

SEQUENCE LISTING

<110> Eli Lilly and Company

<120> CD200R AGONIST ANTIBODIES AND USES THEREOF

<130> X21772

<150> US 62/731204

<151> 2018-09-14

<160> 17

<170> PatentIn version 3.5

<210> 1

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 1

Lys Ala Ser Gly Phe Ser Phe Ser Ser Gly Tyr Tyr Met Ala
1 5 10

<210> 2

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 2

Leu Ile Gly Val Gly Ser Gly Ser Leu Trp Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 3

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 3

Ala Arg His Phe Ala Leu Ser Asp Pro Phe Asn Leu
1 5 10

<210> 4

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 4

Gln Ala Ser Glu Ser Ile Asp Ser Tyr Leu Leu
1 5 10

<210> 5

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 5

Lys Gln Ala Ser Thr Leu Ala Ser
1 5

<210> 6

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 6

Gln Asn Tyr Tyr Asp Ile Ser Ser Asn Asp
1 5 10

<210> 7

<211> 120

<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa at position 1 is either glutamine or pyroglutamic acid

<400> 7

Xaa 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 Phe Ser Phe Ser Ser Gly
20 25 30

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

Met Gly Leu Ile Gly Val Gly Ser Gly Ser Leu Trp Tyr Ala Gln Lys
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 8
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 8

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

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

<210> 9
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa at position 1 is either glutamine or pyroglutamic acid

<220>
 <221> MISC_FEATURE
 <222> (446)..(446)
 <223> Xaa at position 446 is either glycine or absent

<400> 9

Xaa 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 Phe Ser Phe Ser Ser Gly	20	25	30	

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

Met Gly Leu Ile Gly Val Gly Ser Gly Ser Leu Trp Tyr Ala Gln Lys
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 10

<211> 215

<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequences

<400> 10

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

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

Leu Leu Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

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

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

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Asn Tyr Tyr Asp Ile Ser Ser
85 90 95

Asn Asp Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 11
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa at position 1 is either glutamine or pyroglutamic acid

<220>
<221> MISC_FEATURE
<222> (450)..(450)
<223> Xaa at position 450 is either lysine or absent

<400> 11

Xaa 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 Phe Ser Phe Ser Ser Gly
20 25 30

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

Met Gly Leu Ile Gly Val Gly Ser Gly Ser Leu Trp Tyr Ala Gln Lys
50 55 60

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

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

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

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

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

305		310		315		320
Glu Tyr Lys Cys	Lys Val Ser Asn Lys	Ala Leu Pro Ala	Pro Ile Glu			
	325	330	335			
Lys Thr Ile Ser	Lys Ala Lys Gly	Gln Pro Arg Glu	Pro Gln Val Tyr			
	340	345	350			
Thr Leu Pro Pro	Ser Arg Asp Glu	Leu Thr Lys Asn	Gln Val Ser Leu			
	355	360	365			
Thr Cys Leu Val	Lys Gly Phe Tyr	Pro Ser Asp Ile	Ala Val Glu Trp			
	370	375	380			
Glu Ser Asn Gly	Gln Pro Glu Asn	Asn Tyr Lys Thr	Thr Pro Pro Val			
385	390	395	400			
Leu Asp Ser Asp	Gly Ser Phe Phe	Leu Tyr Ser Lys	Leu Thr Val Asp			
	405	410	415			
Lys Ser Arg Trp	Gln Gln Gly Asn	Val Phe Ser Cys	Ser Val Met His			
	420	425	430			
Glu Ala Leu His	Asn His Tyr Thr	Gln Lys Ser Leu	Ser Leu Ser Pro			
	435	440	445			
Gly Xaa						
	450					

<210> 12
 <211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 12	
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt	60
tcctgcaagg catctggatt ctccttcagt agcggctact acatggcatg ggtgcggcag	120
gcccctggac aagggttgga gtggatggga ctgattggtg ttggtagtgg tagcctatgg	180

tacgcgcaga agttccaagg ccgggtcacc atgaccaggg acacgtccac gagcacagtc	240
tacatggagc tgagcagcct gagatctgag gacacggccg tgtattactg tgcgagacat	300
tttgctctgt ctgatccctt taacttgtgg ggccagggca cactcgtcac cgtctcctca	360
gctagcacca agggcccatc ggtcttcccc ctggcaccct gctccaggag cacctccgag	420
agcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg	480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg cacgaagacc	600
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc	660
aaatatggtc ccccatgccc accctgcccga gcacctgagt tcctggggggg accatcagtc	720
ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg	780
tgcgtgggtg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat	840
ggcgtggagg tgcataatgc caagacaaaag ccgcgggagg agcagttcaa cagcacgtac	900
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag	960
tgcaagggtct ccaacaaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa	1020
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag	1080
aaccagggtca gcctgacctg cctgggtcaaa ggcttctacc ccagcgacat cgccgtggag	1140
tgggaaagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	1200
gacggctcct tcttcctcta cagcaggcta accgtggaca agagcaggtg gcaggagggg	1260
aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc	1320
ctctccctgt ctctgggt	1338

