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<110> UCB Biopharma sprl

<120> Antibodies

<130> PF0129-WO

<150> GB1720970.1

<151> 2017-12-15

<160> 47

<170> PatentIn version 3.5

<210> 1

<211> 11

<212> PRT

<213> Rattus norvegicus

<400> 1

Lys Ala Ser Gln Asn Ile Asn Lys Asn Leu Asp

1 5 10

<210> 2

<211> 7

<212> PRT

<213> Rattus norvegicus

<400> 2

Tyr Ala Asn Asn Leu Gln Thr
1 5

<210> 3

<211> 8

<212> PRT

<213> Rattus norvegicus

<400> 3

Tyr Gln Tyr Lys Asn Gly Trp Thr
1 5

<210> 4

<211> 10

<212> PRT

<213> Rattus norvegicus

<400> 4

Gly Phe Thr Phe Asn Asn Ala Ala Met Tyr
1 5 10

<210> 5

<211> 19

<212> PRT

<213> Rattus norvegicus

<400> 5

Arg Ile Arg Thr Lys Pro Asn Asn Tyr Ala Thr Ser Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 6
<211> 7
<212> PRT
<213> Rattus norvegicus

<400> 6

Asp Tyr Ser Arg Gly Asp Arg
1 5

<210> 7
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 7

Tyr Gln Tyr Lys Asn Ala Trp Thr
1 5

<210> 8
<211> 140
<212> PRT
<213> Homo sapiens

<400> 8

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> 9

<211> 106

<212> PRT

<213> Rattus norvegicus

<400> 9

Asn Ile Gln Met Thr Gln Ser Pro Pro Val Leu Ser Ala Ser Val Gly

1 5 10 15

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

20 25 30

Leu Asp Trp Tyr Gln Gln Lys His Gly Glu Ala Pro Lys Leu Leu Met

35 40 45

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

50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Tyr Gln Tyr Lys Asn Gly Trp Thr

85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys

100 105

<210> 10

<211> 118

<212> PRT

<213> Rattus norvegicus

<400> 10

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

1 5 10 15

Ser Leu Lys Ile Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asn Ala

20 25 30

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

35 40 45

Ala Arg Ile Arg Thr Lys Pro Asn Asn Tyr Ala Thr Ser Tyr Ala Asp

50 55 60

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

65 70 75 80

Val Tyr Leu Gln Met Asp Asn Leu Lys Ser Glu Asp Thr Ala Met Tyr

85 90 95

Tyr Cys Thr Ala Asp Tyr Ser Arg Gly Asp Arg Trp Gly Gln Gly Val

100 105 110

Met Val Thr Val Ser Ser

115

<210> 11

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> Rat VL nucleotide

<400> 11

aacatccaga tgacccagtc tcctccagtc ctgtctgcat ctgtgggaga cagagtcact 60

ctcagctgca aagcaagtca gaacattaat aagaacttag actggtatca gcaaaagcat 120

ggagaagctc caaaactcct gatgtattat gcaaacaatt tacaaacggg catcccatca 180

aggttcagtg gcagtggatc tggaacagat tacacgctca ccatcagcag cctgcagcct 240

gaagatgttg ccacatatta ctgctatcag tataagaatg ggtggacgtt cggtggaggc 300

accaagctgg aactgaaa 318

<210> 12

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Rat VH nucleotide

<400> 12

gaaatgcagc tggtggagtc tggtggagga ttggtgcagc ctaaggagtc attgaaaatc 60

tcatgtgcag cctctggatt caccttcaat aatgctgcca tgtactgggt ccgccaggct 120

ccaggaaagg gtctggaatg ggttgctcgc ataagaacta aacctaataa ttatgcaaca 180

tcttatgctg attcagtgaa aggcagattc accatctcca gagatgattc aaaaagcatg 240

gtctacctac aaatggataa cttgaaaagt gaggacacag ccatgtatta ctgtacagca 300

gattactcca gaggtgacag gtggggccaa ggagtcatgg tcacagtctc gagc 354

<210> 13

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> 5811 gL5 V-region

<400> 13

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 Lys Ala Ser Gln Asn Ile Asn Lys Asn
20 25 30

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

35 40 45

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Tyr Gln Tyr Lys Asn Gly Trp Thr
85 90 95

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

<210> 14

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> 5811 gL5 Light chain

<400> 14

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 Lys Ala Ser Gln Asn Ile Asn Lys Asn

