

# SEQUENCE LISTING

<110> DAIICHI SANKYO COMPANY, LIMITED

<120> Anti-CD147 antibody

<130> DSPCT-FP1821

<150> JP2017-145701

<151> 2017-07-27

<160> 152

<170> PatentIn version 3.5

<210> 1

<211> 385

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu Gly Thr  
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His Gly Ala Ser Gly Ala Ala Gly Phe Val Gln Ala Pro Leu Ser Gln  
20 25 30

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

Ser Pro Val Pro Glu Ile Gln Trp Trp Phe Glu Gly Gln Gly Pro Asn  
50 55 60

Asp Thr Cys Ser Gln Leu Trp Asp Gly Ala Arg Leu Asp Arg Val His  
65 70 75 80

Ile His Ala Thr Tyr His Gln His Ala Ala Ser Thr Ile Ser Ile Asp  
85 90 95

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

Asp Pro Asp Arg Asn His Leu Thr Arg Ala Pro Arg Val Lys Trp Val  
115 120 125

Arg Ala Gln Ala Val Val Leu Val Leu Glu Pro Gly Thr Val Phe Thr  
130 135 140

Thr Val Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn  
145 150 155 160

Asp Ser Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val  
165 170 175

Val Leu Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val  
180 185 190

Asp Ser Asp Asp Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu  
195 200 205

Pro Met Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys  
210 215 220

Ala Val Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu  
225 230 235 240

Val Cys Lys Ser Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr  
245 250 255

Lys Ile Thr Asp Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser  
260 265 270

Arg Phe Phe Val Ser Ser Ser Gln Gly Arg Ser Glu Leu His Ile Glu  
275 280 285

Asn Leu Asn Met Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr  
290 295 300

Ser Ser Lys Gly Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser  
305 310 315 320

His Leu Ala Ala Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu  
325 330 335

Val Leu Val Thr Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu  
340 345 350

Asp Val Leu Asp Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser  
355 360 365

Gly Gln His Gln Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser  
370 375 380

Ser  
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<210> 2  
<211> 1158  
<212> DNA  
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cagaggaact cttcctga 1158

<210> 3  
<211> 269  
<212> PRT  
<213> Homo sapiens

<400> 3

Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu Gly Thr  
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His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp  
20 25 30

Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr  
35 40 45

Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu  
50 55 60

Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp  
65 70 75 80

Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr  
85 90 95

Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser  
100 105 110

Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser  
115 120 125

Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp  
130 135 140

Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val  
 145 150 155 160

Ser Ser Ser Gln Gly Arg Ser Glu Leu His Ile Glu Asn Leu Asn Met  
 165 170 175

Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly  
 180 185 190

Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala  
 195 200 205

Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr  
 210 215 220

Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp  
 225 230 235 240

Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln  
 245 250 255

Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser  
 260 265

<210> 4  
 <211> 810  
 <212> DNA  
 <213> Homo sapiens

<400> 4  
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 tgctccttga atgacagcgc cacagaggtc acagggcacc gctggctgaa ggggggcgtg 180  
 gtgctgaagg aggacgcgct gcccggccag aaaacggagt tcaaggtgga ctccgacgac 240  
 cagtggggag agtactcctg cgtcttctc cccgagccca tgggcacggc caacatccag 300  
 ctccacgggc ctccagagt gaaggctgtg aagtcgtcag aacacatcaa cgagggggag 360  
 acggccatgc tggctgcaa gtcagagtcc gtgccacctg tcactgactg ggcttggtac 420  
 aagatcactg actctgagga caaggccctc atgaacggct ccgagagcag gttcttcgtg 480

agttcctcgc agggccggtc agagctacac attgagaacc tgaacatgga ggccgacccc 540  
 ggccagtacc ggtgcaacgg caccagctcc aagggtccg accaggccat catcacgctc 600  
 cgcgtgcgca gccacctggc cgccctctgg cccttcctgg gcatcgtggc tgagggtgctg 660  
 gtgctggtca ccatcatctt catctacgag aagcgccgga agcccgagga cgtcctggat 720  
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<210> 5  
 <211> 552  
 <212> PRT  
 <213> Homo sapiens

<400> 5

Met Asp Asn Met Ser Ile Thr Asn Thr Pro Thr Ser Asn Asp Ala Cys  
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Leu Ser Ile Val His Ser Leu Met Cys His Arg Gln Gly Gly Glu Ser  
 20 25 30

Glu Thr Phe Ala Lys Arg Ala Ile Glu Ser Leu Val Lys Lys Leu Lys  
 35 40 45

Glu Lys Lys Asp Glu Leu Asp Ser Leu Ile Thr Ala Ile Thr Thr Asn  
 50 55 60

Gly Ala His Pro Ser Lys Cys Val Thr Ile Gln Arg Thr Leu Asp Gly  
 65 70 75 80

Arg Leu Gln Val Ala Gly Arg Lys Gly Phe Pro His Val Ile Tyr Ala  
 85 90 95

Arg Leu Trp Arg Trp Pro Asp Leu His Lys Asn Glu Leu Lys His Val  
 100 105 110

Lys Tyr Cys Gln Tyr Ala Phe Asp Leu Lys Cys Asp Ser Val Cys Val  
 115 120 125

Asn Pro Tyr His Tyr Glu Arg Val Val Ser Pro Gly Ile Asp Leu Ser  
130 135 140

Gly Leu Thr Leu Gln Ser Asn Ala Pro Ser Ser Met Met Val Lys Asp  
145 150 155 160

Glu Tyr Val His Asp Phe Glu Gly Gln Pro Ser Leu Ser Thr Glu Gly  
165 170 175

His Ser Ile Gln Thr Ile Gln His Pro Pro Ser Asn Arg Ala Ser Thr  
180 185 190

Glu Thr Tyr Ser Thr Pro Ala Leu Leu Ala Pro Ser Glu Ser Asn Ala  
195 200 205

Thr Ser Thr Ala Asn Phe Pro Asn Ile Pro Val Ala Ser Thr Ser Gln  
210 215 220

Pro Ala Ser Ile Leu Gly Gly Ser His Ser Glu Gly Leu Leu Gln Ile  
225 230 235 240

Ala Ser Gly Pro Gln Pro Gly Gln Gln Gln Asn Gly Phe Thr Gly Gln  
245 250 255

Pro Ala Thr Tyr His His Asn Ser Thr Thr Thr Trp Thr Gly Ser Arg  
260 265 270

Thr Ala Pro Tyr Thr Pro Asn Leu Pro His His Gln Asn Gly His Leu  
275 280 285

Gln His His Pro Pro Met Pro Pro His Pro Gly His Tyr Trp Pro Val  
290 295 300

His Asn Glu Leu Ala Phe Gln Pro Pro Ile Ser Asn His Pro Ala Pro  
305 310 315 320

Glu Tyr Trp Cys Ser Ile Ala Tyr Phe Glu Met Asp Val Gln Val Gly  
325 330 335

Glu Thr Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 340                                                             | 345 | 350 |
| Tyr Val Asp Pro Ser Gly Gly Asp Arg Phe Cys Leu Gly Gln Leu Ser |     |     |
| 355                                                             | 360 | 365 |
| Asn Val His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His Ile Gly |     |     |
| 370                                                             | 375 | 380 |
| Lys Gly Val Gln Leu Glu Cys Lys Gly Glu Gly Asp Val Trp Val Arg |     |     |
| 385                                                             | 390 | 395 |
| Cys Leu Ser Asp His Ala Val Phe Val Gln Ser Tyr Tyr Leu Asp Arg |     |     |
| 405                                                             | 410 | 415 |
| Glu Ala Gly Arg Ala Pro Gly Asp Ala Val His Lys Ile Tyr Pro Ser |     |     |
| 420                                                             | 425 | 430 |
| Ala Tyr Ile Lys Val Phe Asp Leu Arg Gln Cys His Arg Gln Met Gln |     |     |
| 435                                                             | 440 | 445 |
| Gln Gln Ala Ala Thr Ala Gln Ala Ala Ala Ala Ala Gln Ala Ala Ala |     |     |
| 450                                                             | 455 | 460 |
| Val Ala Gly Asn Ile Pro Gly Pro Gly Ser Val Gly Gly Ile Ala Pro |     |     |
| 465                                                             | 470 | 475 |
| Ala Ile Ser Leu Ser Ala Ala Ala Gly Ile Gly Val Asp Asp Leu Arg |     |     |
| 485                                                             | 490 | 495 |
| Arg Leu Cys Ile Leu Arg Met Ser Phe Val Lys Gly Trp Gly Pro Asp |     |     |
| 500                                                             | 505 | 510 |
| Tyr Pro Arg Gln Ser Ile Lys Glu Thr Pro Cys Trp Ile Glu Ile His |     |     |
| 515                                                             | 520 | 525 |
| Leu His Arg Ala Leu Gln Leu Leu Asp Glu Val Leu His Thr Met Pro |     |     |
| 530                                                             | 535 | 540 |
| Ile Ala Asp Pro Gln Pro Leu Asp                                 |     |     |
| 545                                                             | 550 |     |

<210> 6  
 <211> 1659  
 <212> DNA  
 <213> Homo sapiens

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 gaaagtttgg taaagaagct gaaggagaaa aaagatgaat tggattcttt aataacagct 180  
 ataactacaa atggagctca tcctagtaaa tgtgttacca tacagagaac attggatggg 240  
 aggcttcagg tggctggctg gaaaggattt cctcatgtga tctatgcccg tctctggagg 300  
 tggcctgata ttcacaaaaa tgaactaaaa catgttaa at attgtcagta tgcgtttgac 360  
 ttaaaatgtg atagtgtctg tgtgaatcca tatcactacg aacgagttgt atcacctgga 420  
 attgatctct caggattaac actgcagagt aatgctccat caagtatgat ggtgaaggat 480  
 gaatatgtgc atgactttga gggacagcca tcgttgtcca ctgaaggaca ttcaattcaa 540  
 accatccagc atccaccaag taatcgtgca tcgacagaga catacagcac cccagctctg 600  
 ttagcccat ctgagtctaa tgctaccagc actgccaaact ttccaacat tcctgtggct 660  
 tccacaagtc agcctgccag tatactgggg ggcagccata gtgaaggact gttgcagata 720  
 gcatcagggc ctgagccagg acagcagcag aatggattta ctggtcagcc agctacttac 780  
 catcataaca gcactaccac ctggactgga agtaggactg caccatacac acctaatttg 840  
 cctcaccacc aaaacggcca tcttcagcac caccgccta tgccgcccc tcccggacat 900  
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 gttccttcaa gctgccctat tgttactgtt gatggatacg tggacccttc tggaggagat 1080  
 cgcttttgtt tgggtcaact ctccaatgtc cacaggacag aagccattga gagagcaagg 1140  
 ttgcacatag gcaaagggtg gcagttggaa tgtaaagggtg aaggtgatgt ttgggtcagg 1200  
 tgccttagtg accacgcggt ctttgtacag agttactact tagacagaga agctgggcgt 1260  
 gcacctggag atgctgttca taagatctac ccaagtgc at atataaagg ttttgatttg 1320  
 cgtcagtgat atcgacagat gcagcagcag gcggctactg cacaagctgc agcagctgcc 1380

caggcagcag ccgtaggcagg aaacatccct ggcccaggat cagtaggtgg aatagctcca 1440  
gctatcagtc tgtcagctgc tgctggaatt ggtgttgatg accttcgtcg cttatgcata 1500  
ctcaggatga gttttgtgaa aggctgggga ccggattacc caagacagag catcaaagaa 1560  
acaccttgct ggattgaaat tcacttacac cgggccctcc agctcctaga cgaagtactt 1620  
cataccatgc cgattgcaga cccacaacct ttagactga 1659

<210> 7  
<211> 324  
<212> DNA  
<213> Mus musculus

<400> 7  
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ctcacttgctc gggcaagtct ggaaattagt ggtttcttaa gttggcttca gcagaaacca 120  
gatggaacta ttaaagcct gatctacgcc gcatccattt tagattctgg tgtcccaaaa 180  
aggttcagtg gcagtaggtc tgggtcagat tattctctca ccatcagcag cttgagtct 240  
gaagattttg cagactatta ctgtctacaa tatgctagtt atccgtggac gttcgggtga 300  
ggcaccaagc tggaatcaa acgg 324

<210> 8  
<211> 108  
<212> PRT  
<213> Mus musculus

<400> 8

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly  
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Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Leu Glu Ile Ser Gly Phe  
20 25 30

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

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

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

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Tyr Pro Trp  
85 90 95

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

<210> 9

<211> 366

<212> DNA

<213> Mus musculus

<400> 9

|                                                                    |     |
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| tcctgcaagg cttctgggta taccttcaca aactatggaa tgaactgggt gaagcaggct  | 120 |
| ccaggaaagg gtttaaagtg gatgggctgg ataaacacct acactggaga gccaacatat  | 180 |
| gctgatgact tcaagggacg gtttgccttc tctttggaaa cctctgccag cactgcctat  | 240 |
| ttgcagatca acaacctcaa aaatgaggac acggctacat atttctgtgc aagagggggg  | 300 |
| tatggtaact acggggcggg ggctatggac tactgggggtc aaggtagctc agtcaccgtc | 360 |
| tcctca                                                             | 366 |

<210> 10

<211> 122

<212> PRT

<213> Mus musculus

<400> 10

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

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

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

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe  
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys  
85 90 95

Ala Arg Gly Gly Tyr Gly Asn Tyr Gly Ala Gly Ala Met Asp Tyr Trp  
100 105 110

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

<210> 11  
<211> 11  
<212> PRT  
<213> Mus musculus

<400> 11

Arg Ala Ser Leu Glu Ile Ser Gly Phe Leu Ser  
1 5 10

<210> 12  
<211> 7  
<212> PRT  
<213> Mus musculus

<400> 12

Ala Ala Ser Ile Leu Asp Ser  
1 5

<210> 13  
<211> 9  
<212> PRT  
<213> Mus musculus

<400> 13

Leu Gln Tyr Ala Ser Tyr Pro Trp Thr  
1 5

<210> 14  
 <211> 10  
 <212> PRT  
 <213> Mus musculus

<400> 14

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

<210> 15  
 <211> 10  
 <212> PRT  
 <213> Mus musculus

<400> 15

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr  
 1 5 10

<210> 16  
 <211> 13  
 <212> PRT  
 <213> Mus musculus

<400> 16

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

<210> 17  
 <211> 324  
 <212> DNA  
 <213> Rattus norvegicus

<400> 17  
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 gggaaatctc ctgagctcct gatctatggg gcaagtagct tgcaagacgg ggtcccatca 180  
 cggttcagtg gcagtggatc tggcacacag tattctctca agatcagcgg catgcaacct 240  
 gaagatgaag gggtttatta ctgtcaacag gggtacaagt atccattcac gttcgggtca 300  
 gggacgaagt tggaaataaa acgg 324

<210> 18

<211> 108  
 <212> PRT  
 <213> Rattus norvegicus

<400> 18

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

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

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

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

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

Glu Asp Glu Gly Val Tyr Tyr Cys Gln Gln Gly Tyr Lys Tyr Pro Phe  
 85 90 95

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

<210> 19  
 <211> 351  
 <212> DNA  
 <213> Rattus norvegicus

<400> 19

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| acctgttctg tctactggta ctccatcact agtaattact ggggctggat ccggaagttc | 120 |
| ccaggaaata aaatggagtg gatgggatgc ataacctaca gtggtggcac tagctacaac | 180 |
| ccatctctca aaagtcgaat ctccattact agagacacat caaagaatca gttcttcctg | 240 |
| cagttgaact ctgtaactac tgaggacaca gccacatatt actgtgcaag ttcctatacc | 300 |
| agtggtgacg tcgattactg gggccaagga gtcatggtca cagtctcctc a          | 351 |

<210> 20  
 <211> 117  
 <212> PRT  
 <213> Rattus norvegicus

<400> 20

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
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Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn  
 20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met Glu Trp Met  
 35 40 45

Gly Cys Ile Thr Tyr Ser Gly Gly Thr Ser Tyr Asn Pro Ser Leu Lys  
 50 55 60

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

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

Ser Ser Tyr Thr Ser Gly Asp Val Asp Tyr Trp Gly Gln Gly Val Met  
 100 105 110

Val Thr Val Ser Ser  
 115

<210> 21  
 <211> 11  
 <212> PRT  
 <213> Rattus norvegicus

<400> 21

Leu Ala Ser Glu Gly Ile Ser Asn Ser Leu Ala  
 1 5 10

<210> 22  
 <211> 7  
 <212> PRT

<213> Rattus norvegicus

<400> 22

Gly Ala Ser Ser Leu Gln Asp  
1 5

<210> 23

<211> 9

<212> PRT

<213> Rattus norvegicus

<400> 23

Gln Gln Gly Tyr Lys Tyr Pro Phe Thr  
1 5

<210> 24

<211> 10

<212> PRT

<213> Rattus norvegicus

<400> 24

Gly Tyr Ser Ile Thr Ser Asn Tyr Trp Gly  
1 5 10

<210> 25

<211> 9

<212> PRT

<213> Rattus norvegicus

<400> 25

Cys Ile Thr Tyr Ser Gly Gly Thr Ser  
1 5

<210> 26

<211> 9

<212> PRT

<213> Rattus norvegicus

<400> 26

Ser Tyr Thr Ser Gly Asp Val Asp Tyr  
1 5

<210> 27

<211> 449  
<212> DNA  
<213> Artificial Sequence

<220>

<223> DNA comprising DNA sequence coding for human light chain signal sequence and human kappa chain constant region

<400> 27

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gtggatctcc ggcgctacg gcgatatcgt gatgattaaa cgtacgggtg ccgccccctc      120
cgtgttcattc tccccccct ccgacgagca gctgaagtcc ggacaccgct ccgtgggtgtg      180
cctgctgaat aatttctacc ccagagaggc caagggtgcag tggaagggtg acaacgccct      240
gcagtccggg aactcccagg agagcgtgac cgagcaggac agcaaggaca gcacctacag      300
cctgagcagc accctgacct tgagcaaagc cgactacgag aagcacaagg tgtacgcctg      360
cgaggtgacc caccagggcc tgagctcccc cgtcaccaag agcttcaaca gggggggagtg      420
ttagggggccc gtttaaaccg gggaggcta                                     449
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<210> 28  
<211> 1132  
<212> DNA  
<213> Artificial Sequence

<220>

<223> DNA comprising DNA sequence coding for amino acid of human heavy chain signal sequence and human IgG1 constant region