<210> 13
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 13	
gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc	60
atcacctgcc aggccagtga gtcgattgat agctattttac tgtggtacca gcagaaacca	120

gatcagtctc caaagctcct catcaagcag gcatccactc tggcatctgg ggtcccctcg	180
aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct	240
gaagatgctg caacgtatta ctgtcaaaac tattatgata ttagtagtaa tgatttcggc	300
ggagggacca aggtggagat caaacggacc gtggctgcac catctgtctt catcttcccg	360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc	420
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg	540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag	600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgc	645

<210> 14
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 14	
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt	60
tcctgcaagg catctggatt ctccttcagt agcggctact acatggcatg ggtgcggcag	120
gcccctggac aagggttga gtggatggga ctgattgggtg ttggtagtgg tagcctatgg	180
tacgcgcaga agttccaagg ccgggtcacc atgaccaggg acacgtccac gagcacagtc	240
tacatggagc tgagcagcct gagatctgag gacacggccg tgtattactg tgcgagacat	300
tttgctctgt ctgatccctt taacttgtgg ggccagggca cactcgtcac cgtctcctca	360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg	480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttgtg acaaaaactca cacatgcca ccgtgcccag cacctgaact cctgggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt	780

gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900
 agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 1080
 ctgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200
 ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320
 cagaagagcc tctccctgtc tccgggtaag 1350

<210> 15
 <211> 348
 <212> PRT
 <213> Homo sapiens

<400> 15

Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
 1 5 10 15

Thr Ile Phe Leu Val Ala Glu Ala Glu Gly Ala Ala Gln Pro Asn Asn
 20 25 30

Ser Leu Met Leu Gln Thr Ser Lys Glu Asn His Ala Leu Ala Ser Ser
 35 40 45

Ser Leu Cys Met Asp Glu Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val
 50 55 60

Leu Ala Glu Val Asn Thr Ser Trp Pro Val Lys Met Ala Thr Asn Ala
 65 70 75 80

Val Leu Cys Cys Pro Pro Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr
 85 90 95

Trp Glu Ile Ile Leu Arg Gly Gln Pro Ser Cys Thr Lys Ala Tyr Arg
 100 105 110

Lys Glu Thr Asn Glu Thr Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile
115 120 125

Thr Trp Val Ser Arg Pro Asp Gln Asn Ser Asp Leu Gln Ile Arg Pro
130 135 140

Val Ala Ile Thr His Asp Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro
145 150 155 160

Asp Gly Asn Phe His Arg Gly Tyr His Leu Gln Val Leu Val Thr Pro
165 170 175

Glu Leu Thr Leu Phe Gln Asn Arg Asn Arg Thr Ala Val Cys Lys Ala
180 185 190

Val Ala Gly Lys Pro Ala Ala Gln Ile Ser Trp Ile Pro Glu Gly Asp
195 200 205

Cys Ala Thr Lys Gln Glu Tyr Trp Ser Asn Gly Thr Val Thr Val Lys
210 215 220

Ser Thr Cys His Trp Glu Val His Asn Val Ser Thr Val Thr Cys His
225 230 235 240

Val Ser His Leu Thr Gly Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro
245 250 255