20 25 30

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

35 40 45

Tyr Tyr Ala Asn Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Tyr Gln Tyr Lys Asn Gly Trp Thr

85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro

100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr

115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys

130 135 140

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

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

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 15
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> 5811 gL5 V-region nucleotide

<400> 15

gacatccaga tgacccagag cccgagctcc ctgtccgcat cagtggggga tcgcgtgact 60

attacgtgca aagcctcgca gaacatcaac aagaacctcg actggtatca gcagaagcca 120

ggaaaggcgc ctaagctgct gatctactac gccaacaatc tccagaccgg cgtgccctcg 180

cggttctccg gatctgggtc cggtactgat tacaccctga ccattagctc ccttcaaccg 240

gaggacttcg ccacctatta ctgctaccag tacaagaacg gctggacttt tggacaaggc 300

accaaggtcg aaatcaag 318

<210> 16

<211> 639

<212> DNA

<213> Artificial Sequence

<220>

<223> 5811 gL5 Light chain nucleotide

<400> 16

gacatccaga tgacccagag cccgagctcc ctgtccgcat cagtggggga tcgcgtgact 60

attacgtgca aagcctcgca gaacatcaac aagaacctcg actggtatca gcagaagcca 120

ggaaaggcgc ctaagctgct gatctactac gccaacaatc tccagaccgg cgtgccctcg 180

cggttctccg gatctgggtc cggtactgat tacaccctga ccattagctc ccttcaaccg 240

gaggacttcg ccacctatta ctgctaccag tacaagaacg gctggacttt tggacaaggc 300

accaaggtcg aaatcaagcg tacggtggcc gctccctccg tgttcatctt cccaccctcc 360

gacgagcagc tgaagtccgg caccgcctcc gtcgtgtgcc tgctgaacaa cttctacccc 420

cgcgaggcca aggtgcagtg gaaggtggac aacgccctgc agtccggcaa ctcccaggaa 480

tccgtcaccg agcaggactc caaggacagc acctactccc tgtcctccac cctgaccctg 540

tccaaggccg actacgagaa gcacaaggtg tacgcctgcg aagtgaccca ccagggcctg 600

tccagccccg tgaccaagtc cttcaaccgg ggcgagtgc 639

<210> 17

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> 5811 gL8 V-region

<400> 17

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 Lys Ala Ser Gln Asn Ile Asn Lys Asn

20 25 30

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

35 40 45

Tyr Tyr Ala Asn Asn Leu Gln Thr 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 Tyr Gln Tyr Lys Asn Gly Trp Thr

85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 18

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> 5811 gL8 Light chain

<400> 18

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 Lys Ala Ser Gln Asn Ile Asn Lys Asn

20 25 30

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

35 40 45

Tyr Tyr Ala Asn Asn Leu Gln Thr 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 Tyr Gln Tyr Lys Asn Gly Trp Thr

