ala Ala Asp Arg Gly Ala Phe Asp Ile
1 5 10

<210> 43
<211> 108
<212> PRT
<213> Homo sapiens

<400> 43
Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1 5 10 15

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

105

<210> 44

<211> 11

<212> PRT

<213> Homo sapiens

<400> 44

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser

1 5 10

<210> 45

<211> 7

<212> PRT

<213> Homo sapiens

<400> 45

Gly Lys Asn Asn Arg Pro Ser

1 5

<210> 46

<211> 11

<212> PRT

<213> Homo sapiens

<400> 46

Asn Ser Arg Asp Ser Ser Gly Asn His Val Val

1 5 10

<210> 47

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> source

<223> /note="Bbbt0626 VH"

<400> 47

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

1 5 10 15

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

20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

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

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

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

Ala Arg Arg Ser Ser Leu Ala Ala Ala Asp Arg Gly Ala Phe Asp Ile
100 105 110

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

<210> 48

<211> 122

<212> PRT

<213> Homo sapiens

<400> 48

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

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

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

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

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

Gly Arg Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 49

<211> 5

<212> PRT

<213> Homo sapiens

<400> 49

Thr Tyr Ser Ile Thr

1 5

<210> 50

<211> 17

<212> PRT

<213> Homo sapiens

<400> 50

Asp Ile Val Pro Ile Phe Gly Thr Pro Asn Tyr Ala Gln Asn Phe Gln

1 5 10 15

Gly

<210> 51

<211> 13

<212> PRT

<213> Homo sapiens

<400> 51

Arg Gly Ser Tyr Tyr Gly Arg Gly Gly Trp Phe Asp Pro

1 5 10

<210> 52

<211> 122

<212> PRT

<213> Homo sapiens

<400> 52

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

1 5 10 15

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

20 25 30

Ser Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

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

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

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 53
<211> 5
<212> PRT
<213> Homo sapiens

<400> 53
Thr Tyr Ser Ile Thr
1 5

<210> 54
<211> 17
<212> PRT
<213> Homo sapiens

<400> 54
Asp Ile Val Pro Ile Phe Gly Thr Pro Asn Tyr Ala Gln Asn Phe Gln
1 5 10 15

Gly

<210> 55
<211> 13
<212> PRT
<213> Homo sapiens

<400> 55
Arg Gly Ser Tyr Tyr Gly Arg Gly Gly Trp Phe Asp Pro
1 5 10

<210> 56

<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> MISC_FEATURE
<222> (1)..(50)
<223> /note="This sequence may encompass 1-10 'Gly Gly Gly Gly Ser'
repeating units"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 56
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser
50

<210> 57
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 57
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 58
<211> 98

<212> PRT

<213> Homo sapiens

<400> 58

Glu Val Gln Leu Leu 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 Ser Ser Tyr
 20 25 30

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

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

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

<210> 59

<211> 11

<212> PRT

<213> Homo sapiens

<400> 59

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 60

<211> 102

<212> PRT

<213> Homo sapiens

<400> 60

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

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

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

Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile
65 70 75 80

Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
85 90 95

Met Ile Trp His Trp Val
100

<210> 61

<211> 10

<212> PRT

<213> Homo sapiens

<400> 61

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
1 5 10