<400> 28

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gcctccggac tctagagcca ccatgaaaca cctgtggttc ttctcctgc tgggtggcagc      60
tcccagatgg gtgctgagcc aggtgcaatt gtgcaggcgg ttagctcagc ctccaccaag      120
ggcccaagcg tcttccccct ggacacctcc tccaagagca cctctggcgg cacagccgcc      180
ctgggctgcc tgggtcaagga ctacttcccc gaacctgtga ccgtgagctg gaactcaggc      240
gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc      300
ctcagcagcg tgggtaccgt gccctccagc agcttgggca ccagacctc catctgcaac      360
gtgaatcaca agcccagcaa caccaagggt gacaagagag ttgagcccaa atcttgtgac      420
aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctgagtcttc      480
ctcttcccc caaaaccaa ggacacctc atgatctccc ggaccttga ggtcacatgc      540
```

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc  | 600  |
| gtggagggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg | 660  |
| gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc  | 720  |
| aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggc   | 780  |
| cagccccggg aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 840  |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg  | 900  |
| gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac  | 960  |
| ggctccttct tcctctacag caagctcacc gtggacaaga gcagggtggca gcagggcaac | 1020 |
| gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacca gaagagcctc   | 1080 |
| tccctgtctc ccggcaaatt agatatcggg cccgtttaaa cgggggaggc ta          | 1132 |

<210> 29

<211> 1114

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA comprising DNA sequence coding for amino acid of human heavy chain signal sequence and human IgG2 constant region

<400> 29

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ccagcctccg gactctagag ccaccatgaa acacctgtgg ttcttcctcc tgctggtggc  | 60  |
| agctcccaga tgggtgctga gccagggtgca attgtgcagg cggttagctc agcctccacc | 120 |
| aagggccctt ccgtgttccc tctggcccct tgtagccgtt ccaccagcga gtccaccgcc  | 180 |
| gcccttggct gtctggtgaa ggactacttc cctgagcctg tgaccgtgag ctggaactcc  | 240 |
| ggagccctta ccagcggcgt gcacaccttc cctgccgtgc tgcagtccag cggcctttac  | 300 |
| tccctgagct ccgtggtgac cgtgcctagc tccaacttcg gcacccaaac ctacacctgt  | 360 |
| aacgtggacc acaagcctag caacaccaag gtggacaaga ccgtggagcg taagtgttgt  | 420 |
| gtggagtgtc ctcttgtcc tgccccctct gtggccggac cttccgtgtt ccttttcct    | 480 |
| cctaagccta aggacaccct gatgatcagc cgtacccttg aggtgacctg tgtggtggtg  | 540 |
| gacgtgtccc acgaggaccc tgagggtcag ttcaactggt acgtggacgg cgtggagggtg | 600 |
| cacaacgcca agaccaagcc tcgtgaggag caattcaaca gcaccttccg tgtggtgtcc  | 660 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| gtgcttaccg tggtgcacca agactggctg aacggcaagg agtacaagtg taaggtgagc | 720  |
| aacaagggac ttcctgcccc tatcgagaag accatctcca agaccaaggg ccaacctcgt | 780  |
| gagcctcaag tgtacaccct tcctcctagc cgtgaggaga tgaccaagaa ccaagtgtcc | 840  |
| cttacctgtc tggtgaaggg cttctaccct agcgacatcg ccgtggagtg ggagtccaac | 900  |
| ggacaacctg agaacaacta caagaccacc cctcctatgc ttgacagcga cggctccttc | 960  |
| ttcctgtaca gcaagctgac cgtggacaag tcccgttggc aacaaggcaa cgtgttcagc | 1020 |
| tgttccgtga tgcacgaggc cctgcacaac cactacaccc aaaagagcct ttccctgagc | 1080 |
| cctggaaagt gagtttaaac gggggaggct aact                             | 1114 |

<210> 30  
 <211> 702  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Light chain of human chimeric LN22R8

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 30                                                           |     |
| atgggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc  | 60  |
| gacatccaga tgaccagtc tccatcctcc ttatctgcct ctctgggaga aagagtcagt   | 120 |
| ctcacttgtc gggcaagtct ggaaattagt ggtttcttaa gttggcttca gcagaaacca  | 180 |
| gatggaacta ttaaagcct gatctacgcc gcatccattt tagattctgg tgtcccaaaa   | 240 |
| aggttcagtg gcagtaggtc tgggtcagat tattctctca ccatcagcag cttgagtct   | 300 |
| gaagattttg cagactatta ctgtctacaa tatgctagtt atccgtggac gttcgggtgga | 360 |
| ggcaccaagc tggaaatcaa acgggctgtg gccgccccct ccgtgttcat cttccccccc  | 420 |
| tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac  | 480 |
| cccagagagg ccaaggtgca gtggaagggt gacaacgccc tgcaagtcgg gaactcccag  | 540 |
| gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc  | 600 |
| ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc  | 660 |
| ctgagctccc ccgtcaccaa gagcttcaac aggggggaggt gt                    | 702 |

<210> 31

<211> 234  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Light chain of human chimeric LN22R8

<400> 31

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

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

Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Leu Glu  
35 40 45

Ile Ser Gly Phe Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile  
50 55 60

Lys Arg Leu Ile Tyr Ala Ala Ser Ile Leu Asp Ser Gly Val Pro Lys  
65 70 75 80

Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser  
85 90 95

Ser Leu Glu Ser Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala  
100 105 110

Ser Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg  
115 120 125

Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230

<210> 32  
<211> 1413  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Heavy chain IgG1 type of human chimeric LN22R8

<400> 32  
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60  
atccagttgg tgcagtctgg acctgagctg aagaagcctg gagagacagt caagatctcc 120  
tgcaaggctt ctgggtatac cttcacaac tatggaatga actgggtgaa gcaggctcca 180  
ggaaagggtt taaagtggat gggctggata aacacctaca ctggagagcc aacatatgct 240  
gatgacttca agggacggtt tgccttctct ttggaaacct ctgccagcac tgcctatttg 300  
cagatcaaca acctcaaaaa tgaggacacg gctacatatt tctgtgcaag aggggggtat 360  
ggtaactacg gggcgggggc tatggactac tggggtaag gtacctcagt caccgtcagc 420  
tcagcctcca ccaaggggccc aagcgtcttc cccctggcac cctcctcaa gagcacctct 480  
ggcggcacag cgccttggg ctgcctggtc aaggactact tccccgaacc cgtgaccgtg 540  
agctggaact caggcgcctt gaccagcggc gtgcacacct tccccgctgt cctgcagtcc 600  
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag 660  
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720  
cccaaattct gtgacaaaac tcacacatgc ccacctgcc cagcacctga actcctgggg 780  
ggaccctcag tcttctctt cccccaaaa cccaaggaca cctcatgat ctcccgacc 840

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900  
 tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccccggga ggagcagtac 960  
 aacagcacgt accgggtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020  
 aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1080  
 tccaaagcca aaggccagcc ccgggaacca caggtgtaca ccctgcccc atcccgggag 1140  
 gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1200  
 atcgccgtgg agtgggagag caatggccag cccgagaaca actacaagac caccctccc 1260  
 gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1320  
 tggcagcagg gcaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380  
 acccagaaga gcctctcct gtctcccggc aaa 1413

<210> 33  
 <211> 471  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG1 type of human chimeric LN22R8

<400> 33

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

Val Leu Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys  
 20 25 30

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

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

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

Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser  
 85 90 95

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr  
100 105 110

Tyr Phe Cys Ala Arg Gly Gly Tyr Gly Asn Tyr Gly Ala Gly Ala Met  
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr  
130 135 140

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

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu  
225 230 235 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
245 250 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
275 280 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
340 345 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
370 375 380

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

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
450 455 460

Leu Ser Leu Ser Pro Gly Lys  
465 470

<210> 34  
<211> 1401  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Heavy chain IgG2 type of human chimeric LN22R8

<400> 34  
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60  
atccagttgg tgcagtctgg acctgagctg aagaagcctg gagagacagt caagatctcc 120  
tgcaaggctt ctgggtatac cttcacaac tatggaatga actgggtgaa gcaggctcca 180  
ggaaagggtt taaagtggat gggctggata aacacctaca ctggagagcc aacatatgct 240  
gatgacttca agggacggtt tgccttctct ttggaaacct ctgccagcac tgcctatttg 300  
cagatcaaca acctcaaaaa tgaggacacg gctacatatt tctgtgcaag aggggggtat 360  
ggtaactacg gggcgggggc tatggactac tggggtaag gtacctcagt caccgtcagc 420  
tcagcctcca ccaagggcc ttccgtgttc cctctggccc ctgttagccg ttccaccagc 480  
gagtcaccg cgccttgg ctgtctgggtg aaggactact tccctgagcc tgtgaccgtg 540  
agctggaact cgggagccct taccagcggc gtgcacacct tccctgccgt gctgcagtcc 600  
agcggccttt actccctgag ctccgtgggtg accgtgccta gctccaactt cggcacccaa 660  
acctacacct gtaacgtgga ccacaagcct agcaacacca aggtggacaa gaccgtggag 720  
cgtaagtgtt gtgtggagtg tcctccttgt cctgcccctc ctgtggccgg accttccgtg 780  
ttccttttcc ctctaagcc taaggacacc ctgatgatca gccgtacccc tgaggtgacc 840  
tgtgtggtgg tggacgtgtc ccacgaggac cctgaggtgc agttcaactg gtacgtggac 900  
ggcgtggagg tgcacaacgc caagaccaag cctcgtgagg agcaattcaa cagcaccttc 960  
cgtgtggtgt ccgtgcttac cgtggtgcac caagactggc tgaacggcaa ggagtacaag 1020  
tgtaaggtga gcaacaaggg acttcctgcc cctatcgaga agaccatctc caagaccaag 1080  
ggccaacctc gtgagcctca agtgtacacc cttcctccta gccgtgagga gatgaccaag 1140  
aaccaagtgt cccttacctg tctggtgaag ggcttctacc ctagcgacat cgccgtggag 1200  
tgggagtcca acggacaacc tgagaacaac tacaagacca cccctcctat gcttgacagc 1260  
gacggctcct tcttcctgta cagcaagctg accgtggaca agtcccgttg gcaacaaggc 1320  
aacgtgttca gctgttccgt gatgcacgag gccctgcaca accactacac ccaaaagagc 1380  
ctttccctga gccctggaaa g 1401

<210> 35  
<211> 467  
<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain IgG2 type of human chimeric LN22R8

<400> 35

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

Val Leu Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys  
20 25 30

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

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

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

Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser  
85 90 95

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr  
100 105 110

Tyr Phe Cys Ala Arg Gly Gly Tyr Gly Asn Tyr Gly Ala Gly Ala Met  
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr  
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser  
145 150 155 160

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
195 200 205

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys  
210 215 220

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu  
225 230 235 240

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala  
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe  
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly  
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile  
340 345 350

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val  
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
405 410 415

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
450 455 460

Pro Gly Lys  
465

<210> 36  
<211> 1454  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> DNA comprising DNA sequence coding for amino acid sequence of  
human chimera LN22R8\_heavy chain\_ IgG4P type

<400> 36  
ccagcctccg gactctagag ccaccatgaa gcacctgtgg ttctttctgc tgctggtggc 60  
cgctcccaga tgggtgctgt ctcagatcca gctggtgcag agcggccctg agctgaagaa 120  
acccggcgag acagtgaaga tcagctgcaa ggccagcggc tacaccttca ccaactacgg 180  
catgaactgg gtcaagcagg cccctggcaa gggcctgaag tggatgggct ggatcaacac 240  
ctacaccggc gagcccacct acgccgacga cttcaagggc agattcgcct tcagcctgga 300  
aaccagcgcc agcaccgcct acctgcagat caacaacctg aagaacgagg acaccgccac 360  
ctacttttgc gccagaggcg gctacggcaa ttacggcgct ggcgccatgg attactgggg 420  
ccaggaaca agcgtgaccg tgtccagcgc ctctaccaag ggccctagcg tgttcctct 480  
ggccccttgc agcagaagca ccagcgaatc tacagccgcc ctgggctgcc tcgtgaagga 540  
ctactttccc gagcccgtag cagtgtcctg gaactctggc gccctgacaa gcggcgtagc 600  
cacctttcca gccgtgctgc agagcagcgg cctgtactct ctgagcagcg tcgtgactgt 660

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gcccagcagc tctctgggca ccaagaccta cacctgtaac gtggaccaca agcccagcaa  | 720  |
| caccaaggtg gacaagcggg tggaaatctaa gtacggccct ccctgccctc cttgcccagc | 780  |
| ccctgaattt ctgggicggac cctccgtgtt cctgttcccc ccaaagccca aggacaccct | 840  |
| gatgatcagc cggacccccg aagtgacctg cgtgggtgtg gatgtgtccc aggaagatcc  | 900  |
| cgaggtgcag ttcaatttgt acgtggacgg cgtggaagtg cacaacgcca agaccaagcc  | 960  |
| tagagaggaa cagttcaaca gcacctaccg ggtgggtgtc gtgctgacag tgctgcacca  | 1020 |
| ggactggctg aacggcaaag agtacaagtg caaggtgtcc aacaaggac tgcccagctc   | 1080 |
| catcgagaaa accatcagca aggccaaggg ccagccccgc gaaccccagg tgtacacact  | 1140 |
| gcctccaagc caggaagaga tgaccaagaa ccaggtgtcc ctgacctgtc tcgtgaaagg  | 1200 |
| cttctacccc tccgatatcg ccgtggaatg ggagagcaac ggccagcccc agaacaacta  | 1260 |
| caagaccacc ccccctgtgc tggacagcga cggctcattc ttctgtaca gcagactgac   | 1320 |
| cgtggacaag agccggtggc aggaaggcaa cgtgttcagc tgcagcgtga tgcacgaggc  | 1380 |
| cctgcacaac cactacacc agaagtcct gtctctgagc ctgggcaaat gaggtttaaac   | 1440 |
| gggggaggct aact                                                    | 1454 |

<210> 37

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain IgG4P type of human chimeric LN22R8

<400> 37

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | His | Leu | Trp | Phe | Phe | Leu | Leu | Leu | Val | Ala | Ala | Pro | Arg | Trp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Gln | Ile | Gln | Leu | Val | Gln | Ser | Gly | Pro | Glu | Leu | Lys | Lys |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Glu | Thr | Val | Lys | Ile | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asn | Tyr | Gly | Met | Asn | Trp | Val | Lys | Gln | Ala | Pro | Gly | Lys | Gly | Leu |
| 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |

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

Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser  
85 90 95

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr  
100 105 110

Tyr Phe Cys Ala Arg Gly Gly Tyr Gly Asn Tyr Gly Ala Gly Ala Met  
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr  
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser  
145 150 155 160

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys  
210 215 220

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu  
225 230 235 240

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu  
245 250 255

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
275 280 285

Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu  
290 295 300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr  
305 310 315 320

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser  
340 345 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
355 360 365

Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val  
370 375 380

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr  
420 425 430

Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val  
435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
450 455 460

Ser Leu Gly Lys  
465

<210> 38  
<211> 1137  
<212> DNA  
<213> Artificial Sequence

<220>

<223> DNA comprising DNA sequence coding for amino acid of human heavy chain signal sequence and human IgG1LALA constant region

<400> 38  
ccagcctccg gactctagag ccaccatgaa acacctgtgg ttcttcctcc tgctggtggc 60  
agctcccaga tgggtgctga gccagggtgca attgtgcagg cggttagctc agcctccacc 120  
aagggcccaa gcgtcttccc cctggcaccc tcctccaaga gcacctctgg cggcacagcc 180  
gccctgggct gcctggtcaa ggactacttc cccgaacccg tgaccgtgag ctggaactca 240  
ggcgccctga ccagcggcgt gcacaccttc cccgctgtcc tgcagtcctc aggactctac 300  
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 360  
aacgtgaatc acaagcccag caacaccaag gtggacaaga gagttgagcc caaatcttgt 420  
gacaaaactc acacatgccc accctgcccga gcacctgaag ccgcgggggg accctcagtc 480  
ttctcttccc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 540  
tgctggtggg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 600  
ggcgtggagg tgcataatgc caagacaaag ccccgaggagg agcagtacaa cagcacgtac 660  
cgggtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 720  
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 780  
ggccagcccc gggaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 840  
aaccagggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 900  
tgggagagca atggccagcc cgagaacaac tacaagacca cccctcccgt gctggactcc 960  
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggc 1020  
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac ccagaagagc 1080  
ctctccctgt ctcccggcaa atgagatatc gggcccgttt aaacggggga ggctaac 1137

<210> 39  
<211> 1117  
<212> DNA  
<213> Artificial Sequence

<220>

<223> DNA comprising DNA sequence coding for amino acid of human heavy chain signal sequence and human IgG4P constant region

<400> 39