85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro

100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr

115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys

130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu

145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser

165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala

180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe

195 200 205

Asn Arg Gly Glu Cys

210

<210> 19

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> 5811 V-region nucleotide

<400> 19

gacatccaga tgacccagag cccgagctcc ctgtccgcat cagtggggga tcgcgtgact 60

attacgtgca aagcctcgca gaacatcaac aagaacctcg actggtatca gcagaagcca 120

ggaaaggcgc ctaagctgct gatctactac gccaacaatc tccagaccgg cgtgccctcg 180

cggttctccg gatctgggtc cggtactgat ttcaccctga ccattagctc ccttcaaccg 240

gaggacttcg ccacctatta ctgctaccag tacaagaacg gctggacttt tggacaaggc 300

accaaggtcg aaatcaag 318

<210> 20

<211> 639

<212> DNA

<213> Artificial Sequence

<220>

<223> 5811 gL8 Light chain nucleotide

<400> 20

gacatccaga tgacccagag cccgagctcc ctgtccgcat cagtggggga tcgcgtgact 60

attacgtgca aagcctcgca gaacatcaac aagaacctcg actggtatca gcagaagcca 120

ggaaaggcgc ctaagctgct gatctactac gccaacaatc tccagaccgg cgtgccctcg 180

cggttctccg gatctgggtc cggtactgat ttcaccctga ccattagctc ccttcaaccg 240

gaggacttcg ccacctatta ctgctaccag tacaagaacg gctggacttt tggacaaggc 300

accaaggtcg aaatcaagcg tacggtggcc gctccctccg tgttcatctt cccaccctcc 360

gacgagcagc tgaagtccgg caccgcctcc gtcgtgtgcc tgctgaacaa cttctacccc 420

cgcgaggcca aggtgcagtg gaaggtggac aacgccctgc agtccggcaa ctcccaggaa 480

tccgtcaccg agcaggactc caaggacagc acctactccc tgtcctccac cctgaccctg 540

tccaaggccg actacgagaa gcacaaggtg tacgcctgcg aagtgaccca ccagggcctg 600

tccagccccg tgaccaagtc cttcaaccgg ggcgagtgc 639

<210> 21

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> 5811 gL14 V-region

<400> 21

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 Lys Ala Ser Gln Asn Ile Asn Lys Asn

20 25 30

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

35 40 45

Tyr Tyr Ala Asn Asn Leu Gln Thr 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 Tyr Gln Tyr Lys Asn Ala Trp Thr

85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 22

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> 5811 gL14 Light chain

<400> 22

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 Lys Ala Ser Gln Asn Ile Asn Lys Asn
20 25 30

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

Tyr Tyr Ala Asn Asn Leu Gln Thr 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 Tyr Gln Tyr Lys Asn Ala Trp Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr

115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys

130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu

145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser

165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala

180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe

195 200 205

Asn Arg Gly Glu Cys

210

<210> 23

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> 5811 gL14 V-region nucleotide

<400> 23

gacatccaga tgacccagag cccgagctcc ctgtccgcat cagtggggga tcgcgtgact 60

attacgtgca aagcctcgca gaacatcaac aagaacctcg actggtatca gcagaagcca 120

ggaaaggcgc ctaagctgct gatctactac gccaacaatc tccagaccgg cgtgccctcg 180

cggttctccg gatctgggtc cggtactgat ttcaccctga ccattagctc ccttcaaccg 240

gaggacttcg ccacctatta ctgctaccag tacaagaacg cttggacttt tggacaaggc 300

accaaggtcg aaatcaag 318

<210> 24

<211> 639

<212> DNA

<213> Artificial Sequence

<220>

<223> 5811 gL14 Light chain nucleotide

<400> 24

gacatccaga tgacccagag cccgagctcc ctgtccgcat cagtggggga tcgcgtgact 60

attacgtgca aagcctcgca gaacatcaac aagaacctcg actggtatca gcagaagcca 120

ggaaaggcgc ctaagctgct gatctactac gccaacaatc tccagaccgg cgtgccctcg 180

cggttctccg gatctgggtc cggtactgat ttcaccctga ccattagctc ccttcaaccg 240

gaggacttcg ccacctatta ctgctaccag tacaagaacg cttggacttt tggacaaggc 300

accaaggtcg aaatcaagcg tacggtggcc gctccctccg tgttcatctt cccaccctcc 360

gacgagcagc tgaagtccgg caccgcctcc gtcgtgtgcc tgctgaacaa cttctacccc 420

cgcgaggcca aggtgcagtg gaaggtggac aacgccctgc agtccggcaa ctcccaggaa 480

tccgtcaccg agcaggactc caaggacagc acctactccc tgtcctccac cctgaccctg 540

tccaaggccg actacgagaa gcacaaggtg tacgcctgcg aagtgaccca ccagggcctg 600

tccagccccg tgaccaagtc cttcaaccgg ggcgagtgc 639

<210> 25

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> 5811 gH4 V-region

<400> 25

Glu 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 Asn Asn Ala

20 25 30

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

35 40 45

Ala Arg Ile Arg Thr Lys Pro Asn Asn Tyr Ala Thr Ser Tyr Ala Asp

50 55 60

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

65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Thr Ala Asp Tyr Ser Arg Gly Asp Arg Trp Gly Gln Gly Thr

100 105 110

Met Val Thr Val Ser Ser

115

<210> 26

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> 5811 gH4 Heavy chain

<400> 26

Glu 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 Asn Asn Ala
20 25 30

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

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

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

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Thr Ala Asp Tyr Ser Arg Gly Asp Arg Trp Gly Gln Gly Thr

100 105 110

Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro

115 120 125

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

130 135 140

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

145 150 155 160

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

165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

180 185 190

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

195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys

210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu

225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln

260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu

290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys

325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

355 360 365

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

370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln

405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys

435 440 445

<210> 27

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> 5811 gH4 V-region nucleotide