Val Pro Gly Ala Lys Lys Ser Ala Lys Leu Tyr Ile Pro Tyr Ile Ile
260 265 270

Leu Thr Ile Ile Ile Leu Thr Ile Val Gly Phe Ile Trp Leu Leu Lys
275 280 285

Val Asn Gly Cys Arg Lys Tyr Lys Leu Asn Lys Thr Glu Ser Thr Pro
290 295 300

Val Val Glu Glu Asp Glu Met Gln Pro Tyr Ala Ser Tyr Thr Glu Lys
305 310 315 320

Asn Asn Pro Leu Tyr Asp Thr Thr Asn Lys Val Lys Ala Ser Gln Ala
325 330 335

Leu Gln Ser Glu Val Asp Thr Asp Leu His Thr Leu
340 345

<210> 16
<211> 349
<212> PRT
<213> *Macaca fascicularis*

<400> 16

Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
1 5 10 15

Ala Val Phe Leu Val Ala Glu Ala Glu Gly Ala Ala Gln Ser Asn Asn
20 25 30

Ser Leu Met Leu Gln Thr Ser Lys Glu Asn His Thr Leu Ala Ser Asn
35 40 45

Ser Leu Cys Met Asp Glu Lys Gln Ile Thr Gln Asn His Ser Lys Val
50 55 60

Leu Ala Glu Val Asn Ile Ser Trp Pro Val Gln Met Ala Arg Asn Ala
65 70 75 80

Val Leu Cys Cys Pro Pro Ile Glu Phe Arg Asn Leu Ile Val Ile Thr
85 90 95

Trp Glu Ile Ile Leu Arg Gly Gln Pro Ser Cys Thr Lys Thr Tyr Arg
100 105 110

Lys Asp Thr Asn Glu Thr Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile
115 120 125

Thr Trp Val Ser Thr Pro Asp Gln Asn Ser Asp Leu Gln Ile His Pro
130 135 140

Val Ala Ile Thr His Asp Gly Tyr Tyr Arg Cys Ile Met Ala Thr Pro
145 150 155 160

Asp Gly Asn Phe His Arg Gly Tyr His Leu Gln Val Leu Val Thr Pro
165 170 175

Glu Val Thr Leu Phe Glu Ser Arg Asn Arg Thr Ala Val Cys Lys Ala
180 185 190

Val Ala Gly Lys Pro Ala Ala Gln Ile Ser Trp Ile Pro Ala Gly Asp
195 200 205

Cys Ala Pro Thr Glu Gln Glu Tyr Trp Gly Asn Gly Thr Val Thr Val
210 215 220

Lys Ser Thr Cys His Trp Glu Gly His Asn Val Ser Thr Val Thr Cys
225 230 235 240

His Val Ser His Leu Thr Gly Asn Lys Ser Leu Tyr Ile Glu Leu Leu
245 250 255

Pro Val Pro Gly Ala Lys Lys Ser Ala Lys Leu Tyr Met Pro Tyr Val
260 265 270

Ile Leu Thr Ile Ile Ile Leu Thr Ile Val Gly Phe Ile Trp Leu Leu
275 280 285

Lys Ile Ser Gly Cys Arg Lys Tyr Asn Leu Asn Lys Thr Glu Ser Thr
290 295 300

Ser Val Val Glu Glu Asp Glu Met Gln Pro Tyr Ala Ser Tyr Thr Glu
305 310 315 320

Lys Asn Asn Pro Leu Tyr Asp Thr Thr Asn Lys Val Lys Ala Ser Gln
325 330 335

Ala Leu Gln Ser Glu Val Gly Thr Asp Leu His Thr Leu
340 345

<210> 17

<211> 278

<212> PRT

<213> Macaca fascicularis

<400> 17

Met His Thr Leu Gly Lys Met Ser Ala Ser Arg Leu Leu Ile Ser Ile
1 5 10 15

Ile Ile Met Val Ser Ala Ser Ser Ser Ser Cys Met Asp Gly Lys Gln
20 25 30

Met Thr Gln Asn Tyr Ser Lys Met Ser Ala Glu Gly Asn Ile Ser Gln
35 40 45

Pro Val Leu Met Asp Thr Asn Ala Met Leu Cys Cys Pro Pro Ile Glu
50 55 60

Phe Arg Asn Leu Ile Val Ile Val Trp Glu Ile Ile Ile Arg Gly Gln
65 70 75 80

Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys Glu
85 90 95

Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Thr Pro Asp Gln
100 105 110

Asn Ser Asp Leu Gln Ile His Pro Val Ala Ile Thr His Asp Gly Tyr
115 120 125

Tyr Arg Cys Ile Met Ala Thr Pro Asp Gly Asn Phe His Arg Gly Tyr
130 135 140

His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Ser Arg
145 150 155 160

Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala Gln
165 170 175

Ile Ser Trp Ile Pro Ala Gly Asp Cys Ala Pro Thr Glu His Glu Tyr
180 185 190

Trp Gly Asn Gly Thr Val Thr Val Glu Ser Met Cys His Trp Gly Asp
195 200 205

His Asn Ala Ser Thr Met Thr Cys His Val Ser His Leu Thr Gly Asn
210 215 220

Lys Ser Leu Tyr Ile Lys Leu Asn Ser Gly Leu Arg Thr Ser Gly Ser
225 230 235 240

Pro Ala Leu Asp Leu Leu Ile Ile Leu Tyr Val Lys Leu Ser Leu Phe
245 250 255

Val Val Ile Leu Val Thr Thr Gly Phe Val Phe Phe Gln Arg Ile Asn
260 265 270

Tyr Val Arg Lys Ser Leu
275