```
ccagcctccg gactctagag ccaccatgaa acacctgtgg ttcttcctcc tgctggtggc      60
agctcccaga tgggtgctga gccagggtgca attgtgcagg cggttagctc agcctccacc    120
aagggcccta gcgtgttccc tctggcccct tgtagcagaa gcaccagcga gtctacagcc      180
gccctgggct gcctcgtgaa ggactacttt cccgagcccc tgaccgtgtc ctggaactct      240
ggcgctctga caagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac      300
tctctgtcca gcgtcgtgac tgtgcccagc agctctctgg gcaccaagac ctacacctgt      360
aacgtggacc acaagcccag caacaccaag gtggacaagc gggtggaatc taagtacggc      420
cctccctgcc ctcttgccc agccccgaa tttctgggcg gaccctccgt gttcctgttc      480
cccccaaagc ccaaggacac cctgatgatc agccggaccc ccgaagtgaac ctgcgtggtg      540
gtggatgtgt cccaggaaga tcccgagggtg cagttcaatt ggtacgtgga cggcgtggaa      600
gtgcacaacg ccaagaccaa gcctagagag gaacagttca acagcaccta ccgggtgggtg      660
tccgtgctga cagtgtgca ccaggactgg ctgaacggca aagagtacaa gtgcaagggtg      720
tccaacaagg gcctgcccag ctccatcgag aaaaccatca gcaaggccaa gggccagccc      780
cgcgaaacccc aggtgtacac actgcctcca agccaggaag agatgaccaa gaatcaggtg      840
tccctgacct gtctcgtgaa aggcttctac ccctccgata tcgccgtgga atgggagagc      900
aacggccagc ccgagaacaa ctacaagacc accccccctg tgctggactc cgatgggtca      960
ttcttcctgt acagcagact gaccgtggac aagagccggt ggcaggaagg caacgtgttc     1020
agctgctccg tgatgcacga ggccctgcac aaccactaca ccagaagtc cctgtctctg     1080
agcctgggca aatgagtta aacggggggag gctaact                                1117
```

<210> 40

<211> 702

<212> DNA

<213> Artificial Sequence

<220>

<223> Light chain of human chimeric 2P10F2

<400> 40  
atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60  
gacatccaga tgacacagtc tccagcttcc ctgtctgcat ctctgggaga aactgtctcc 120  
atcgaatgtc ttgcaagtga gggcatttcc aatagtttag cgtggtatca gcagaagcca 180  
gggaaatctc ctcagctcct gatctatggt gcaagtagct tgcaagacgg ggtcccatca 240  
cggttcagtg gcagtggatc tggcacacag tattctctca agatcagcgg catgcaacct 300  
gaagatgaag gggtttatta ctgtcaacag ggttacaagt atccattcac gttcgggtca 360  
gggacgaagt tggaaataaa acgggctgtg gccgccccct ccgtgttcat cttccccccc 420  
tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480  
cccagagagg ccaaggtgca gtggaagggt gacaacgccc tgcagtccgg gaactccag 540  
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600  
ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660  
ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt 702

<210> 41  
<211> 234  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Light chain of human chimeric 2P10F2

<400> 41

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

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

Ala Ser Leu Gly Glu Thr Val Ser Ile Glu Cys Leu Ala Ser Glu Gly  
35 40 45

Ile Ser Asn Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro  
50 55 60

Gln Leu Leu Ile Tyr Gly Ala Ser Ser Leu Gln Asp Gly Val Pro Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Gln | Tyr | Ser | Leu | Lys | Ile | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Met | Gln | Pro | Glu | Asp | Glu | Gly | Val | Tyr | Tyr | Cys | Gln | Gln | Gly | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Tyr | Pro | Phe | Thr | Phe | Gly | Ser | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu | Gln | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp | Ser | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Ser | Leu | Ser | Ser | Thr | Leu | Thr | Leu | Ser | Lys | Ala | Asp | Tyr | Glu | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Lys | Val | Tyr | Ala | Cys | Glu | Val | Thr | His | Gln | Gly | Leu | Ser | Ser | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Thr | Lys | Ser | Phe | Asn | Arg | Gly | Glu | Cys |     |     |     |     |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     |     |

<210> 42  
 <211> 1398  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG1LALA type of human chimeric 2P10F2

<400> 42  
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag

60

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gtgcagcttc aggagtcagg acctggcctt gtgaaaccct cacagtcact ctccctcacc  | 120  |
| tgttctgtca ctggttactc catcactagt aattactggg gctggatccg gaagttccca  | 180  |
| ggaaataaaa tggagtggat gggatgcata acctacagtg gtggcactag ctacaacca   | 240  |
| tctctcaaaa gtcgaatctc cattactaga gacacatcaa agaatacagtt cttcctgcag | 300  |
| ttgaactctg taactactga ggacacagcc acatattact gtgcaagttc ctataccagt  | 360  |
| ggtgacgtcg attactgggg ccaaggagtc atggtcacag tcagctcagc ctccaccaag  | 420  |
| ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc  | 480  |
| ctgggctgcc tgggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc | 540  |
| gccctgacca gcggcggtgca caccttcccc gctgtcctgc agtcctcagg actctactcc | 600  |
| ctcagcagcg tggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac   | 660  |
| gtgaatcaca agcccagcaa caccaagggtg gacaagagag ttgagcccaa atcttgtgac | 720  |
| aaaactcaca catgcccacc ctgcccagca cctgaagccg cgggggggacc ctcagtcttc | 780  |
| ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc    | 840  |
| gtgggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc | 900  |
| gtggaggtgc ataatgccaa gacaaaagccc cgggaggagc agtacaacag cacgtaccgg | 960  |
| gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc  | 1020 |
| aaggtctcca acaaagccct ccagcccc atcgagaaaa ccatctcca agccaaaggc     | 1080 |
| cagccccggg aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 1140 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg   | 1200 |
| gagagcaatg gccagcccga gaacaactac aagaccacc ctcccgtgct ggactccgac   | 1260 |
| ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac  | 1320 |
| gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacca gaagagcctc   | 1380 |
| tcctgtctc ccggcaaa                                                 | 1398 |

<210> 43  
 <211> 466  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Heavy chain IgG1LALA type of human chimeric 2P10F2

<400> 43

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

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

Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile  
35 40 45

Thr Ser Asn Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met  
50 55 60

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

Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln  
85 90 95

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

Tyr Cys Ala Ser Ser Tyr Thr Ser Gly Asp Val Asp Tyr Trp Gly Gln  
115 120 125

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

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

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
195 200 205

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp  
225 230 235 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly  
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
275 280 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg  
305 310 315 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
340 345 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
355 360 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val

|                                                                 |                                 |     |
|-----------------------------------------------------------------|---------------------------------|-----|
| 405                                                             | 410                             | 415 |
| Leu Asp Ser Asp Gly Ser Phe Phe                                 | Leu Tyr Ser Lys Leu Thr Val Asp |     |
| 420                                                             | 425                             | 430 |
| Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His |                                 |     |
| 435                                                             | 440                             | 445 |
| Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro |                                 |     |
| 450                                                             | 455                             | 460 |
| Gly Lys                                                         |                                 |     |
| 465                                                             |                                 |     |

<210> 44  
 <211> 1386  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG2 type of human chimeric 2P10F2

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 44                                                           |     |
| atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag  | 60  |
| gtgcagcttc aggagtcagg acctggcctt gtgaaacctt cacagtcact ctccctcacc  | 120 |
| tgtttctgtca ctggttactc catcactagt aattactggg gctggatccg gaagttccca | 180 |
| ggaaataaaa tggagtggat gggatgcata acctacagtg gtggcactag ctacaacca   | 240 |
| tctctcaaaa gtcgaatctc cattactaga gacacatcaa agaatcagtt cttcctgcag  | 300 |
| ttgaactctg taactactga ggacacagcc acatattact gtgcaagttc ctataccagt  | 360 |
| ggtgacgtcg attactgggg ccaaggagtc atgggtcacag tcagctcagc ctccaccaag | 420 |
| ggcccttccg tggtccctct ggcccttgt agccgttcca ccagcgagtc caccgccgcc   | 480 |
| cttggctgtc tggagaagga ctacttcctt gaggctgtga ccgtgagctg gaactccgga  | 540 |
| gcccttacca gcggcgtgca caccttcctt gccgtgtgtc agtccagcgg cttttactcc  | 600 |
| ctgagctccg tggtgaccgt gcctagctcc aacttcggca cccaaacctt cacctgtaac  | 660 |
| gtggaccaca agcctagcaa caccaagggt gacaagaccg tggagcgtaa gtgttgtgtg  | 720 |
| gagtgtcctc cttgtcctgc ccctcctgtg gccggacctt ccgtgttcct tttccctcct  | 780 |

aagcctaagg acaccctgat gatcagccgt acccctgagg tgacctgtgt ggtggtggac 840  
gtgtccacg aggaccctga ggtgcagttc aactggtacg tggacggcgt ggaggtgcac 900  
aacgccaaga ccaagcctcg tgaggagcaa ttcaacagca ccttccgtgt ggtgtccgtg 960  
cttaccgtgg tgcaccaaga ctggctgaac ggcaaggagt acaagtgtaa ggtgagcaac 1020  
aagggacttc ctgcccctat cgagaagacc atctccaaga ccaagggcca acctcgtgag 1080  
cctcaagtgt acacccttcc tcctagccgt gaggagatga ccaagaacca agtgtccctt 1140  
acctgtctgg tgaagggtt ctaccctagc gacatcgccg tggagtggga gtccaacgga 1200  
caacctgaga acaactacaa gaccaccct cctatgcttg acagcgacgg ctccttcttc 1260  
ctgtacagca agctgaccgt ggacaagtcc cgttggcaac aaggcaacgt gttcagctgt 1320  
tccgtgatgc acgaggccct gcacaaccac tacacccaaa agagcctttc cctgagccct 1380  
ggaaag 1386

<210> 45  
<211> 462  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Heavy chain IgG2 type of human chimeric 2P10F2

<400> 45

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

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

Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile  
35 40 45

Thr Ser Asn Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met  
50 55 60

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

Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln  
85 90 95

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

Tyr Cys Ala Ser Ser Tyr Thr Ser Gly Asp Val Asp Tyr Trp Gly Gln  
115 120 125

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

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala  
145 150 155 160

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
195 200 205

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys  
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val  
225 230 235 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe  
245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
275 280 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
 290 295 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val  
 305 310 315 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
 325 330 335

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
 340 345 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
 355 360 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
 370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
 385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp  
 405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
 420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
 435 440 445

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

<210> 46  
 <211> 1389  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG4P type of human chimeric 2P10F2

<400> 46

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag  | 60   |
| gtgcagcttc aggagtcagg acctggcctt gtgaaacctt cacagtcact ctccctcacc  | 120  |
| tgtttctgtca ctggttactc catcactagt aattactggg gctggatccg gaagttccca | 180  |
| ggaaataaaa tggagtggat gggatgcata acctacagtg gtggcactag ctacaacca   | 240  |
| tctctcaaaa gtcgaatctc cattactaga gacacatcaa agaatacagt cttcctgcag  | 300  |
| ttgaactctg taactactga ggacacagcc acataattact gtgcaagttc ctataccagt | 360  |
| ggtgacgtcg attactgggg ccaaggagtc atggtcacag tcagctcagc ctccaccaag  | 420  |
| ggccctagcg tgttccctct ggccccttgt agcagaagca ccagcgagtc tacagccgcc  | 480  |
| ctgggctgcc tcgtgaagga ctactttccc gagcccgtga ccgtgtcctg gaactctggc  | 540  |
| gctctgacaa gcggcgtgca cacctttcca gccgtgctgc agagcagcgg cctgtactct  | 600  |
| ctgtccagcg tcgtgactgt gcccagcagc tctctgggca ccaagaccta cacctgtaac  | 660  |
| gtggaccaca agcccagcaa caccaagggtg gacaagcggg tggaatctaa gtacggccct | 720  |
| ccctgccctc cttgcccagc ccctgaattt ctgggcggac cctccgtgtt cctgttcccc  | 780  |
| ccaaagccca aggacaccct gatgatcagc cggacccccg aagtgacctg cgtgggtggtg | 840  |
| gatgtgtccc aggaagatcc cgagggtcag ttcaattggt acgtggacgg cgtggaagtg  | 900  |
| cacaacgcca agaccaagcc tagagaggaa cagttcaaca gcacctaccg ggtggtgtcc  | 960  |
| gtgctgacag tgctgcacca ggactggctg aacggcaaag agtacaagtg caaggtgtcc  | 1020 |
| aacaagggcc tgcccagctc catcgagaaa accatcagca aggccaaggg ccagccccgc  | 1080 |
| gaaccccagg tgtacacact gcctccaagc caggaagaga tgaccaagaa tcaggtgtcc  | 1140 |
| ctgacctgtc tcgtgaaagg cttctacccc tccgatatcg ccgtggaatg ggagagcaac  | 1200 |
| ggccagcccc agaacaacta caagaccacc cccctgtgc tggactccga tggctcattc   | 1260 |
| ttcctgtaca gcagactgac cgtggacaag agccggtggc aggaaggcaa cgtgttcagc  | 1320 |
| tgctccgtga tgcacgaggc cctgcacaac cactacacc agaagtcctt gtctctgagc   | 1380 |
| ctgggcaaa                                                          | 1389 |

<210> 47  
 <211> 463  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Heavy chain IgG4P type of human chimeric 2P10F2

<400> 47

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

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

Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile  
35 40 45

Thr Ser Asn Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met  
50 55 60

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

Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln  
85 90 95

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

Tyr Cys Ala Ser Ser Tyr Thr Ser Gly Asp Val Asp Tyr Trp Gly Gln  
115 120 125

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

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala  
145 150 155 160

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
195 200 205

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys  
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro  
225 230 235 240

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val  
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu  
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser  
305 310 315 320

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile  
340 345 350

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
355 360 365

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg  
420 425 430

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
435 440 445

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

<210> 48  
<211> 324  
<212> DNA  
<213> Rattus norvegicus

<400> 48  
gatgtccaga tgaccagtc tccatcttat cttgctgcgt ctcttgagaa aagtgtttcc 60  
atcagttgca aggcaagtaa gagcattagc aataatttag cctgggtatca ggagaaacct 120  
gggaaagcaa ataagcttct tattcactct ggggtcaactt tgcaatctgg aactccatcg 180  
aggttcagtg gcagtggatc tggtagacat ttcacgtca ccatcagaag cctggagttt 240  
gaagattttg cagtctatta ctgtcaacag tataatgaat acccactcac gttcgggttct 300  
gggaccaagc tggagatcaa acgg 324

<210> 49  
<211> 108  
<212> PRT  
<213> Rattus norvegicus

<400> 49

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

Glu Ser Val Ser Ile Ser Cys Lys Ala Ser Lys Ser Ile Ser Asn Asn  
20 25 30

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

His Ser Gly Ser Thr Leu Gln Ser Gly Thr Pro Ser Arg Phe Ser Gly  
 50 55 60

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

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

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

<210> 50  
 <211> 363  
 <212> DNA  
 <213> Rattus norvegicus

<400> 50  
 gaggtgcagc tgggtggagtc tgggggaggc ctagtgcagc ctggaaggct cctgaaactc 60  
 tcctgtgcag cctcaggatt cactttcagt aactattaca tggcctgggt ccgccaggct 120  
 ccaaagaagg gtctggagtg ggtcgcaacc attactacca gtggtagcag accttactat 180  
 ccagactccg tgaaaggccg attcactatc tccagagata atgcaaaaag cagcctatac 240  
 ctgcaaataa acagtctgaa gtctgaggac acggccactt attactgtgc aagacatatt 300  
 tattactatg atggttaccc ctttgcttac tggggccaag gcactctggg cactgtctct 360  
 tca 363

<210> 51  
 <211> 121  
 <212> PRT  
 <213> Rattus norvegicus

<400> 51

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

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

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

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

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

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

Ala Arg His Ile Tyr Tyr Tyr Asp Gly Tyr Pro Phe Ala Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 52  
<211> 11  
<212> PRT  
<213> Rattus norvegicus

<400> 52

Lys Ala Ser Lys Ser Ile Ser Asn Asn Leu Ala  
1 5 10

<210> 53  
<211> 7  
<212> PRT  
<213> Rattus norvegicus

<400> 53

Ser Gly Ser Thr Leu Gln Ser  
1 5

<210> 54  
<211> 9  
<212> PRT  
<213> Rattus norvegicus

<400> 54

Gln Gln Tyr Asn Glu Tyr Pro Leu Thr  
1 5

<210> 55  
<211> 10  
<212> PRT  
<213> Rattus norvegicus

<400> 55

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

<210> 56  
<211> 10  
<212> PRT  
<213> Rattus norvegicus

<400> 56

Thr Ile Thr Thr Ser Gly Ser Arg Pro Tyr  
1 5 10

<210> 57  
<211> 12  
<212> PRT  
<213> Rattus norvegicus

<400> 57

His Ile Tyr Tyr Tyr Asp Gly Tyr Pro Phe Ala Tyr  
1 5 10

<210> 58  
<211> 324  
<212> DNA  
<213> Rattus norvegicus

<400> 58  
gacatccaga tgaccagtc tccttcactc ctgtctgcat ctgtgggagg cagaatcact 60  
ctcaactgca aagcaagtca gaatctctat aagaacttag cctgggtatca gcagaagctt 120  
ggagaagctc ccaaactcct gattgataat gcaaacagtt tgcaaacggg catcccatca 180  
aggttcagtg gcagtggatc tggtagagat ttcacactca ccatcagcag cctgcagcct 240  
gaagatgttg ccacatattt ctgccagcag tattatagcg ggtagtacac gtttggagct 300

gggaccaagc tggaactgaa acgg

324

<210> 59  
<211> 108  
<212> PRT  
<213> Rattus norvegicus

<400> 59

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

Gly Arg Ile Thr Leu Asn Cys Lys Ala Ser Gln Asn Leu Tyr Lys Asn  
20 25 30

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

Asp Asn Ala Asn Ser Leu Gln Thr 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 Gln Pro  
65 70 75 80

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

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

<210> 60  
<211> 354  
<212> DNA  
<213> Rattus norvegicus

<400> 60

gaggtgcagc tgggtggagtc tgatggaggc ttagtgcagc ctggaaggct cctaaaactc 60

tcctgtgcag cctcaggatt cactttcagt gactattaca tggcctgggt ccgccaggct 120

ccaacgaagg ggctggagtg ggtcgcaacc attagttatg atggtagtaa cacttactat 180

cgagactccg tgaagggccg attcactatc tccagagata atgcaaaaag caccctatac 240

ctgcaaatgg acagtctgag gtctggggac acggccactt attactgtgc aagattttac 300

aacaactact acttttgatta ctggggccaa ggagtcatgg tcacagtctc ctca

354

<210> 61  
<211> 118  
<212> PRT  
<213> Rattus norvegicus

<400> 61

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr  
20 25 30

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

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

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

Leu Gln Met Asp Ser Leu Arg Ser Gly Asp Thr Ala Thr Tyr Tyr Cys  
85 90 95

Ala Arg Phe Tyr Asn Asn Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Val  
100 105 110

Met Val Thr Val Ser Ser  
115

<210> 62  
<211> 11  
<212> PRT  
<213> Rattus norvegicus

<400> 62

Lys Ala Ser Gln Asn Leu Tyr Lys Asn Leu Ala  
1 5 10

<210> 63  
<211> 7  
<212> PRT  
<213> Rattus norvegicus

<400> 63

Asn Ala Asn Ser Leu Gln Thr  
1 5

<210> 64  
<211> 9  
<212> PRT  
<213> Rattus norvegicus

<400> 64

Gln Gln Tyr Tyr Ser Gly Ser Tyr Thr  
1 5

<210> 65  
<211> 10  
<212> PRT  
<213> Rattus norvegicus

<400> 65

Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ala  
1 5 10

<210> 66  
<211> 10  
<212> PRT  
<213> Rattus norvegicus

<400> 66

Thr Ile Ser Tyr Asp Gly Ser Asn Thr Tyr  
1 5 10

<210> 67  
<211> 9  
<212> PRT  
<213> Rattus norvegicus

<400> 67

Phe Tyr Asn Asn Tyr Tyr Phe Asp Tyr

1

5

<210> 68  
 <211> 324  
 <212> DNA  
 <213> Rattus norvegicus

<400> 68  
 gacatccaga tgaccagac tccatcctcc atgcctgcat ctctgggaga gagagtcacc 60  
 atcagttgca gagcaagtca gggattatgc aattatctaa actggtatca gcagaaacca 120  
 gatggaacga ttaaaccct gatctactac acatccaatt tacaatctgg tgtcccatca 180  
 aggttcagtg gcagtgggtc tgggacagat tattctctca ccatcagcag cctggagcct 240  
 gaagattttg caatgtattt ctgccaacag tatgatagtt ctctcggac gttcgggtgga 300  
 ggcaccaagc tggaattgaa acgg 324

<210> 69  
 <211> 108  
 <212> PRT  
 <213> Rattus norvegicus

<400> 69

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

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

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

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

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

Glu Asp Phe Ala Met Tyr Phe Cys Gln Gln Tyr Asp Ser Ser Pro Arg  
 85 90 95

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

<210> 70  
 <211> 351  
 <212> DNA  
 <213> Rattus norvegicus

<400> 70  
 cagggtacagc tgcagcaatc tggggctgaa ctggtgaagc ctgggtcctc agtgaaaatt 60  
 tcctgcaagg cttctggcta caccttcacc agtgacttta tgcactggat aaaacagcag 120  
 cctggaaatg gccttgagtg gattgggtgg atttatcctg gagatgggtga tacagagtac 180  
 aatcaaaagt tcaatgggaa ggcaacactc actgcagaca aatcctccag cacagcctat 240  
 atgcagctca gcagcctgac atctgaggac tctgcagtct atttctgtgc aaggggacgg 300  
 gggatatgtta tggatgcctg gggtaagga gcttcagtca ctgtctcctc a . 351

<210> 71  
 <211> 117  
 <212> PRT  
 <213> Rattus norvegicus

<400> 71  
 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Asp  
 20 25 30  
 Phe Met His Trp Ile Lys Gln Gln Pro Gly Asn Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Trp Ile Tyr Pro Gly Asp Gly Asp Thr Glu Tyr Asn Gln Lys Phe  
 50 55 60  
 Asn 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

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

Val Thr Val Ser Ser  
 115

<210> 72  
 <211> 11  
 <212> PRT  
 <213> Rattus norvegicus

<400> 72

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Asn  
 1 5 10

<210> 73  
 <211> 7  
 <212> PRT  
 <213> Rattus norvegicus

<400> 73

Tyr Thr Ser Asn Leu Gln Ser  
 1 5

<210> 74  
 <211> 9  
 <212> PRT  
 <213> Rattus norvegicus

<400> 74

Gln Gln Tyr Asp Ser Ser Pro Arg Thr  
 1 5

<210> 75  
 <211> 10  
 <212> PRT  
 <213> Rattus norvegicus

<400> 75

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

<210> 76  
 <211> 10  
 <212> PRT  
 <213> Rattus norvegicus

<400> 76

Trp Ile Tyr Pro Gly Asp Gly Asp Thr Glu  
 1 5 10

<210> 77  
 <211> 8  
 <212> PRT  
 <213> Rattus norvegicus

<400> 77

Gly Arg Gly Tyr Val Met Asp Ala  
 1 5

<210> 78  
 <211> 324  
 <212> DNA  
 <213> Rattus norvegicus

<400> 78

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gatgtccaga tgaccagtc tccatcttat cttgctgcgt ctcctggaga aagtgtttcc   | 60  |
| atcagttgca aggcaagtaa aagcattaac acatacttag cctgggtatca ggagaaacct | 120 |
| gggaaaacga ataagcttct tatctactct ggggtcaactt tgcaatctgg aactccatcg | 180 |
| agattcagtg gcagtggatc tgggtacagat ttcacgctca ccatcagaag cctggagcct | 240 |
| gaagattttg cagtctacta ctgtcaacag cataatgaat accccttcac gttcggtca   | 300 |
| gggacgaagt tggaaataaa acgg                                         | 324 |

<210> 79  
 <211> 108  
 <212> PRT  
 <213> Rattus norvegicus

<400> 79

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

Glu Ser Val Ser Ile Ser Cys Lys Ala Ser Lys Ser Ile Asn Thr 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 | Thr | Pro | Ser | Arg | Phe | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Arg | Ser | Leu | Glu | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Asp | Phe | Ala | Val | Tyr | Tyr | Cys | Gln | Gln | His | Asn | Glu | Tyr | Pro | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Gly | Ser | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg |     |     |     |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |     |

<210> 80  
 <211> 357  
 <212> DNA  
 <213> Rattus norvegicus

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 80                                                           |     |
| gaggtgcagc tgggtggagtc tgggggaggc ctagtgcagc ctggaaggtc tctgaaacta | 60  |
| tcctgtggag cctctggatt cacattcaat aactactgga tgacctgggt ccgccaggct  | 120 |
| ccaggggaagg ggctggagtg ggttgcattc attactaaag ctggtggtag cacttactat | 180 |
| cgagactctg tgaagggccg attcactatc tccagagata atgcaaaaag caccctatat  | 240 |
| ctgcaaatga acagtctgag gtctgaggac acggccactt attactgtac aagagaactg  | 300 |
| ggagagttct atgttatgga tgcctggggc caaggagctt cagtcactgt ctcctca     | 357 |

<210> 81  
 <211> 119  
 <212> PRT  
 <213> Rattus norvegicus

|                                                                 |    |
|-----------------------------------------------------------------|----|
| <400> 81                                                        |    |
| Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg |    |
| 1                                                               | 15 |
|                                                                 | 5  |
|                                                                 | 10 |

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

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

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

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

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

Thr Arg Glu Leu Gly Glu Phe Tyr Val Met Asp Ala Trp Gly Gln Gly  
100 105 110

Ala Ser Val Thr Val Ser Ser  
115

<210> 82  
<211> 11  
<212> PRT  
<213> Rattus norvegicus

<400> 82

Lys Ala Ser Lys Ser Ile Asn Thr Tyr Leu Ala  
1 5 10

<210> 83  
<211> 7  
<212> PRT  
<213> Rattus norvegicus

<400> 83

Ser Gly Ser Thr Leu Gln Ser  
1 5

<210> 84  
<211> 9  
<212> PRT

<213> Rattus norvegicus

<400> 84

Gln Gln His Asn Glu Tyr Pro Phe Thr  
1 5

<210> 85

<211> 10

<212> PRT

<213> Rattus norvegicus

<400> 85

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

<210> 86

<211> 10

<212> PRT

<213> Rattus norvegicus

<400> 86

Ser Ile Thr Lys Ala Gly Gly Ser Thr Tyr  
1 5 10

<210> 87

<211> 10

<212> PRT

<213> Rattus norvegicus

<400> 87

Glu Leu Gly Glu Phe Tyr Val Met Asp Ala  
1 5 10

<210> 88

<211> 1117

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA comprising DNA sequence coding for amino acid of human heavy chain signal sequence and human IgG4PFALA constant region

<400> 88

ccagcctccg gactctagag ccaccatgaa acacctgtgg ttcttcctcc tgctggtggc 60

|                                                                    |      |
|--------------------------------------------------------------------|------|
| agctcccaga tgggtgctga gccaggtgca attgtgcagg cggttagctc agcctccacc  | 120  |
| aagggcccta gcgtgttccc tctggcccct tgtagcagaa gcaccagcga gtctacagcc  | 180  |
| gccctgggct gcctcgtgaa ggactacttt cccgagcccg tgaccgtgtc ctggaactct  | 240  |
| ggcgctctga caagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac  | 300  |
| tctctgtcca gcgtcgtgac tgtgcccagc agctctcttg gcaccaagac ctacacctgt  | 360  |
| aacgtggacc acaagcccag caacaccaag gtggacaagc gggtggaatc taagtacggc  | 420  |
| cctccctgcc ctcttgccc agcccctgaa gccgcgggcg gaccctccgt gttcctgttc   | 480  |
| cccccaaagc ccaaggacac cctgatgatc agccggaccc ccgaagtgac ctgcgtgggtg | 540  |
| gtggatgtgt cccaggaaga tcccagggtg cagttcaatt ggtacgtgga cggcgtggaa  | 600  |
| gtgcacaacg ccaagaccaa gcctagagag gaacagttca acagcaccta ccgggtgggtg | 660  |
| tccgtgctga cagtgtgca ccaggactgg ctgaacggca aagagtacaa gtgcaagggtg  | 720  |
| tccaacaagg gcctgcccag ctccatcgag aaaaccatca gcaaggccaa gggccagccc  | 780  |
| cgcgaacccc aggtgtacac actgcctcca agccaggaag agatgaccaa gaatcaggtg  | 840  |
| tccctgacct gtctcgtgaa aggcttctac cctccgata tcgccgtgga atgggagagc   | 900  |
| aacggccagc ccgagaacaa ctacaagacc acccccttg tgctggactc cgatggctca   | 960  |
| ttcttctgt acagcagact gaccgtggac aagagccggt ggcaggaagg caacgtgttc   | 1020 |
| agctgctccg tgatgcacga ggcctgcac aaccactaca ccagaagtc cctgtctctg    | 1080 |
| agcctgggca aatgagttta aacgggggag gctaact                           | 1117 |

<210> 89

<211> 702

<212> DNA

<213> Artificial Sequence

<220>

<223> Light chain of human chimeric rat\_CD147\_#84

<400> 89

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc  | 60  |
| gatgtccaga tgaccagtc tccatcttat cttgctgcgt ctcttgaga aagtgtttcc   | 120 |
| atcagttgca aggcaagtaa gagcattagc aataatttag cctggtatca ggagaaacct | 180 |
| gggaaagcaa ataagcttct tattcactct gggtaactt tgcaatctgg aactccatcg  | 240 |

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aggttcagtg gcagtggatc tggtagatg ttcacgctca ccatcagaag cctggagttt      300
gaagattttg cagtctatta ctgtcaacag tataatgaat acccactcac gttcggttct      360
gggaccaagc tggagatcaa acggacgggtg gccgccccct ccgtgttcat cttccccccc      420
tccgacgagc agctgaagtc cggcaccgcc tccgtgggtg gcctgctgaa taacttttac      480
cccagagagg ccaagggtgca gtggaagggtg gacaacgccc tgcagtccgg gaactcccag      540
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc      600
ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc      660
ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt                          702

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<210> 90
<211> 234
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Light chain of human chimeric rat_CD147_#84