<400> 27

gaagtgcagc ttgtggagag cggaggtgga ctcgtgaagc ctggcggatc tctgcgcctg 60

tcctgcgccg cctcggggtt cacctttaac aatgccgcaa tgtattgggt cagacaggcc 120

ccgggaaagg gtttggaatg ggtggctagg attcggacta agcccaacaa ctacgcgacc 180

tcctacgccg atagcgtgaa gggcagattc accatctccc gggacgactc aaagaacacg 240

ctgtacctcc aaatgaactc cctgaaaacc gaggacaccg ccgtgtacta ctgcaccgcg 300

gactactccc ggggcgatcg ctggggacag gggactatgg tcactgtctc gagt 354

<210> 28

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> 5811 gH4 Heavy chain nucleotide

<400> 28

gaagtgcagc ttgtggagag cggaggtgga ctcgtgaagc ctggcggatc tctgcgcctg 60

tcctgcgccg cctcggggtt cacctttaac aatgccgcaa tgtattgggt cagacaggcc 120

ccgggaaagg gtttggaatg ggtggctagg attcggacta agcccaacaa ctacgcgacc 180

tcctacgccg atagcgtgaa gggcagattc accatctccc gggacgactc aaagaacacg 240

ctgtacctcc aaatgaactc cctgaaaacc gaggacaccg ccgtgtacta ctgcaccgcg 300

gactactccc ggggcgatcg ctggggacag gggactatgg tcactgtctc gagtgcctcc 360

accaagggcc cctccgtgtt ccctctggcc ccttgctccc ggtccacctc cgagtctacc 420

gccgctctgg gctgcctggt caaggactac ttccccgagc ccgtgacagt gtcctggaac 480

tctggcgccc tgacctccgg cgtgcacacc ttccctgccg tgctgcagtc ctccggcctg 540

tactccctgt cctccgtcgt gaccgtgccc tcctccagcc tgggcaccaa gacctacacc 600

tgtaacgtgg accacaagcc ctccaacacc aaggtggaca agcgggtgga atctaagtac 660

ggccctccct gccccccctg ccctgcccct gaatttctgg gcggaccttc cgtgttcctg 720

ttcccccaa agcccaagga caccctgatg atctcccgga cccccgaagt gacctgcgtg 780

gtggtggacg tgtcccagga agatcccgag gtccagttca attggtacgt ggacggcgtg 840

gaagtgcaca atgccaagac caagcccaga gaggaacagt tcaactccac ctaccgggtg 900

gtgtccgtgc tgaccgtgct gcaccaggac tggctgaacg gcaaagagta caagtgcaag 960

gtgtccaaca agggcctgcc ctccagcatc gaaaagacca tctccaaggc caagggccag 1020

ccccgcgagc cccaggtgta caccctgccc cctagccagg aagagatgac caagaaccag 1080

gtgtccctga cctgtctggt caagggcttc taccctccg acattgccgt ggaatgggag 1140

tccaacggcc agcccgagaa caactacaag accacccccc ctgtgctgga cagcgacggc 1200

tccttcttcc tgtactctcg gctgaccgtg gacaagtccc ggtggcagga aggcaacgtc 1260

ttctcctgct ccgtgatgca cgaggccctg cacaaccact acacccagaa gtccctgtcc 1320

ctgagcctgg gcaag 1335

<210> 29

<211> 107

<212> PRT

<213> Homo sapiens

<400> 29

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 Trp
85 90 95

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

<210> 30
<211> 116
<212> PRT
<213> Homo sapiens

<400> 30

Glu 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 Asn Ala

20 25 30

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

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
50 55 60

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

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

Tyr Cys Thr Thr Asp Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 31

<211> 321

<212> DNA

<213> Homo sapiens

<400> 31

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta ccccttggac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 32

<211> 348

<212> DNA

<213> Homo sapiens

<400> 32

gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggGtc ccttagactc 60

tcctgtgcag cctctggatt cactttcagt aacgcctgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaaaagca aaactgatgg tgggacaaca 180

gactacgctg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300

gatgcttttg atgtctgggg ccaagggaca atggtcaccg tctcttca 348

<210> 33

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> Rabbit Fc human 68-140 a-syn