```

```

<400> 90

```

```

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

```

```

Gly Ala Tyr Gly Asp Val Gln Met Thr Gln Ser Pro Ser Tyr Leu Ala
20          25          30

```

```

Ala Ser Pro Gly Glu Ser Val Ser Ile Ser Cys Lys Ala Ser Lys Ser
35          40          45

```

```

Ile Ser Asn Asn Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Asn
50          55          60

```

```

Lys Leu Leu Ile His Ser Gly Ser Thr Leu Gln Ser Gly Thr Pro Ser
65          70          75          80

```

```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg
85          90          95

```

```

Ser Leu Glu Phe Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn

```

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 100                                                             | 105 | 110 |
| Glu Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg |     |     |
| 115                                                             | 120 | 125 |
| Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln |     |     |
| 130                                                             | 135 | 140 |
| Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr |     |     |
| 145                                                             | 150 | 155 |
| Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser |     |     |
| 165                                                             | 170 | 175 |
| Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr |     |     |
| 180                                                             | 185 | 190 |
| Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys |     |     |
| 195                                                             | 200 | 205 |
| His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro |     |     |
| 210                                                             | 215 | 220 |
| Val Thr Lys Ser Phe Asn Arg Gly Glu Cys                         |     |     |
| 225                                                             | 230 |     |

<210> 91  
 <211> 1410  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG1 type of human chimeric rat\_CD147\_#84

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 91                                                          |     |
| atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag | 60  |
| gtgcagctgg tggagtctgg gggaggccta gtgcagcctg gaaggctcct gaaactctcc | 120 |
| tgtgcagcct caggattcac tttcagtaac tattacatgg cctgggtccg ccaggctcca | 180 |
| aagaagggtc tggagtgggt cgcaaccatt actaccagtg gtagcagacc ttactatcca | 240 |
| gactccgtga aaggccgatt cactatctcc agagataatg caaaaagcag cctatacctg | 300 |

```

caaatgaaca gtctgaagtc tgaggacacg gccacttatt actgtgcaag acatatttat      360
tactatgatg gttacccctt tgcttactgg ggccaaggca ctctggtcac tgtcagctca      420
gcctccacca agggcccaag cgtcttcccc ctggcaccct cctccaagag cacctctggc      480
ggcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccctg gaccgtgagc      540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc ccgctgtcct gcagtcctca      600
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc      720
aaatcttgtg aaaaaactca cacatgccc cctgcccag cacctgaact cctggggggga      780
ccctcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct      840
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cccgggagga gcagtacaac      960
agcacgtacc ggggtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag     1020
gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1080
aaagccaaag gccagccccg ggaaccacag gtgtacaccc tgccccatc ccgggaggag     1140
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc     1200
gccgtggagt gggagagcaa tggccagccc gagaacaact acaagaccac ccctcccgtg     1260
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg     1320
cagcagggca acgtcttctc atgtccgtg atgcatgagg ctctgcacaa ccactacacc     1380
cagaagagcc tctccctgtc tcccggcaaa                                     1410

```

```

<210> 92
<211> 470
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Heavy chain IgG1 type of human chimeric rat_CD147_#84

```

```

<400> 92

```

```

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1           5           10           15

```

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Ser Asn Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Lys Lys Gly Leu  
50 55 60

Glu Trp Val Ala Thr Ile Thr Thr Ser Gly Ser Arg Pro Tyr Tyr Pro  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser  
85 90 95

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

Tyr Tyr Cys Ala Arg His Ile Tyr Tyr Tyr Asp Gly Tyr Pro Phe Ala  
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

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

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro  
 225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
 245 250 255

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 275 280 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
 305 310 315 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
 355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 420 425 430

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

435

440

445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 450 455 460

Ser Leu Ser Pro Gly Lys  
 465 470

<210> 93  
 <211> 1398  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG2 type of human chimeric rat\_CD147\_#84

<400> 93  
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag 60  
 gtgcagctgg tggagcttgg gggaggccta gtgcagcctg gaaggctcct gaaactctcc 120  
 tgtgcagcct caggattcac tttcagtaac tattacatgg cctgggtccg ccaggctcca 180  
 aagaagggtc tggagtgggt cgcaaccatt actaccagtg gtagcagacc ttactatcca 240  
 gactccgtga aaggccgatt cactatctcc agagataatg caaaaagcag cctatacctg 300  
 caaatgaaca gtctgaagtc tgaggacacg gccacttatt actgtgcaag acatatttat 360  
 tactatgatg gttacccctt tgcttactgg ggccaaggca ctctggtcac tgtcagctca 420  
 gcctccacca agggcccttc cgtgttcctt ctggcccctt gtagccgttc caccagcgag 480  
 tccaccgccg cccttgggtg tctggtgaag gactacttcc ctgagcctgt gaccgtgagc 540  
 tggaactccg gagcccttac cagcggcgtg cacaccttcc ctgccgtgct gcagtccagc 600  
 ggcctttact ccctgagctc cgtgggtgacc gtgcctagct ccaacttcgg cacccaaacc 660  
 tacacctgta acgtggacca caagcctagc aacaccaagg tggacaagac cgtggagcgt 720  
 aagtgttggtg tggagtgtcc tccttgtcct gccctcctg tggccggacc ttccgtgttc 780  
 cttttccctc ctaagcctaa ggacaccctg atgatcagcc gtaccctga ggtgacctgt 840  
 gtggtggtgg acgtgtccca cgaggaccct gaggtgcagt tcaactggta cgtggacggc 900  
 gtggaggtgc acaacgcca gaccaagcct cgtgaggagc aattcaacag caccttccgt 960  
 gtggtgtccg tgcttaccgt ggtgcaccaa gactggctga acggcaagga gtacaagtgt 1020

aaggtgagca acaagggact tcctgcccct atcgagaaga ccattctcaa gaccaagggc 1080  
caacctcgtg agcctcaagt gtacaccctt cctcctagcc gtgaggagat gaccaagaac 1140  
caagtgtccc ttacctgtct ggtgaagggc ttctacccta gcgacatcgc cgtggagtgg 1200  
gagtccaacg gacaacctga gaacaactac aagaccaccc ctcctatgct tgacagcgac 1260  
ggctccttct tcctgtacag caagctgacc gtggacaagt cccgttggca acaaggcaac 1320  
gtgttcagct gttccgtgat gcacgaggcc ctgcacaacc actacacca aaagagcctt 1380  
tccttgagcc ctggaaaag 1398

<210> 94  
<211> 466  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Heavy chain IgG2 type of human chimeric rat\_CD147\_#84

<400> 94

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Ser Asn Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Lys Lys Gly Leu  
50 55 60

Glu Trp Val Ala Thr Ile Thr Thr Ser Gly Ser Arg Pro Tyr Tyr Pro  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser  
85 90 95

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

Tyr Tyr Cys Ala Arg His Ile Tyr Tyr Tyr Asp Gly Tyr Pro Phe Ala  
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn  
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg  
225 230 235 240

Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly  
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
275 280 285

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg  
305 310 315 320

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys  
 325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu  
 340 345 350

Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
 355 360 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
 370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
 385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met  
 405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
 420 425 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
 435 440 445

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

Gly Lys  
 465

<210> 95  
 <211> 1401  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG4P type of human chimeric rat\_CD147\_#84

<400> 95  
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag 60  
 gtgcagctgg tggagtctgg gggaggccta gtgcagcctg gaaggtccct gaaactctcc 120

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tgtgcagcct caggattcac tttcagtaac tattacatgg cctgggtccg ccaggctcca  | 180  |
| aagaagggtc tggagtgggt cgcaaccatt actaccagtg gtagcagacc ttactatcca  | 240  |
| gactccgtga aaggccgatt cactatctcc agagataatg caaaaagcag cctataacctg | 300  |
| caaatgaaca gtctgaagtc tgaggacacg gccacttatt actgtgcaag acatatttat  | 360  |
| tactatgatg gttacccctt tgcttactgg ggccaaggca ctctggtcac tgtcagctca  | 420  |
| gcctccacca agggccctag cgtgttcctt ctggccccctt gtagcagaag caccagcgag | 480  |
| tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc  | 540  |
| tggaactctg gcgctctgac aagcggcgtg cacacctttc cagccgtgct gcagagcagc  | 600  |
| ggcctgtact ctctgtccag cgtcgtgact gtgcccagca gctctctggg caccaagacc  | 660  |
| tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct  | 720  |
| aagtacggcc ctccctgccc tccttgccca gcccctgaat ttctgggagg accctccgtg  | 780  |
| ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc  | 840  |
| tgcgtggtgg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac  | 900  |
| ggcgtggaag tgcacaacgc caagaccaag cctagagagg aacagttcaa cagcacctac  | 960  |
| cgggtggtgt ccgtgctgac agtgctgcac caggactggc tgaacggcaa agagtacaag  | 1020 |
| tgcaaggtgt ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag  | 1080 |
| ggccagcccc gcgaaccca ggtgtacaca ctgcctccaa gccaggaaga gatgaccaag   | 1140 |
| aatcaggtgt ccctgacctg tctcgtgaaa ggcttctacc cctccgatat cgccgtggaa  | 1200 |
| tgggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggactcc   | 1260 |
| gatggctcat tcttctgta cagcagactg accgtggaca agagccggtg gcaggaaggc   | 1320 |
| aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc  | 1380 |
| ctgtctctga gcctgggcaa a                                            | 1401 |

<210> 96  
 <211> 467  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG4P type of human chimeric rat\_CD147\_#84

<400> 96

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Ser Asn Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Lys Lys Gly Leu  
50 55 60

Glu Trp Val Ala Thr Ile Thr Thr Ser Gly Ser Arg Pro Tyr Tyr Pro  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser  
85 90 95

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

Tyr Tyr Cys Ala Arg His Ile Tyr Tyr Tyr Asp Gly Tyr Pro Phe Ala  
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
 210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
 225 230 235 240

Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
 275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
450 455 460

Leu Gly Lys  
465

<210> 97  
<211> 1410  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Heavy chain IgG1LALA type of human chimeric rat\_CD147\_#84

<400> 97  
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag 60  
gtgcagctgg tggagtctgg gggaggccta gtgcagcctg gaaggctcct gaaactctcc 120  
tgtgcagcct caggattcac tttcagtaac tattacatgg cctgggtccg ccaggctcca 180  
aagaagggtc tggagtgggt cgcaaccatt actaccagtg gtagcagacc ttactatcca 240  
gactccgtga aaggccgatt cactatctcc agagataatg caaaaagcag cctatacctg 300  
caaatgaaca gtctgaagtc tgaggacacg gccacttatt actgtgcaag acatatttat 360  
tactatgatg gttacccctt tgcttactgg ggccaaggca ctctggtcac tgtcagctca 420  
gcctccacca agggcccaag cgtcttcccc ctggcaccct cctccaagag cacctctggc 480  
ggcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccgt gaccgtgagc 540  
tggaactcag gcgccctgac cagcggcgtg cacaccttcc ccgctgtcct gcagtcctca 600  
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 720  
aaatcttgtg aaaaaactca cacatgcccc ccctgcccag cacctgaagc cgcgggggga 780  
ccctcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840

gaggtcacat gcgtgggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900  
 tacgtggacg gcgtgggaggt gcataatgcc aagacaaagc cccgggagga gcagtacaac 960  
 agcacgtacc ggggtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020  
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080  
 aaagccaaag gccagccccg ggaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
 atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1200  
 gccgtggagt gggagagcaa tggccagccc gagaacaact acaagaccac ccctcccgtg 1260  
 ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1320  
 cagcagggca acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacc 1380  
 cagaagagcc tctccctgtc tcccggcaaa 1410

<210> 98

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain IgG1LALA type of human chimeric rat\_CD147\_#84

<400> 98

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
 20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 35 40 45

Ser Asn Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Lys Lys Gly Leu  
 50 55 60

Glu Trp Val Ala Thr Ile Thr Thr Ser Gly Ser Arg Pro Tyr Tyr Pro  
 65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser  
 85 90 95

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

Tyr Tyr Cys Ala Arg His Ile Tyr Tyr Tyr Asp Gly Tyr Pro Phe Ala  
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

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

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro  
225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
245 250 255

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
275 280 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
305 310 315 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
450 455 460

Ser Leu Ser Pro Gly Lys  
465 470

<210> 99

<211> 1401

<212> DNA

<213> Artificial Sequence

<220>

<223> Heavy chain IgG4PFALA type of human chimeric rat\_CD147\_#84

<400> 99  
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag 60  
gtgcagctgg tggagtctgg gggaggccta gtgcagcctg gaaggctcct gaaactctcc 120  
tgtgcagcct caggattcac tttagtaac tattacatgg cctgggtccg ccaggctcca 180  
aagaagggtc tggagtgggt cgcaaccatt actaccagtg gtagcagacc ttactatcca 240  
gactccgtga aaggccgatt cactatctcc agagataatg caaaaagcag cctatacctg 300  
caaatgaaca gtctgaagtc tgaggacacg gccacttatt actgtgcaag acatatttat 360  
tactatgatg gttacccctt tgcttactgg ggccaaggca ctctggtcac tgtcagctca 420  
gcctccacca agggccctag cgtgttcct ctggcccctt gtagcagaag caccagcgag 480  
tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 540  
tggaactctg gcgctctgac aagcggcgtg cacacctttc cagccgtgct gcagagcagc 600  
ggcctgtact ctctgtccag cgtcgtgact gtgcccagca gctctctggg caccaagacc 660  
tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 720  
aagtacggcc ctccctgccc tccttgcca gccctgaag ccgcgggcgg accctccgtg 780  
ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 840  
tgcgtggtgg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac 900  
ggcgtggaag tgcacaacgc caagaccaag cctagagagg aacagttcaa cagcacctac 960  
cgggtggtgt ccgtgctgac agtgctgcac caggactggc tgaacggcaa agagtacaag 1020  
tgcaaggtgt ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag 1080  
ggccagcccc gcgaaccca ggtgtacaca ctgcctccaa gccaggaaga gatgaccaag 1140  
aatcaggtgt ccctgacctg tctcgtgaaa ggcttctacc cctccgatat cgccgtggaa 1200  
tgggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggactcc 1260  
gatggctcat tcttctgta cagcagactg accgtggaca agagccggtg gcaggaaggc 1320  
aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1380  
ctgtctctga gcctgggcaa a 1401

<210> 100  
<211> 467  
<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain IgG4PFALA type of human chimeric rat\_CD147\_#84

<400> 100

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Ser Asn Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Lys Lys Gly Leu  
50 55 60

Glu Trp Val Ala Thr Ile Thr Thr Ser Gly Ser Arg Pro Tyr Tyr Pro  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser  
85 90 95

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

Tyr Tyr Cys Ala Arg His Ile Tyr Tyr Tyr Asp Gly Tyr Pro Phe Ala  
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
225 230 235 240

Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly  
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
 420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Leu Gly Lys  
 465

<210> 101  
 <211> 702  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Light chain of human chimeric rat\_CD147\_#101

<400> 101  
 atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60  
 gacatccaga tgaccagtc tccttcactc ctgtctgcat ctgtgggagg cagaatcact 120  
 ctcaactgca aagcaagtca gaatctctat aagaacttag cctggatatca gcagaagctt 180  
 ggagaagctc ccaaactcct gattgataat gcaaacagtt tgcaaacggg catcccatca 240  
 aggttcagtg gcagtggatc tggtagatc ttacactca ccatcagcag cctgcagcct 300  
 gaagatgttg ccacatattt ctgccagcag tattatagcg ggtcgtacac gtttggagct 360  
 gggaccaagc tggaactgaa acggacgggtg gccgccccct ccgtgttcat cttccccccc 420  
 tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480  
 cccagagagg ccaaggtgca gtggaagggtg gacaacgccc tgtagtccgg gaactccag 540  
 gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600  
 ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660  
 ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt 702

<210> 102  
<211> 234  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Light chain of human chimeric rat\_CD147\_#101

<400> 102

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

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

Ala Ser Val Gly Gly Arg Ile Thr Leu Asn Cys Lys Ala Ser Gln Asn  
35 40 45

Leu Tyr Lys Asn Leu Ala Trp Tyr Gln Gln Lys Leu Gly Glu Ala Pro  
50 55 60

Lys Leu Leu Ile Asp Asn Ala Asn Ser Leu Gln Thr Gly Ile Pro Ser  
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
85 90 95

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

Ser Gly Ser Tyr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg  
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser

|                                                                 |     |  |     |  |     |
|-----------------------------------------------------------------|-----|--|-----|--|-----|
|                                                                 | 165 |  | 170 |  | 175 |
| Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr |     |  |     |  |     |
|                                                                 | 180 |  | 185 |  | 190 |
| Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys |     |  |     |  |     |
|                                                                 | 195 |  | 200 |  | 205 |
| His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro |     |  |     |  |     |
|                                                                 | 210 |  | 215 |  | 220 |
| Val Thr Lys Ser Phe Asn Arg Gly Glu Cys                         |     |  |     |  |     |
|                                                                 | 225 |  | 230 |  |     |

<210> 103  
 <211> 1389  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG2 of human chimeric rat\_CD147\_#101

<400> 103  
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag 60  
 gtgcagctgg tggagtctga tggaggctta gtgcagcctg gaaggtcctt aaaactctcc 120  
 tgtgcagcct caggattcac tttcagtac tattacatgg cctgggtccg ccaggctcca 180  
 acgaaggggc tggagtgggt cgcaaccatt agttatgatg gtagtaacac ttactatcga 240  
 gactccgtga agggccgatt cactatctcc agagataatg caaaaagcac cctatacctg 300  
 caaatggaca gtctgaggtc tggggacacg gccacttatt actgtgcaag attttacaac 360  
 aactactact ttgattactg gggccaagga gtcattgtca cagtcagctc agcctccacc 420  
 aagggccctt ccgtgttccc tctggcccct ttagaccgtt ccaccagcga gtccaccgcc 480  
 gcccttggct gtctggtgaa ggactacttc cctgagcctg tgaccgtgag ctggaactcc 540  
 ggagccctta ccagcggcgt gcacaccttc cctgccgtgc tgcagtccag cggcctttac 600  
 tccctgagct ccgtggtgac cgtgcctagc tccaacttcg gcacccaaac ctacacctgt 660  
 aacgtggacc acaagcctag caacaccaag gtggacaaga ccgtggagcg taagtgttgt 720  
 gtggagtgtc ctccttgtcc tgcccctcct gtggccggac cttccgtgtt ccttttccct 780

cctaagccta aggacaccct gatgatcagc cgtacccttg aggtgacctg tgtggtggtg 840  
 gacgtgtccc acgaggaccc tgaggtgcag ttcaactggt acgtggacgg cgtggagggtg 900  
 cacaacgcca agaccaagcc tcgtgaggag caattcaaca gcaccttccg tgtggtgtcc 960  
 gtgcttaccg tgggtgcacca agactggctg aacggcaagg agtacaagtg taaggtagc 1020  
 aacaagggac ttctgcccc tatcgagaag accatctcca agaccaaggg ccaacctcgt 1080  
 gagcctcaag tgtacaccct tcctcctagc cgtgaggaga tgaccaagaa ccaagtgtcc 1140  
 cttacctgtc tgggtgaaggg cttctaccct agcgacatcg ccgtggagtg ggagtccaac 1200  
 ggacaacctg agaacaacta caagaccacc cctcctatgc ttgacagcga cggctccttc 1260  
 ttctgttaca gcaagctgac cgtggacaag tcccgttggc aacaaggcaa cgtgttcagc 1320  
 tgttccgtga tgcacgaggc cctgcacaac cactacaccc aaaagagcct ttccctgagc 1380  
 cctggaaag 1389

<210> 104

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain IgG2 of human chimeric rat\_CD147\_#101

<400> 104

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Asp Gly Gly Leu Val Gln  
 20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 35 40 45

Ser Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Thr Lys Gly Leu  
 50 55 60

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

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser  
85 90 95

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

Tyr Tyr Cys Ala Arg Phe Tyr Asn Asn Tyr Tyr Phe Asp Tyr Trp Gly  
115 120 125

Gln Gly Val Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala  
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
195 200 205

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His  
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys  
225 230 235 240

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val  
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu  
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
 290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser  
 305 310 315 320

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
 325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile  
 340 345 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
 370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
 385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser  
 405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg  
 420 425 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
 435 440 445

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

<210> 105

<211> 1392

<212> DNA

<213> Artificial Sequence

<220>

<223> Heavy chain IgG4P of human chimeric rat\_CD147\_#101

<400> 105

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag  | 60   |
| gtgcagctgg tggagtctga tggaggctta gtgcagcctg gaaggctcct aaaactctcc  | 120  |
| tgtgcagcct caggattcac tttcagtga c tattacatgg cctgggtccg ccaggctcca | 180  |
| acgaaggggc tggagtgggt cgcaaccatt agttatgatg gtagtaacac ttactatcga  | 240  |
| gactccgtga agggccgatt cactatctcc agagataatg caaaaagcac cctatacctg  | 300  |
| caaatggaca gtctgaggtc tggggacacg gccacttatt actgtgcaag attttacaac  | 360  |
| aactactact ttgattactg gggccaagga gtcattgtca cagtcagctc agcctccacc  | 420  |
| aagggcccta gcgtgttccc tctggcccct tgtagcagaa gcaccagcga gtctacagcc  | 480  |
| gccctgggct gcctcgtgaa ggactacttt cccgagcccg tgaccgtgtc ctggaactct  | 540  |
| ggcgctctga caagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac  | 600  |
| tctctgtcca gcgtcgtgac tgtgcccagc agctctctgg gcaccaagac ctacacctgt  | 660  |
| aacgtggacc acaagcccag caacaccaag gtggacaagc ggggtggaatc taagtacggc | 720  |
| cctccctgcc ctccctgccc agcccctgaa tttctgggcg gaccctccgt gttcctgttc  | 780  |
| ccccaaaagc ccaaggacac cctgatgatc agccggaccc ccgaagtga cctgcgtggtg  | 840  |
| gtggatgtgt cccaggaaga tcccagggtg cagttcaatt ggtacgtgga cggcgtggaa  | 900  |
| gtgcacaacg ccaagaccaa gcctagagag gaacagttca acagcaccta ccgggtggtg  | 960  |
| tccgtgctga cagtgtgca ccaggactgg ctgaacggca aagagtacaa gtgcaagggtg  | 1020 |
| tccaacaagg gcctgcccag ctccatcgag aaaaccatca gcaaggccaa gggccagccc  | 1080 |
| cgcgaacccc aggtgtacac actgcctcca agccaggaag agatgaccaa gaatcagggtg | 1140 |
| tccctgacct gtctcgtgaa aggcttctac ccctccgata tcgccgtgga atgggagagc  | 1200 |
| aacggccagc ccgagaacaa ctacaagacc accccctg tgctggactc cgatggctca    | 1260 |
| tttttctgt acagcagact gaccgtggac aagagccggt ggcaggaagg caacgtgttc   | 1320 |
| agctgctccg tgatgcacga ggccctgcac aaccactaca ccagaagtc cctgtctctg   | 1380 |
| agcctgggca aa                                                      | 1392 |

<210> 106

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain IgG4P of human chimeric rat\_CD147\_#101

<400> 106

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Asp Gly Gly Leu Val Gln  
20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Ser Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Thr Lys Gly Leu  
50 55 60

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

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser  
85 90 95

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

Tyr Tyr Cys Ala Arg Phe Tyr Asn Asn Tyr Tyr Phe Asp Tyr Trp Gly  
115 120 125

Gln Gly Val Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala  
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
195 200 205

Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His  
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly  
225 230 235 240

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe 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 Gln Glu Asp Pro  
275 280 285

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
290 295 300

Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys Ser  
420 425 430

Arg Trp Gln Glu 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 Leu Gly Lys  
450 455 460

<210> 107

<211> 1392

<212> DNA

<213> Artificial Sequence

<220>

<223> Heavy chain IgG4PFALA of human chimeric rat\_CD147\_#101

<400> 107

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag  | 60  |
| gtgcagctgg tggagtctga tggaggctta gtgcagcctg gaaggctcct aaaactctcc  | 120 |
| tgtgcagcct caggattcac tttcagtac tattacatgg cctgggtccg ccaggctcca   | 180 |
| acgaaggggc tggagtgggt cgcaaccatt agttatgatg gtagtaacac ttactatcga  | 240 |
| gactccgtga agggccgatt cactatctcc agagataatg caaaaagcac cctatacctg  | 300 |
| caaatggaca gtctgaggtc tggggacacg gccacttatt actgtgcaag attttacaac  | 360 |
| aactactact ttgattactg gggccaagga gtcattgtca cagtcagctc agcctccacc  | 420 |
| aagggcccta gcgtgttccc tctggcccct ttagcagaa gcaccagcga gtctacagcc   | 480 |
| gccctgggct gcctcgtgaa ggactacttt cccgagcccg tgaccgtgtc ctggaactct  | 540 |
| ggcgctctga caagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac  | 600 |
| tctctgtcca gcgtcgtgac tgtgcccagc agctctctgg gcaccaagac ctacacctgt  | 660 |
| aacgtggacc acaagcccag caacaccaag gtggacaagc ggggtggaatc taagtacggc | 720 |
| cctccctgcc ctcttgccc agcccctgaa gccgcgggag gaccctccgt gttcctgttc   | 780 |
| ccccaaagc ccaaggacac cctgatgatc agccggaccc ccgaagtgc ctgcgtgggtg   | 840 |

gtggatgtgt cccaggaaga tcccgagggtg cagttcaatt ggtacgtgga cggcgtggaa 900  
 gtgcacaacg ccaagaccaa gcctagagag gaacagttca acagcaccta ccgggtgggtg 960  
 tccgtgctga cagtgtctgca ccaggactgg ctgaacggca aagagtacaa gtgcaagggtg 1020  
 tccaacaagg gcctgcccag ctccatcgag aaaaccatca gcaaggccaa gggccagccc 1080  
 cgcgaacccc aggtgtacac actgcctcca agccaggaag agatgaccaa gaatcaggtg 1140  
 tccctgacct gtctcgtgaa aggcttctac ccctccgata tcgccgtgga atgggagagc 1200  
 aacggccagc ccgagaacaa ctacaagacc accccccctg tgctggactc cgatgggtca 1260  
 ttcttctctgt acagcagact gaccgtggac aagagccggt ggcaggaagg caacgtgttc 1320  
 agctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgtctctg 1380  
 agcctgggca aa 1392

<210> 108

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain IgG4PFALA of human chimeric rat\_CD147\_#101

<400> 108

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Asp Gly Gly Leu Val Gln  
 20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 35 40 45

Ser Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Thr Lys Gly Leu  
 50 55 60

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

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser  
 85 90 95

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

Tyr Tyr Cys Ala Arg Phe Tyr Asn Asn Tyr Tyr Phe Asp Tyr Trp Gly  
115 120 125

Gln Gly Val Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala  
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
195 200 205

Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His  
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly  
225 230 235 240

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gln Glu Asp Pro  
275 280 285

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
290 295 300

Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys Ser  
420 425 430

Arg Trp Gln Glu 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 Leu Gly Lys  
450 455 460

<210> 109

<211> 702

<212> DNA

<213> Artificial Sequence

<220>

<223> Light chain of human chimeric rat\_CD147\_#110

<400> 109

atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gacatccaga tgaccagac tccatcctcc atgcctgcat ctctgggaga gagagtcacc 120

atcagttgca gagcaagtca gggatttagc aattatctaa actggtatca gcagaaacca 180  
 gatggaacga ttaaaccct gatctactac acatccaatt tacaatctgg tgtcccatca 240  
 aggttcagtg gcagtgggtc tgggacagat tattctctca ccatcagcag cctggagcct 300  
 gaagattttg caatgtattt ctgccaacag tatgatagtt ctctcggac gttcgggtgga 360  
 ggcaccaagc tggaattgaa acggacgggtg gccgccccct ccgtgttcat cttccccccc 420  
 tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480  
 cccagagagg ccaagggtgca gtggaagggtg gacaacgccc tgcagtccgg gaactccag 540  
 gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600  
 ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660  
 ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt 702