<400> 33

Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys Thr Val Glu
1 5 10 15

Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys Lys Asp Gln
20 25 30

Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile Leu Glu Asp
35 40 45

Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro Ser Glu Glu
50 55 60

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

Ser Thr Cys Ser Lys Pro Thr Cys Pro Pro Pro Glu Leu Leu Gly Gly

85 90 95

Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile

100 105 110

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Asp

115 120 125

Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg

130 135 140

Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg

145 150 155 160

Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys

165 170 175

Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu

180 185 190

Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr

195 200 205

Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu
210 215 220

Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp
225 230 235 240

Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Ala Val
245 250 255

Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro
260 265 270

Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met His
275 280 285

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

Gly Lys
305

<210> 34

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> 5811 rat-mouse chimeric light chain

<400> 34

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

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

Leu Asp Trp Tyr Gln Gln Lys His Gly Glu Ala Pro Lys Leu Leu Met
35 40 45

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

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

Glu Asp Val Ala Thr Tyr Tyr Cys Tyr Gln Tyr Lys Asn Gly Trp Thr

85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg Thr Asp Ala Ala Pro
100 105 110

Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly
115 120 125

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
130 135 140

Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn
145 150 155 160

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
165 170 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
180 185 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
195 200 205

Asn Arg Asn Glu Cys

210

<210> 35

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<223> 5811 rat-mouse chimeric heavy chain

<400> 35

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

1 5 10 15

Ser Leu Lys Ile Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asn Ala

20 25 30

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

35 40 45

Ala Arg Ile Arg Thr Lys Pro Asn Asn Tyr Ala Thr Ser Tyr Ala Asp

50 55 60

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

65 70 75 80

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

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

Met Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro
115 120 125

Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly
130 135 140

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

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

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

Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser

195 200 205

Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro

210 215 220

Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro

225 230 235 240

Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys

245 250 255

Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp

260 265 270

Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu

275 280 285

Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met

290 295 300

His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser

305 310 315 320

Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly

325 330 335

Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln

340 345 350

Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe

355 360 365

Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu

370 375 380

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

385 390 395 400

Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn

405 410 415

Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr

420 425 430

Glu Lys Ser Leu Ser His Ser Pro Gly Lys

435 440

<210> 36

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> 5811 rat-mouse chimeric Fab-His heavy chain

<400> 36

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

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

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

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

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

Val Tyr Leu Gln Met Asp Asn Leu Lys Ser Glu Asp Thr Ala Met Tyr

85 90 95

Tyr Cys Thr Ala Asp Tyr Ser Arg Gly Asp Arg Trp Gly Gln Gly Val

100 105 110

Met Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro

115 120 125

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

130 135 140

Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn

145 150 155 160

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

165 170 175

Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr

180 185 190

Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser

195 200 205

Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys His His His His

210 215 220

His His His His His His

225 230

<210> 37

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> fragment of C-terminus of alpha synuclein

<400> 37

Glu Glu Gly Ala Pro Gln Glu Gly Ile Leu

1 5 10

<210> 38

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> fragment of C-terminus of alpha synuclein

<400> 38

Gln Glu Gly Ile Leu Glu Asp Met Pro Val
1 5 10

<210> 39
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> fragment of C-terminus of alpha synuclein

<400> 39

Gly Ile Leu Glu Asp Met Pro Val Asp Pro
1 5 10

<210> 40
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> fragment of C-terminus of alpha synuclein

<400> 40

Leu Glu Asp Met Pro Val Asp Pro Asp Asn

1 5 10

<210> 41

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> fragment of C-terminus of alpha synuclein

<400> 41

Asp Met Pro Val Asp Pro Asp Asn Glu Ala

1 5 10

<210> 42

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> fragment of C-terminus of alpha synuclein

<400> 42

Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu

1 5 10

<210> 43

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> fragment of C-terminus of alpha synuclein

<400> 43

Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro

1 5 10

<210> 44

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> fragment of C-terminus of alpha synuclein

<400> 44

Asp Asn Glu Ala Tyr Glu Met Pro Ser Glu

1 5 10

<210> 45

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> fragment of C-terminus of alpha synuclein

<400> 45

Glu Ala Tyr Glu Met Pro Ser Glu Glu Gly
1 5 10

<210> 46

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> fragment of C-terminus of alpha synuclein

<400> 46

Tyr Glu Met Pro Ser Glu Glu Gly Tyr Gln
1 5 10

<210> 47

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> fragment of C-terminus of alpha synuclein

<400> 47

Met Pro Ser Glu Glu Gly Tyr Gln Asp Tyr
1 5 10