<210> 110

<211> 234

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain of human chimeric rat\_CD147\_#110

<400> 110

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

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

Ala Ser Leu Gly Glu Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Gly  
 35 40 45

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Ile  
 50 55 60

Lys Pro Leu Ile Tyr Tyr Thr Ser Asn Leu Gln Ser Gly Val Pro Ser  
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 85                                                              | 90  | 95  |
| Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Phe Cys Gln Gln Tyr Asp |     |     |
| 100                                                             | 105 | 110 |
| Ser Ser Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg |     |     |
| 115                                                             | 120 | 125 |
| Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln |     |     |
| 130                                                             | 135 | 140 |
| Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr |     |     |
| 145                                                             | 150 | 155 |
| Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser |     |     |
| 165                                                             | 170 | 175 |
| Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr |     |     |
| 180                                                             | 185 | 190 |
| Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys |     |     |
| 195                                                             | 200 | 205 |
| His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro |     |     |
| 210                                                             | 215 | 220 |
| Val Thr Lys Ser Phe Asn Arg Gly Glu Cys                         |     |     |
| 225                                                             | 230 |     |

<210> 111  
 <211> 1386  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG2 of human chimeric rat\_CD147\_#110

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 111                                                         |     |
| atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag | 60  |
| gtacagctgc agcaatctgg ggctgaactg gtgaagcctg ggtcctcagt gaaaatttcc | 120 |
| tgcaaggctt ctggctacac cttcaccagt gactttatgc actggataaa acagcagcct | 180 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ggaaatggcc ttgagtggat tgggtggatt tatcctggag atggtgatac agagtacaat  | 240  |
| caaaagttca atgggaaggc aacactcact gcagacaaat cctccagcac agcctatatg  | 300  |
| cagctcagca gcctgacatc tgaggactct gcagtctatt tctgtgcaag gggacggggg  | 360  |
| tatgttatgg atgcctgggg tcaaggagct tcagtcactg tcagctcagc ctccaccaag  | 420  |
| ggcccttccg tgttccctct ggccccttgt agccgttcca ccagcgagtc caccgccgcc  | 480  |
| cttggctgtc tggatgaagga ctacttccct gagcctgtga ccgtgagctg gaactccgga | 540  |
| gcccttacca gcggcgtagc caccttccct gccgtgctgc agtccagcgg cttttactcc  | 600  |
| ctgagctccg tggtagcgt gcctagctcc aacttcggca cccaaaccta cacctgtaac   | 660  |
| gtggaccaca agcctagcaa caccaagggtg gacaagaccg tggagcgtaa gtgttgtgtg | 720  |
| gagtgtcctc cttgtcctgc ccctcctgtg gccggacctt ccgtgttcct tttccctcct  | 780  |
| aagcctaagg acaccctgat gatcagccgt acccctgagg tgacctgtgt ggtggtggac  | 840  |
| gtgtcccacg aggaccctga ggtgcagttc aactggtagc tggacggcgt ggaggtgcac  | 900  |
| aacgccaaga ccaagcctcg tgaggagcaa ttcaacagca ccttcctgtgt ggtgtccgtg | 960  |
| cttaccgtgg tgcaccaaga ctggctgaac ggcaaggagt acaagtgtaa ggtgagcaac  | 1020 |
| aagggacttc ctgcccctat cgagaagacc atctccaaga ccaagggcca acctcgtgag  | 1080 |
| cctcaagtgt acacccttcc tcctagccgt gaggagatga ccaagaacca agtgtccctt  | 1140 |
| acctgtctgg tgaagggtt ctaccctagc gacatcgccg tggagtggga gtccaacgga   | 1200 |
| caacctgaga acaactacaa gaccaccct cctatgcttg acagcgacgg ctcttcttc    | 1260 |
| ctgtacagca agctgaccgt ggacaagtcc cgtttgcaac aaggcaacgt gttcagctgt  | 1320 |
| tccgtgatgc acgaggccct gcacaaccac tacacccaaa agagcctttc cctgagccct  | 1380 |
| ggaaag                                                             | 1386 |

<210> 112

<211> 462

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain IgG2 of human chimeric rat\_CD147\_#110

<400> 112

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

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

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

Thr Ser Asp Phe Met His Trp Ile Lys Gln Gln Pro Gly Asn Gly Leu  
 50 55 60

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

Gln Lys Phe Asn Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
 85 90 95

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

Tyr Phe Cys Ala Arg Gly Arg Gly Tyr Val Met Asp Ala Trp Gly Gln  
 115 120 125

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

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala  
 145 150 155 160

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
 180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
 195 200 205

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys  
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val  
225 230 235 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe  
245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
275 280 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
290 295 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val  
305 310 315 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
325 330 335

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
340 345 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
355 360 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp  
405 410 415

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

420

425

430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
 435 440 445

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

&lt;210&gt; 113

&lt;211&gt; 1389

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Heavy chain IgG4P of human chimeric rat\_CD147\_#110

&lt;400&gt; 113

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atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag      60
gtacagctgc agcaatctgg ggctgaactg gtgaagcctg ggtcctcagt gaaaatttcc      120
tgcaaggctt ctggctacac cttcaccagt gactttatgc actggataaa acagcagcct      180
ggaaatggcc ttgagtggat tgggtggatt tatcctggag atggtgatac agagtacaat      240
caaaagttca atgggaaggc aacactcact gcagacaaat cctccagcac agcctatatg      300
cagctcagca gcctgacatc tgaggactct gcagtctatt tctgtgcaag gggacggggg      360
tatgttatgg atgcctgggg tcaaggagct tcagtcactg tcagctcagc ctccaccaag      420
ggccctagcg tgttccctct ggccccttgt agcagaagca ccagcgagtc tacagccgcc      480
ctgggctgcc tcgtgaagga ctactttccc gagcccgtga ccgtgtcctg gaactctggc      540
gctctgacaa gcggcgtgca cacctttcca gccgtgctgc agagcagcgg cctgtactct      600
ctgtccagcg tcgtgactgt gcccagcagc tctctgggca ccaagaccta cacctgtaac      660
gtggaccaca agcccagcaa caccaagggt gacaagcggg tggaatctaa gtacggccct      720
ccctgccctc cttgcccagc ccctgaattt ctgggcggac cctccgtgtt cctgttcccc      780
ccaaagccca aggacaccct gatgatcagc cggacccccg aagtgacctg cgtggtggtg      840
gatgtgtccc aggaagatcc cgagggtcag ttcaattggt acgtggacgg cgtggaagtg      900
cacaacgcca agaccaagcc tagagaggaa cagttcaaca gcacctaccg ggtggtgtcc      960
gtgctgacag tgctgcacca ggactggctg aacggcaaag agtacaagtg caagggtgtcc     1020

```

aacaagggcc tgcccagctc catcgagaaa accatcagca aggccaaggg ccagccccgc 1080  
gaaccccagg tgtacacact gcctccaagc caggaagaga tgaccaagaa tcaggtgtcc 1140  
ctgacctgtc tcgtgaaagg cttctacccc tccgatatcg ccgtggaatg ggagagcaac 1200  
ggccagccccg agaacaacta caagaccacc cccctgtgctc tggactccga tggctcattc 1260  
ttcctgtaca gcagactgac cgtggacaag agccgggtggc aggaaggcaa cgtgttcagc 1320  
tgctccgtga tgcacgaggc cctgcacaac cactacaccc agaagtcctt gtctctgagc 1380  
ctgggcaaaa 1389

<210> 114

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain IgG4P of human chimeric rat\_CD147\_#110

<400> 114

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

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

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

Thr Ser Asp Phe Met His Trp Ile Lys Gln Gln Pro Gly Asn Gly Leu  
50 55 60

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

Gln Lys Phe Asn Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
85 90 95

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

Tyr Phe Cys Ala Arg Gly Arg Gly Tyr Val Met Asp Ala Trp Gly Gln  
115 120 125

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

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala  
145 150 155 160

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
195 200 205

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys  
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro  
225 230 235 240

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val  
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu  
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser  
305 310 315 320

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
 325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile  
 340 345 350

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
 355 360 365

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
 370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
 385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
 405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg  
 420 425 430

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
 435 440 445

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

<210> 115

<211> 1389

<212> DNA

<213> Artificial Sequence

<220>

<223> Heavy chain IgG4PFALA of human chimeric rat\_CD147\_#110

<400> 115

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtacagctgc agcaatctgg ggctgaactg gtgaagcctg ggtcctcagt gaaaatttcc 120

tgcaaggctt ctggctacac cttcaccagt gactttatgc actggataaa acagcagcct 180

ggaaatggcc ttgagtggat tgggtggatt tatcctggag atggtgatac agagtacaat 240

|                                                                    |      |
|--------------------------------------------------------------------|------|
| caaaagttca atgggaaggc aacactcact gcagacaaat cctccagcac agcctatatg  | 300  |
| cagctcagca gcctgacatc tgaggactct gcagtctatt tctgtgcaag gggacggggg  | 360  |
| tatgttatgg atgcctgggg tcaaggagct tcagtcactg tcagctcagc ctccaccaag  | 420  |
| ggccctagcg tgttcctctt ggccccttgt agcagaagca ccagcgagtc tacagccgcc  | 480  |
| ctgggctgcc tcgtgaagga ctactttccc gagcccgtga ccgtgtcctg gaactctggc  | 540  |
| gctctgacaa gcggcgtgca cacctttcca gccgtgctgc agagcagcgg cctgtactct  | 600  |
| ctgtccagcg tcgtgactgt gcccagcagc tctctgggca ccaagaccta cacctgtaac  | 660  |
| gtggaccaca agcccagcaa caccaagggtg gacaagcggg tggaatctaa gtacggccct | 720  |
| ccctgccctc cttgccagc ccctgaagcc gcgggcggac cctccgtgtt cctgttcccc   | 780  |
| ccaaagccca aggacaccct gatgatcagc cggacccccg aagtgacctg cgtgggtggtg | 840  |
| gatgtgtccc aggaagatcc cgagggtcag ttcaattggt acgtggacgg cgtggaagtg  | 900  |
| cacaacgcca agaccaagcc tagagaggaa cagttcaaca gcacctaccg ggtggtgtcc  | 960  |
| gtgctgacag tgctgcacca ggactggctg aacggcaaag agtacaagtg caagggtgtcc | 1020 |
| aacaagggcc tgcccagctc catcgagaaa accatcagca aggccaaagg ccagccccgc  | 1080 |
| gaaccccagg tgtacacact gcctccaagc caggaagaga tgaccaagaa tcagggtgtcc | 1140 |
| ctgacctgtc tcgtgaaagg cttctacccc tccgatatcg ccgtggaatg ggagagcaac  | 1200 |
| ggccagcccc agaacaacta caagaccacc cccctgtgc tggactccga tggctcattc   | 1260 |
| ttcctgtaca gcagactgac cgtggacaag agccgggtggc aggaaggcaa cgtgttcagc | 1320 |
| tgctccgtga tgcacgaggc cctgcacaac cactacaccc agaagtcctt gtctctgagc  | 1380 |
| ctgggcaaa                                                          | 1389 |

<210> 116

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain IgG4PFALA of human chimeric rat\_CD147\_#110

<400> 116

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | His | Leu | Trp | Phe | Phe | Leu | Leu | Leu | Val | Ala | Ala | Pro | Arg | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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

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

Thr Ser Asp Phe Met His Trp Ile Lys Gln Gln Pro Gly Asn Gly Leu  
50 55 60

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

Gln Lys Phe Asn Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
85 90 95

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

Tyr Phe Cys Ala Arg Gly Arg Gly Tyr Val Met Asp Ala Trp Gly Gln  
115 120 125

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

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala  
145 150 155 160

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
195 200 205

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys  
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro  
 225 230 235 240

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val  
 245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
 260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu  
 275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
 290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser  
 305 310 315 320

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
 325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile  
 340 345 350

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
 355 360 365

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
 370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
 385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
 405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg  
 420 425 430

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
435 440 445

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

<210> 117  
<211> 702  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Light chain of human chimeric rat\_CD147\_#131

<400> 117  
atgggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60  
gatgtccaga tgaccagtc tccatcttat cttgctgcgt ctcttgaga aagtgtttcc 120  
atcagttgca aggcaagtaa aagcattaac acatacttag cctggatatca ggagaaacct 180  
gggaaaacga ataagcttct tatctactct ggggtcaactt tgcaatctgg aactccatcg 240  
agattcagtg gcagtggatc tggtagatc ttacgctca ccatcagaag cctggagcct 300  
gaagattttg cagtctacta ctgtcaacag cataatgaat accccttcac gttcgggtca 360  
gggacgaagt tggaaataaa acggacgggt gccgccccct ccgtgttcat cttccccccc 420  
tccgacgagc agctgaagtc cggcaccgcc tccgtgggtg gcctgctgaa taacttctac 480  
cccagagagg ccaaggtgca gtggaagggt gacaacgccc tgagtcagg gaactcccag 540  
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600  
ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660  
ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt 702

<210> 118  
<211> 234  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Light chain of human chimeric rat\_CD147\_#131

<400> 118

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| 1   | 5   | 10  | 15  |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| Gly | Ala | Tyr | Gly | Asp | Val | Gln | Met | Thr | Gln | Ser | Pro | Ser | Tyr | Leu | Ala |  |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |  |
| Ala | Ser | Pro | Gly | Glu | Ser | Val | Ser | Ile | Ser | Cys | Lys | Ala | Ser | Lys | Ser |  |  |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |  |
| Ile | Asn | Thr | Tyr | Leu | Ala | Trp | Tyr | Gln | Glu | Lys | Pro | Gly | Lys | Thr | Asn |  |  |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |  |
| Lys | Leu | Leu | Ile | Tyr | Ser | Gly | Ser | Thr | Leu | Gln | Ser | Gly | Thr | Pro | Ser |  |  |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |  |  |
| Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Arg |  |  |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |  |
| Ser | Leu | Glu | Pro | Glu | Asp | Phe | Ala | Val | Tyr | Tyr | Cys | Gln | Gln | His | Asn |  |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |  |
| Glu | Tyr | Pro | Phe | Thr | Phe | Gly | Ser | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg |  |  |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |
| Thr | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln |  |  |  |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |  |
| Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr |  |  |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |
| Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu | Gln | Ser |  |  |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |  |
| Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp | Ser | Thr |  |  |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |  |
| Tyr | Ser | Leu | Ser | Ser | Thr | Leu | Thr | Leu | Ser | Lys | Ala | Asp | Tyr | Glu | Lys |  |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |
| His | Lys | Val | Tyr | Ala | Cys | Glu | Val | Thr | His | Gln | Gly | Leu | Ser | Ser | Pro |  |  |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230

<210> 119  
 <211> 1392  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG2 of human chimeric rat\_CD147\_#131

<400> 119  
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag 60  
 gtgcagctgg tggagtctgg gggaggccta gtgcagcctg gaaggtctct gaaactatcc 120  
 tgtggagcct ctggattcac attcaataac tactggatga cctgggtccg ccaggctcca 180  
 gggaaggggc tggagtgggt tgcatccatt actaaagctg gtggtagcac ttactatcga 240  
 gactctgtga agggccgatt cactatctcc agagataatg caaaaagcac cctatatctg 300  
 caaatgaaca gtctgaggtc tgaggacacg gccacttatt actgtacaag agaactggga 360  
 gagttctatg ttatggatgc ctgggggtcaa ggagcttcag tcactgtcag ctgagcctcc 420  
 accaagggcc cttccgtgtt ccctctggcc ccttgtagcc gttccaccag cgagtccacc 480  
 gccgcccttg gctgtctggt gaaggactac ttccctgagc ctgtgaccgt gagctggaac 540  
 tccggagccc ttaccagcgg cgtgcacacc ttccctgccg tgctgcagtc cagcggcctt 600  
 tactccctga gctccgtggt gaccgtgcct agctccaact tcggcaccca aacctacacc 660  
 tgtaacgtgg accacaagcc tagcaacacc aaggtggaca agaccgtgga gcgtaagtgt 720  
 tgtgtggagt gtcctccttg tcctgcccct cctgtggccg gaccttccgt gttccttttc 780  
 cctcctaagc ctaaggacac cctgatgata agccgtaccc ctgaggtgac ctgtgtggtg 840  
 gtggacgtgt cccacgagga ccctgaggtg cagttcaact ggtacgtgga cggcgtggag 900  
 gtgcacaacg ccaagaccaa gcctcgtgag gagcaattca acagcacctt ccgtgtggtg 960  
 tccgtgctta ccgtgggtgca ccaagactgg ctgaacggca aggagtacaa gtgtaagggtg 1020  
 agcaacaagg gacttcctgc ccctatcgag aagaccatct ccaagaccaa gggccaacct 1080  
 cgtgagcctc aagtgtacac ccttcctcct agccgtgagg agatgaccaa gaaccaagtg 1140

|                                                                   |      |
|-------------------------------------------------------------------|------|
| tcccttacct gtctggtgaa gggcttctac cctagcgaca tcgccgtgga gtgggagtcc | 1200 |
| aacggacaac ctgagaacaa ctacaagacc acccctccta tgcttgacag cgacggctcc | 1260 |
| ttcttcctgt acagcaagct gaccgtggac aagtcccgtt ggcaacaagg caacgtgttc | 1320 |
| agctgttccg tgatgcacga ggccctgcac aaccactaca cccaaaagag cttttccctg | 1380 |
| agccctggaa ag                                                     | 1392 |

<210> 120  
 <211> 464  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG2 of human chimeric rat\_CD147\_#131

<400> 120

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | His | Leu | Trp | Phe | Phe | Leu | Leu | Leu | Val | Ala | Ala | Pro | Arg | Trp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Glu | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Arg | Ser | Leu | Lys | Leu | Ser | Cys | Gly | Ala | Ser | Gly | Phe | Thr | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Asn | Tyr | Trp | Met | Thr | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Trp | Val | Ala | Ser | Ile | Thr | Lys | Ala | Gly | Gly | Ser | Thr | Tyr | Tyr | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ser | Val | Lys | Gly | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Asn | Ala | Lys | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Tyr | Leu | Gln | Met | Asn | Ser | Leu | Arg | Ser | Glu | Asp | Thr | Ala | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Cys | Thr | Arg | Glu | Leu | Gly | Glu | Phe | Tyr | Val | Met | Asp | Ala | Trp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
145 150 155 160

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr  
165 170 175

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
180 185 190

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
195 200 205

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp  
210 215 220

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys  
225 230 235 240

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
290 295 300

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val  
305 310 315 320

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
325 330 335

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 340 |     | 345 |     | 350 |     |     |     |     |     |     |     |     |     |     |
| Ile | Ser | Lys | Thr | Lys | Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Pro | Pro | Ser | Arg | Glu | Glu | Met | 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 | Met | 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 | Lys |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |

<210> 121  
 <211> 1395  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain IgG4P of human chimeric rat\_CD147\_#131

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 121                                                          |     |
| atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag  | 60  |
| gtgcagctgg tggagtctgg gggaggccta gtgcagcctg gaaggtctct gaaactatcc  | 120 |
| tgtggagcct ctggattcac attcaataac tactggatga cctgggtccg ccaggctcca  | 180 |
| gggaaggggc tggagtgggt tgcattcatt actaaagctg gtggtagcac ttactatcga  | 240 |
| gactctgtga agggccgatt cactatctcc agagataatg caaaaagcac cctatatctg  | 300 |
| caaatgaaca gtctgaggtc tgaggacacg gccacttatt actgtacaag agaactggga  | 360 |
| gagttctatg ttatggatgc ctgggggtcaa ggagcttcag tcactgtcag ctcagcctcc | 420 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| accaagggcc ctagcgtggt ccctctggcc cttttagca gaagcaccag cgagtctaca  | 480  |
| gccgccctgg gctgcctcgt gaaggactac tttcccgagc ccgtgaccgt gtcctggaac | 540  |
| tctggcgctc tgacaagcgg cgtgcacacc tttccagccg tgctgcagag cagcggcctg | 600  |
| tactctctgt ccagcgtcgt gactgtgccc agcagctctc tgggcaccaa gacctacacc | 660  |
| tgtaacgtgg accacaagcc cagcaacacc aaggtggaca agcgggtgga atctaagtac | 720  |
| ggccctccct gccctccttg cccagcccct gaatttctgg gcggaccctc cgtgttcctg | 780  |
| ttcccccaa agcccaagga caccctgatg atcagccgga ccccggaagt gacctgcgtg  | 840  |
| gtggtgatg tgtcccagga agatcccag gtgcagttca attggtacgt ggacggcgtg   | 900  |
| gaagtgcaca acgccaagac caagcctaga gaggaacagt tcaacagcac ctaccgggtg | 960  |
| gtgtccgtgc tgacagtgc gcaccaggac tggctgaacg gcaaagagta caagtgaag   | 1020 |
| gtgtccaaca agggcctgcc cagctccatc gagaaaacca tcagcaaggc caagggccag | 1080 |
| ccccgcgaac cccaggtgta cacactgcct ccaagccagg aagagatgac caagaatcag | 1140 |
| gtgtccctga cctgtctcgt gaaaggcttc taccctccg atatcgccgt ggaatgggag  | 1200 |
| agcaacggcc agcccgagaa caactacaag accaccccc ctgtgctgga ctccgatggc  | 1260 |
| tcattcttcc tgtacagcag actgaccgtg gacaagagcc ggtggcagga aggcaacgtg | 1320 |
| ttcagctgct ccgtgatgca cgaggccctg cacaaccact acaccagaa gtccctgtct  | 1380 |
| ctgagcctgg gcaaa                                                  | 1395 |

<210> 122

<211> 465

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain IgG4P of human chimeric rat\_CD147\_#131

<400> 122

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | His | Leu | Trp | Phe | Phe | Leu | Leu | Leu | Val | Ala | Ala | Pro | Arg | Trp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Glu | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Pro Gly Arg Ser Leu Lys Leu Ser Cys Gly Ala Ser Gly Phe Thr Phe  
35 40 45

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

Glu Trp Val Ala Ser Ile Thr Lys Ala Gly Gly Ser Thr Tyr Tyr Arg  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser  
85 90 95

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

Tyr Tyr Cys Thr Arg Glu Leu Gly Glu Phe Tyr Val Met Asp Ala Trp  
115 120 125

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
145 150 155 160

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr  
165 170 175

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
180 185 190

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
195 200 205

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr  
225 230 235 240

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro  
245 250 255

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp  
275 280 285

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
290 295 300

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val  
305 310 315 320

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
325 330 335

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys  
340 345 350

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
355 360 365

Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr  
370 375 380

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu  
385 390 395 400

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu  
405 410 415

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys  
420 425 430

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
435 440 445

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

450                      455                      460  
  
 Lys  
 465  
  
 <210> 123  
 <211> 466  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> #84H1hIgG2  
  
 <400> 123  
  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1                      5                      10                      15  
  
 Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
                     20                      25                      30  
  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
                     35                      40                      45  
  
 Ser Asn Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
                     50                      55                      60  
  
 Glu Trp Val Ser Thr Ile Thr Thr Ser Gly Ser Arg Pro Tyr Tyr Ala  
 65                      70                      75                      80  
  
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn  
                     85                      90                      95  
  
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
                     100                      105                      110  
  
 Tyr Tyr Cys Ala Arg His Ile Tyr Tyr Tyr Asp Gly Tyr Pro Phe Ala  
                     115                      120                      125  
  
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
                     130                      135                      140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn  
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg  
225 230 235 240

Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly  
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
275 280 285

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg  
305 310 315 320

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys  
325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu  
340 345 350

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 355 |     | 360 |     | 365 |     |     |     |     |     |     |     |     |     |     |     |
| Thr | Leu | Pro | Pro | Ser | Arg | Glu | Glu | Met | Thr | Lys | Asn | Gln | Val | Ser | Leu |
| 370 |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Thr | Cys | Leu | Val | Lys | Gly | Phe | Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Glu | Ser | Asn | Gly | Gln | Pro | Glu | Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Met |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Leu | Asp | Ser | Asp | Gly | Ser | Phe | Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Lys | Ser | Arg | Trp | Gln | Gln | Gly | Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Ala | Leu | His | Asn | His | Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro |
| 450 |     |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Gly | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 465 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 124  
 <211> 1398  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> #84H1hIgG2

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 124                                                         |     |
| atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgaa | 60  |
| gtgcagctgg ttgagtctgg cggaggactg gttcaacctg gcggaagcct gagactgtct | 120 |
| tgtgccgcca gcggcttcac cttcagcaac tactatatgg cctgggtccg acaggcccct | 180 |
| ggcaaaggac ttgaatgggt gtccaccatc accaccagcg gcagcagacc ttactacgcc | 240 |
| gatagcgtga agggcagatt caccatcagc cgggacaaca gcaagaacac cctgtacctg | 300 |
| cagatgaaca gcctgagagc cgaggacacc gccgtgtact attgcgccag acacatctac | 360 |
| tactacgacg gctacccctt cgcctattgg ggccaggga cactggtcac agttagctca  | 420 |

gcctccacca agggcccttc cgtgttccct ctggcccctt gtagccgttc caccagcgag 480  
tccaccgccg cccttggctg tctggtgaag gactacttcc ctgagcctgt gaccgtgagc 540  
tggaactccg gagcccttac cagcggcgtg cacaccttcc ctgccgtgct gcagtccagc 600  
ggcctttact ccctgagctc cgtggtgacc gtgcctagct ccaacttcgg cacccaaacc 660  
tacacctgta acgtggacca caagcctagc aacaccaagg tggacaagac cgtggagcgt 720  
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<210> 125  
<211> 467  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> #84H1hIgG4P

<400> 125

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
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Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Ser Asn Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Ser Thr Ile Thr Thr Ser Gly Ser Arg Pro Tyr Tyr Ala  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn  
85 90 95

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

Tyr Tyr Cys Ala Arg His Ile Tyr Tyr Tyr Asp Gly Tyr Pro Phe Ala  
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
225 230 235 240

Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly  
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

450

455

460

Leu Gly Lys

465

&lt;210&gt; 126

&lt;211&gt; 1401

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; #84H1hIgG4P

&lt;400&gt; 126

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 ctgtctctga gcctgggcaa a 1401

<210> 127  
 <211> 234  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> #84L2h

<400> 127

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser  
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Gly Ala Tyr Gly Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu Ser  
 20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Lys Ser  
 35 40 45

Ile Ser Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Asn  
 50 55 60

Lys Leu Leu Ile His Ser Gly Ser Thr Leu Gln Ser Gly Thr Pro Ser  
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
 85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn  
 100 105 110

Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
 115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
 130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
 145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
 165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
 180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
 195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
 210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230

<210> 128  
 <211> 702  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> #84L2h

<400> 128  
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 ggaaaggcca acaagctgct gatccacagc ggcagcacac tgcagtctgg cacccttagc 240  
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 gaggacttcg ccacctacta ctgccagcag tacaacgagt accctctgac ctttggccag 360  
 ggcaccaagg tggaaatcaa gcgtacgggt gccgccccct ccgtgttcat cttccccccc 420  
 tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480

cccagagagg ccaaggtgca gtggaagggtg gacaacgccc tgcagtcgga gaactcccag 540  
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600  
ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660  
ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt 702

<210> 129  
<211> 463  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> #101H1hIgG2

<400> 129

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
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Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Ser Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

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

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser  
85 90 95

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

Tyr Tyr Cys Ala Arg Phe Tyr Asn Asn Tyr Tyr Phe Asp Tyr Trp Gly  
115 120 125

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

|                                                                 |     |     |     |         |
|-----------------------------------------------------------------|-----|-----|-----|---------|
| 130                                                             |     | 135 |     | 140     |
| Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala |     |     |     |         |
| 145                                                             |     | 150 |     | 155 160 |
| Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val |     |     |     |         |
|                                                                 | 165 |     | 170 | 175     |
| Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala |     |     |     |         |
|                                                                 | 180 |     | 185 | 190     |
| Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val |     |     |     |         |
|                                                                 | 195 |     | 200 | 205     |
| Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His |     |     |     |         |
|                                                                 | 210 |     | 215 | 220     |
| Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys |     |     |     |         |
| 225                                                             |     | 230 |     | 235 240 |
| Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val |     |     |     |         |
|                                                                 | 245 |     | 250 | 255     |
| Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr |     |     |     |         |
|                                                                 | 260 |     | 265 | 270     |
| Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu |     |     |     |         |
|                                                                 | 275 |     | 280 | 285     |
| Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys |     |     |     |         |
|                                                                 | 290 |     | 295 | 300     |
| Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser |     |     |     |         |
| 305                                                             |     | 310 |     | 315 320 |
| Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys |     |     |     |         |
|                                                                 | 325 |     | 330 | 335     |
| Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile |     |     |     |         |
|                                                                 | 340 |     | 345 | 350     |

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
 370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
 385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser  
 405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg  
 420 425 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
 435 440 445

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

<210> 130  
 <211> 1389  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> #101H1hIgG2

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 tgtgccgcca gcggcttcac cttcagcgac tactatatgg cctgggtccg acaggcccct 180  
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 aactactact tcgactactg gggccagggc accctggtca cagttagctc agcctccacc 420

aagggccctt ccgtgttccc tctggcccct tgtagccgtt ccaccagcga gtccaccgcc 480  
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cctggaaag 1389

<210> 131  
<211> 464  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> #101H1hIgG4P

<400> 131

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
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Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Ser Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

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

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser  
85 90 95

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

Tyr Tyr Cys Ala Arg Phe Tyr Asn Asn Tyr Tyr Phe Asp Tyr Trp Gly  
115 120 125

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala  
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
195 200 205

Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His  
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly  
225 230 235 240

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe 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 | Gln | Glu | Asp | Pro |  |  |  |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |     |
| Glu | Val | Gln | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala |  |  |  |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |     |
| Lys | Thr | Lys | Pro | Arg | Glu | Glu | Gln | Phe | 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 | Gly | Leu | Pro | Ser | Ser | 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 | Gln | Glu | Glu | Met | 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 | Arg | Leu | Thr | Val | Asp | Lys | Ser |  |  |  |     |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |  |     |
| Arg | Trp | Gln | Glu | 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 | Leu | Gly | Lys |  |  |  |     |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |  |     |

<210> 132  
<211> 1392  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> #101H1hIgG4P

<400> 132  
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tgtgccgcca gcggcttcac cttcagcgac tactatatgg cctgggtccg acaggcccct 180  
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aactactact tcgactactg gggccagggc accctgggtca cagttagctc agcctccacc 420  
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tccaacaagg gcctgcccag ctccatcgag aaaaccatca gcaaggccaa gggccagccc 1080  
cgcgaacccc aggtgtacac actgcctcca agccaggaag agatgaccaa gaatcagggtg 1140  
tccctgacct gtctcgtgaa aggcttctac ccctccgata tcgccgtgga atgggagagc 1200  
aacggccagc ccgagaacaa ctacaagacc accccctg tgctggactc cgatggctca 1260

ttcttcctgt acagcagact gaccgtggac aagagccggt ggcaggaagg caacgtgttc 1320  
 agctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgtctctg 1380  
 agcctgggca aa 1392

<210> 133  
 <211> 234  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> #101L2h

<400> 133

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser  
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Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser  
 20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Lys Ala Ser Gln Asn  
 35 40 45

Leu Tyr Lys Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
 50 55 60

Lys Leu Leu Ile Asp Asn Ala Asn Ser Leu Gln Thr Gly Ile Pro Ser  
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
 85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Tyr Tyr  
 100 105 110

Ser Gly Ser Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
 115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
 130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
 145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
 165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
 180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
 195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
 210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230

<210> 134  
 <211> 702  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> #101L2h

<400> 134  
 atgggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60  
 gatatccaga tgacacagag ccctagcagc ctgtctgccg gcgtgggaga tagagtgacc 120  
 atcaactgca aggccagcca gaacctgtac aagaacctgg cctgggtatca gcagaagccc 180  
 ggcaaggctc ctaagctgct gatcgacaac gccaacagcc tgcagaccgg cattcccagc 240  
 agattttctg gcagcggctc cggcaccgat ttcacctga ccatatctag cctgcagcct 300  
 gaggacttcg ccacctactt ttgccagcag tactacagcg gcagctacac ctttggccag 360  
 ggcaccaagg tggaaatcaa gcgtacgggtg gccgccccct ccgtgttcat cttccccccc 420  
 tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480  
 cccagagagg ccaagggtgca gtggaagggtg gacaacgccc tgcagtccgg gaactcccag 540  
 gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600

ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660

ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt 702

<210> 135

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> #110H1hIgG4P

<400> 135

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

Val Leu 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 Ser Asp Phe Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
50 55 60

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

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

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

Tyr Tyr Cys Ala Arg Gly Arg Gly Tyr Val Met Asp Ala Trp Gly Gln  
115 120 125

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

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala  
145 150 155 160

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
195 200 205

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys  
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro  
225 230 235 240

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val  
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu  
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser  
305 310 315 320

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile  
340 345 350

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
355 360 365

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
 370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
 385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
 405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg  
 420 425 430

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
 435 440 445

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

<210> 136  
 <211> 1389  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> #110H1hIgG4P

<400> 136  
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 gttcagctgg ttcagtctgg cgccgaagtg aagaaacctg ggcctctgt gaagggtgtcc 120  
 tgcaaggcca gcggctacac ctttaccagc gacttcatgc actgggtccg acaggctcca 180  
 ggacagggac ttgaatggat gggctggatc tatcccggcg acggcgacac cgagtacaac 240  
 cagaaattcc agggcagagt gacctgacc agagacacca gcatcagcac cgcctacatg 300  
 gaactgagcc ggctgagatc cgatgacacc gccgtgtact actgcgccag aggcagaggc 360  
 tatgtgatgg atgcttgggg ccagggcacc accgttacag ttagctcagc ctccaccaag 420  
 ggccctagcg tgttccctct ggccccttgt agcagaagca ccagcgagtc tacagccgcc 480  
 ctgggctgcc tcgtgaagga ctactttccc gagcccgtga ccgtgtcctg gaactctggc 540  
 gctctgacaa gcggcgtgca cacctttcca gccgtgctgc agagcagcgg cctgtactct 600

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ctgtccagcg tcgtgactgt gcccagcagc tctctgggca ccaagaccta cacctgtaac  | 660  |
| gtggaccaca agcccagcaa caccaagggtg gacaagcggg tggaatctaa gtacggccct | 720  |
| ccctgccctc cttgcccagc ccctgaattt ctgggcggac cctccgtgtt cctgttcccc  | 780  |
| ccaaagccca aggacaccct gatgatcagc cggacccccg aagtgacctg cgtggtggtg  | 840  |
| gatgtgtccc aggaagatcc cgagggtcag ttcaattggt acgtggacgg cgtggaagtg  | 900  |
| cacaacgcca agaccaagcc tagagaggaa cagttcaaca gcacctaccg ggtgggtgtcc | 960  |
| gtgctgacag tgctgcacca ggactggctg aacggcaaag agtacaagtg caagggtgtcc | 1020 |
| aacaagggcc tgcccagctc catcgagaaa accatcagca aggccaaggg ccagccccgc  | 1080 |
| gaaccccagg tgtacacact gcctccaagc caggaagaga tgaccaagaa tcagggtgtcc | 1140 |
| ctgacctgtc tcgtgaaagg cttctacccc tccgatatcg ccgtggaatg ggagagcaac  | 1200 |
| ggccagcccc agaacaacta caagaccacc cccctgtgc tggactccga tggctcattc   | 1260 |
| ttcctgtaca gcagactgac cgtggacaag agccgggtggc aggaaggcaa cgtgttcagc | 1320 |
| tgctccgtga tgcacgaggc cctgcacaac cactacacc agaagtcctt gtctctgagc   | 1380 |
| ctgggcaaa                                                          | 1389 |

<210> 137  
 <211> 234  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> #110L4h

<400> 137

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Gln | Thr | Gln | Val | Phe | Ile | Ser | Leu | Leu | Leu | Trp | Ile | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Tyr | Gly | Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Val | Gly | Asp | Arg | Val | Thr | Ile | Thr | Cys | Arg | Ala | Ser | Gln | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Asn | Tyr | Leu | Asn | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Ile |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Pro | Leu | Ile | Tyr | Tyr | Thr | Ser | Asn | Leu | Gln | Ser | Gly | Val | Pro | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Tyr | Thr | Leu | Thr | Ile | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Leu | Gln | Pro | Glu | Asp | Phe | Ala | Thr | Tyr | Phe | Cys | Gln | Gln | Tyr | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Pro | Arg | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Val | Glu | Ile | Lys | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu | Gln | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp | Ser | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Ser | Leu | Ser | Ser | Thr | Leu | Thr | Leu | Ser | Lys | Ala | Asp | Tyr | Glu | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Lys | Val | Tyr | Ala | Cys | Glu | Val | Thr | His | Gln | Gly | Leu | Ser | Ser | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Thr | Lys | Ser | Phe | Asn | Arg | Gly | Glu | Cys |     |     |     |     |     |     |
| 225 |     |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     |

<210> 138  
 <211> 702  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> #110L4h

<400> 138

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atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc      60
gatatccaga tgacacagag ccctagcagc ctgtctgcca gcgtgggaga cagagtgacc      120
atcacctgta gagccagcca gggcatcagc aactacctga actggtatca gcagaagccc      180
ggcaaggcca tcaagcccct gatctactac accagcaacc tgcagagcgg cgtgcccagc      240
agattttctg gctctggcag cggcaccgac tacaccctga ccatatctag cctgcagcct      300
gaggacttcg ccacctactt ttgccagcag tacgacagca gcccagaac ctttggcggc      360
ggaacaaagg tggaatcaa gcgtacgggt gccgccccct ccgtgttcat cttccccccc      420
tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac      480
cccagagagg ccaaggtgca gtggaagggt gacaacgccc tgcagtccgg gaactcccag      540
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc      600
ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc      660
ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt                          702
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<210> 139

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> #131H2hIgG2

<400> 139

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1           5           10          15
```

```
Val Leu Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20          25          30
```

```
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35          40          45
```

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

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

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser  
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Gly Thr Ala Val  
100 105 110

Tyr Tyr Cys Thr Arg Glu Leu Gly Glu Phe Tyr Val Met Asp Ala Trp  
115 120 125

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
145 150 155 160

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr  
165 170 175

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
180 185 190

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
195 200 205

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp  
210 215 220

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys  
225 230 235 240

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
 290 295 300

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val  
 305 310 315 320

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
 325 330 335

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr  
 340 345 350

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
 355 360 365

Pro Pro Ser Arg Glu Glu Met 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 Met 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 Lys  
 450 455 460

<210> 140

<211> 1392

<212> DNA

<213> Artificial Sequence

<220>

<223> #131H2hIgG2.

<400> 140

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag  | 60   |
| gttcagctgg ttgaatctgg tggcggagtg gtgcagcctg gcagatctct gagactgtct  | 120  |
| tgtgccgcca gcggcttcac cttcaacaac tactggatga cctgggtccg acaggcccct  | 180  |
| ggcaaaggac ttgaatgggt cgccagcatc accaaggctg gcggctctac ctactacgcc  | 240  |
| gatagcgtga agggcagatt caccatcagc cgggacaaca gcaagagcac cctgtacctg  | 300  |
| cagatgaaca gcctgagagc cgagggcaca gccgtgtact actgtacaag agagctgggc  | 360  |
| gagttctacg tgatggatgc ctggggccag ggcaccacag ttacagttag ctacgcctcc  | 420  |
| accaagggcc cttccgtgtt ccctctggcc ccttgtagcc gttccaccag cgagtccacc  | 480  |
| gccgcccttg gctgtctgggt gaaggactac ttccctgagc ctgtgaccgt gagctggaac | 540  |
| tccggagccc ttaccagcgg cgtgcacacc ttccctgccg tgctgcagtc cagcggcctt  | 600  |
| tactccctga gctccgtgggt gaccgtgcct agctccaact tcggcaccca aacctacacc | 660  |
| tgtaacgtgg accacaagcc tagcaacacc aagggtggaca agaccgtgga gcgtaagtgt | 720  |
| tgtgtggagt gtcctccttg tcctgcccct cctgtggccg gaccttccgt gttccttttc  | 780  |
| cctcctaagc ctaaggacac cctgatgac agccgtaccc ctgaggtgac ctgtgtgggtg  | 840  |
| gtggacgtgt cccacgagga ccctgagggtg cagttcaact ggtacgtgga cggcgtggag | 900  |
| gtgcacaacg ccaagaccaa gcctcgtgag gagcaattca acagcacctt ccgtgtgggtg | 960  |
| tccgtgctta ccgtggtgca ccaagactgg ctgaacggca aggagtacaa gtgtaagggtg | 1020 |
| agcaacaagg gacttcctgc ccctatcgag aagaccatct ccaagaccaa gggccaacct  | 1080 |
| cgtgagcctc aagtgtacac ctttcctcct agccgtgagg agatgaccaa gaaccaagtg  | 1140 |
| ttccttacct gtctggtgaa gggcttctac cctagcgaca tcgccgtgga gtgggagtcc  | 1200 |
| aacggacaac ctgagaacaa ctacaagacc acccctccta tgcttgacag cgacggctcc  | 1260 |
| ttcttcctgt acagcaagct gaccgtggac aagtcccgtt ggcaacaagg caacgtgttc  | 1320 |
| agctgttccg tgatgcacga ggccctgcac aaccactaca cccaaaagag cctttccctg  | 1380 |
| agccctggaa ag                                                      | 1392 |

<210> 141  
 <211> 234  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> #131L2h

<400> 141

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

Gly Ala Tyr Gly Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu Ser  
 20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Lys Ser  
 35 40 45

Ile Asn Thr Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn  
 50 55 60

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
 85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn  
 100 105 110

Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
 115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
 130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
 145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
 165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230

<210> 142  
<211> 702  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> #131L2h

<400> 142  
atgggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60  
gacgttcaga tgacacagag ccctagcagc ctgtctgccg gcgtggggaga cagagtgacc 120  
atcacatgca aggccagcaa gagcatcaac acctacctgg cctgggtatca agagaagccc 180  
ggcaagacca acaagctgct gatctacagc ggacagcacac tgcagagcgg cacccttct 240  
agattttccg gctctggcag cggcaccgac ttcaccctga ccatatctag cctgcagcct 300  
gaggacttcg ccacctacta ctgccagcag cacaacgagt accccttcac ctttggccag 360  
ggcaccaagc tggaaatcaa gcgtacgggtg gccgccccct ccgtgttcat cttccccccc 420  
tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480  
cccagagagg ccaaggtgca gtggaagggtg gacaacgccc tgcagtccgg gaactcccag 540  
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600  
ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660  
ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt 702

<210> 143  
<211> 17

<212> PRT  
<213> Homo sapiens

<400> 143

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

Gln

<210> 144  
<211> 17  
<212> PRT  
<213> Macaca fascicularis

<400> 144

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

Leu

<210> 145  
<211> 457  
<212> PRT  
<213> Homo sapiens

<400> 145

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

Gln Pro Pro Ala Pro Gln Asp Glu Pro Val Phe Ala Gln Leu Lys Pro  
20 25 30

Val Leu Gly Ala Ala Asn Pro Ala Arg Asp Ala Ala Leu Phe Pro Gly  
35 40 45

Glu Glu Leu Lys His Ala His His Arg Pro Gln Ala Gln Pro Ala Pro  
50 55 60

Ala Gln Ala Pro Gln Pro Ala Gln Pro Pro Ala Thr Gly Pro Arg Leu  
65 70 75 80

Pro Pro Glu Asp Leu Val Gln Thr Arg Cys Glu Met Glu Lys Tyr Leu  
85 90 95

Thr Pro Gln Leu Pro Pro Val Pro Ile Ile Pro Glu His Lys Lys Tyr  
100 105 110

Arg Arg Asp Ser Ala Ser Val Val Asp Gln Phe Phe Thr Asp Thr Glu  
115 120 125

Gly Leu Pro Tyr Ser Ile Asn Met Asn Val Phe Leu Pro Asp Ile Thr  
130 135 140

His Leu Arg Thr Gly Leu Tyr Lys Ser Gln Arg Pro Cys Val Thr His  
145 150 155 160

Ile Lys Thr Glu Pro Val Ala Ile Phe Ser His Gln Ser Glu Thr Thr  
165 170 175

Ala Pro Pro Pro Ala Pro Thr Gln Ala Leu Pro Glu Phe Thr Ser Ile  
180 185 190

Phe Ser Ser His Gln Thr Ala Ala Pro Glu Val Asn Asn Ile Phe Ile  
195 200 205

Lys Gln Glu Leu Pro Thr Pro Asp Leu His Leu Ser Val Pro Thr Gln  
210 215 220

Gln Gly His Leu Tyr Gln Leu Leu Asn Thr Pro Asp Leu Asp Met Pro  
225 230 235 240

Ser Ser Thr Asn Gln Thr Ala Ala Met Asp Thr Leu Asn Val Ser Met  
245 250 255

Ser Ala Ala Met Ala Gly Leu Asn Thr His Thr Ser Ala Val Pro Gln  
260 265 270

Thr Ala Val Lys Gln Phe Gln Gly Met Pro Pro Cys Thr Tyr Thr Met  
275 280 285

Pro Ser Gln Phe Leu Pro Gln Gln Ala Thr Tyr Phe Pro Pro Ser Pro  
 290 295 300

Pro Ser Ser Glu Pro Gly Ser Pro Asp Arg Gln Ala Glu Met Leu Gln  
 305 310 315 320

Asn Leu Thr Pro Pro Pro Ser Tyr Ala Ala Thr Ile Ala Ser Lys Leu  
 325 330 335

Ala Ile His Asn Pro Asn Leu Pro Thr Thr Leu Pro Val Asn Ser Gln  
 340 345 350

Asn Ile Gln Pro Val Arg Tyr Asn Arg Arg Ser Asn Pro Asp Leu Glu  
 355 360 365

Lys Arg Arg Ile His Tyr Cys Asp Tyr Pro Gly Cys Thr Lys Val Tyr  
 370 375 380

Thr Lys Ser Ser His Leu Lys Ala His Leu Arg Thr His Thr Gly Glu  
 385 390 395 400

Lys Pro Tyr Lys Cys Thr Trp Glu Gly Cys Asp Trp Arg Phe Ala Arg  
 405 410 415

Ser Asp Glu Leu Thr Arg His Tyr Arg Lys His Thr Gly Ala Lys Pro  
 420 425 430

Phe Gln Cys Gly Val Cys Asn Arg Ser Phe Ser Arg Ser Asp His Leu  
 435 440 445

Ala Leu His Met Lys Arg His Gln Asn  
 450 455

<210> 146  
 <211> 1374  
 <212> DNA  
 <213> Homo sapiens

<400> 146  
 atggctacaa ggggtgctgag catgagcgcc cgcctgggac ccgtgccccca gccgccggcg

60

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ccgcaggacg agccggtgtt cgcgcagctc aagccggtgc tgggcgccgc gaatccggcc  | 120  |
| cgcgacgcgg cgctctttccc cggcgaggag ctgaagcacg cgcaccaccg cccgcaggcg | 180  |
| cagcccgcgc ccgcgcaggc cccgcagccg gcccagccgc ccgccaccgg cccgcggctg  | 240  |
| cctccagagg acctggtcca gacaagatgt gaaatggaga agtatctgac acctcagctt  | 300  |
| cctccagttc ctataattcc agagcataaa aagtatagac gagacagtgc ctcagtcgta  | 360  |
| gaccagttct tctactgacac tgaagggtta ccttacagta tcaacatgaa cgtcttcctc | 420  |
| cctgacatca ctcacctgag aactggcctc taaaaatccc agagaccgtg cgtaacacac  | 480  |
| atcaagacag aacctgttgc cattttcagc caccagagtg aaacgactgc cctcctccg   | 540  |
| gccccgacct aggccctccc tgagttcacc agtatattca gctcacacca gaccgcagct  | 600  |
| ccagagggtga acaatatttt catcaaaca gaacttccta caccagatct tcatctttct  | 660  |
| gtccctacct agcagggcca cctgtaccag ctactgaata caccggatct agatatgccc  | 720  |
| agttctacaa atcagacagc agcaatggac actcttaatg tttctatgtc agctgccatg  | 780  |
| gcaggcctta acacacacac ctctgctgtt ccgcagactg cagtgaaaca attccagggc  | 840  |
| atgccccctt gcacatacac aatgccaagt cagtttcttc cacaacaggc cacttacttt  | 900  |
| ccccgctcac caccaagctc agagcctgga agtccagata gacaagcaga gatgctccag  | 960  |
| aatttaacct cacctccatc ctatgctgct acaattgctt ctaaactggc aattcacaat  | 1020 |
| ccaaatttac ccaccacct gccagttaac tcacaaaaca tccaacctgt cagatacaat   | 1080 |
| agaaggagta accccgattt ggagaaacga cgcattccact actgcgatta ccctggttgc | 1140 |
| aaaaaagttt ataccaagtc ttctcattta aaagctcacc tgaggactca cactggtgaa  | 1200 |
| aagccataca agtgtacctg ggaaggctgc gactggagggt tcgcgcgatc ggatgagctg | 1260 |
| acccgccact accggaagca cacaggcgcc aagcccttcc agtgcggggt gtgcaaccgc  | 1320 |
| agcttctcgc gctctgacca cctggccctg catatgaaga ggcaccagaa ctga        | 1374 |

<210> 147  
 <211> 463  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> #110H13hIgG4P

<400> 147

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

Val Leu 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 Ser Asp Phe Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
50 55 60

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

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

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

Tyr Tyr Cys Ala Arg Gly Arg Gly Tyr Val Met Asp Ala Trp Gly Gln  
115 120 125

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

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala  
145 150 155 160

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
195 200 205

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys  
 210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro  
 225 230 235 240

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val  
 245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
 260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu  
 275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
 290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser  
 305 310 315 320

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
 325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile  
 340 345 350

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
 355 360 365

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
 370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
 385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
 405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg  
420 425 430

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
435 440 445

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

<210> 148  
<211> 1389  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> #110H13hIgG4P

<400> 148  
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gttcagctgg ttcaagtctgg cgccgaagtg aagaaacctg ggcctctgt gaaggtgtcc 120  
tgcaaggcca gcggtctacac ctttaccagc gacttcatgc actgggtccg acaggctcca 180  
ggacagggac ttgaatggat gggctggatc tatcccggcg acggcgatac agagtacgcc 240  
cagaaattcc agggcagagt gaccatgacc agagacacca gcatcagcac cgcctacatg 300  
gaactgagcc ggctgagatc cgatgacacc gccgtgtact actgcgccag aggcagaggc 360  
tatgtgatgg atgcttgggg ccagggcacc accgttacag ttagctcagc ctccaccaag 420  
ggccctagcg tgttccctct ggccccttgt agcagaagca ccagcgagtc tacagccgcc 480  
ctgggctgcc tcgtgaagga ctactttccc gagcccgtga ccgtgtcctg gaactctggc 540  
gctctgacaa gcggcgtgca cacctttcca gccgtgctgc agagcagcgg cctgtactct 600  
ctgtccagcg tcgtgactgt gcccagcagc tctctgggca ccaagacctc cacctgtaac 660  
gtggaccaca agcccagcaa caccaagggtg gacaagcggg tggaatctaa gtacggccct 720  
ccctgccctc cttgcccagc ccctgaattt ctgggcggac cctccgtgtt cctgttcccc 780  
caaagccca aggacacct gatgatcagc cggacccccg aagtgacctg cgtggtggtg 840  
gatgtgtccc aggaagatcc cgagggtcag ttcaattggt acgtggacgg cgtggaagtg 900  
cacaacgcca agaccaagcc tagagaggaa cagttcaaca gcacctaccg ggtggtgtcc 960

gtgctgacag tgctgcacca ggactggctg aacggcaaag agtacaagtg caaggtgtcc 1020  
 aacaagggcc tgcccagctc catcgagaaa accatcagca aggcccaagg ccagccccgc 1080  
 gaaccccagg tgtacacact gcctccaagc caggaagaga tgaccaagaa tcaggtgtcc 1140  
 ctgacctgtc tcgtgaaagg cttctacccc tccgatatcg ccgtggaatg ggagagcaac 1200  
 ggccagcccc agaacaacta caagaccacc ccccctgtgc tggactccga tggctcattc 1260  
 ttctgttaca gcagactgac cgtggacaag agccgggtggc aggaaggcaa cgtgttcagc 1320  
 tgctccgtga tgcacgaggc cctgcacaac cactacaccc agaagtcctt gtctctgagc 1380  
 ctgggcaaa 1389

<210> 149  
 <211> 234  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> #110L2h

<400> 149

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

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

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly  
 35 40 45

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
 50 55 60

Lys Pro Leu Ile Tyr Tyr Thr Ser Asn Leu Gln Ser Gly Val Pro Ser  
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser  
 85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp  
 100 105 110

Ser Ser Pro Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230

<210> 150  
<211> 702  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> #110L2h

<400> 150  
atgggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60  
gatatccaga tgacacagag ccctagcagc ctgtctgccg gcgtgggaga cagagtgacc 120  
atcacctgta gagccagcca gggcatcagc aactacctga actggtatca gcagaagccc 180  
ggcaaggccc ctaagcctct gatctactac accagcaacc tgcagagcgg cgtgcccagc 240  
agattttctg gctctggcag cggcaccgac tacaccctga ccatatctag cctgcagcct 300

gaggacttcg ccacctacta ctgccagcag tacgacagca gccccagaac atttggcgga 360  
ggcaccaagg tggaaatcaa gcgtacgggtg gccgccccct ccgtgttcat cttccccccc 420  
tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480  
cccagagagg ccaaggtgca gtggaagggtg gacaacgccc tgcagtccgg gaactcccag 540  
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600  
ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660  
ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt 702

<210> 151  
<211> 234  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> #110L12h

<400> 151

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

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

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly  
35 40 45

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
50 55 60

Lys Pro Leu Ile Tyr Tyr Thr Ser Asn Leu Gln Ser Gly Val Pro Ser  
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp  
100 105 110

Ser Ser Pro Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230

<210> 152  
<211> 702  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> #110L12h

<400> 152  
atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60  
gatatccaga tgacacagag ccctagcagc ctgtctgcca gcgtgggaga cagagtgacc 120  
atcacctgta gagccagcca gggcatcagc aactacctga actggtatca gcagaagccc 180  
ggcaaggccc ctaagcctct gatctactac accagcaacc tgcagagcgg cgtgcccagc 240  
agattttctg gctctggcag cggcaccgac ttcaccctga ccatatctag cctgcagcct 300  
gaggacttcg ccacctacta ctgccagcag tacgacagca gccccagaac atttggcggg 360

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| ggcaccaagg | tggaatcaa  | gcgtacggtg  | gccgccccct | ccgtgttcat | cttccccccc | 420 |
| tccgacgagc | agctgaagtc | cggcaccgcc  | tccgtggtgt | gcctgctgaa | taacttctac | 480 |
| cccagagagg | ccaaggtgca | gtggaagggtg | gacaacgccc | tcagtcctgg | gaactcccag | 540 |
| gagagcgtga | ccgagcagga | cagcaaggac  | agcacctaca | gcctgagcag | caccctgacc | 600 |
| ctgagcaaag | ccgactacga | gaagcacaag  | gtgtacgcct | gcgaggtgac | ccaccagggc | 660 |
| ctgagctccc | ccgtcaccaa | gagcttcaac  | aggggggagt | gt         |            | 702 |