

KR2016011428_Sequence Listing.TXT

<110> DINONA
 <120> Anti-CD43 antibody and use thereof for treating cancer
 <130> OPP20162379KR
 <150> US 62/240,276
 <151> 2015-10-12
 <150> AU 2016901555
 <151> 2016-04-28
 <160> 134
 <170> KopatentIn 2.0
 <210> 1
 <211> 366
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Quickchange mutant Combo A heavy chain variable region (VH) nucleotide sequence

<400> 1
 caggtgcagc tggtgcagag cggcgccgag gtgaagaaac ctggcgccag cgtgaagggtg 60
 tcctgcaagg ccagcggcta cagcatcggc ggctactaca tgaactgggt gcgccaggct 120
 cctggacagg gcctggaatg gatgggcccgg atcaacccca acagcggcga cagcttctac 180
 aaccagaaat tcaagggcag ggtgaccacg acccgcgaca ccagcaccag caccatgtac 240
 atggaactga gcagcctgag aagcgaggac accgccgtgt actactgcgc cagagagggc 300
 tattacggcg gcagaggcta cgccctggat tactggggcc agggcaccct ggtgaccgtg 360
 tcctcc 366

<210> 2
 <211> 122
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Quickchange mutant Combo A VH amino acid sequence

<400> 2
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
 20 25 30
 Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Ser Gly Asp Ser Phe Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Thr Thr Arg Asp Thr Ser Thr Ser Thr Met Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

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85

90

95

Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110

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

<210> 3
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Quickchange mutant Combo A light chain variable region (VL)
nucleotide sequence

<400> 3
gacatccaga tgacccggag ccctagcagc gtgtccgccg gcgtgggcgg cagagtgtcc 60
atcacctgtc ggaccagcca ggacatcagc aactacctga actggtatca gcagaagccc 120
gacggcaccg tcaagctgct gatctacaac accagccggc tgcacagcgg cgtgccaaagc 180
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagctc cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcggccag 300
ggtatcaagc tggagatcaa gcgt 324

<210> 4
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Quickchange mutant Combo A VL amino acid sequence

<400> 4
Asp Ile Gln Met Thr Arg Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15
Gly Arg Val Pro Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45
Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Ile Lys Leu Glu Ile Lys Arg
100 105

<210> 5
<211> 366
<212> DNA

<213> Artificial Sequence

<220>

<223> 257-10 (Round 2 variant) VH nucleotide sequence

<400> 5
cagggtgcagc tgggtgcagag cggcgccgag gtgaagaagc ccggcgccag cgtcaagggtg 60
tcctgcaagg ccagcggcta caccttcaac ggctacttca tgaactgggt gaggcaggcc 120
cctgggcagg gactggagcg gatgggccgc atcaaccca acaacggcga cagcttctac 180
aaccagaagt tccagggccg cgtcaccatg acccgcgaca ccagcaccag caccgtgtac 240
atggagctgc ccagcctgcg cagcgaggac accgccgtgt actactgcgc cagggagggc 300
tactacggcg gcagaggcta cgccctggac tactggggcc agggcacctt ggtgaccgtg 360
tcctcc 366

<210> 6

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> 257-10 (Round 2 variant) VH amino acid sequence

<400> 6
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Gly Tyr
20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Arg Met
35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Pro Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 7

<211> 325

<212> DNA

<213> Artificial Sequence

<220>

<223> 257-10 (Round 2 variant) VL nucleotide sequence

<400> 7
gacaccaga tgaccagag cccttcttct gtctccgcca gcgtgggcga ccgcgtgacc 60

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atcacctgcc gcaccagcca ggacatcagc aactacctga actggtatca gcagaagccc	120
ggcaaggccc ccaagctgct gatctacaac accagcaggc tccactctgg agtccccagc	180
cgcttctccg gctccgggtc tggaaccgac ttcaccctga ccatcagctc cctgcagccc	240
gaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcgggcag	300
gggaccaagc tggagatcaa gcgta	325

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

<220>
 <223> 257-10 (Round 2 variant) VL amino acid sequence

<400> 8
 Asp Thr Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 9
 <211> 366
 <212> DNA
 <213> Artificial sequence

<220>
 <223> 456-D10 VH nucleotide sequence

<400> 9 caggtgcagc tggtgcagag cggcgccgag gtgaagaagc ccggcgccag cgtcaagggtg	60
tcctgcaagg ccagcggcta caccttcaac ggctacttca tgaactgggt gaggcaggcc	120
cctgggcagg gactggagcg gatgggccgc atcaacccca acaacggcga cagcttctac	180
aaccagaagt tccagggccg cgtcaccatg acccgcgaca ccagcaccag caccgtgtac	240
atggagctgc ccagcctgcg cagcgaggac accgccgtgt actactgcgc cagggagggc	300
tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtgaccgtg	360
tcctcc	366

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<210> 10
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 456-D10 VH amino acid

<400> 10
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Gly Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Arg Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Pro Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 11
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 456-D10 VL nucleotide sequence

<400> 11
 gacacccaga tgacccagag cccttcttct gtctccgcca gcgtgggcga ccgcgtgacc 60
 atcacctgcc gcaccagcca ggacatcagc aactacctga actggtatca gcaggagccc 120
 ggcaaggccc ccaagctgct gatctacaac accagcaggc tccactctgg agtccccagc 180
 cgcttctccg gctccgggtc tggaaccgac ttcaccctga ccatcagctc cctgcagccc 240
 gaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcgggcag 300
 gggaccaagc tggagatcaa gcgg 324

<210> 12
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 456-D10 VL amino acid sequence

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<400>      12
Asp Thr Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
  1          5          10          15
Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
          20          25          30
Leu Asn Trp Tyr Gln Gln Glu Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35          40          45
Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
          65          70          75          80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
          85          90          95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
          100          105

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<210>      13
<211>      366
<212>      DNA
<213>      Artificial Sequence

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<220>
<223>      324-B10 VH nucleotide sequence

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<400>      13
caggtgcagc tggtgcagag cggcgccgag gtgaagaaac ctggcgccag cgtgaagggtg      60
tcctgcaagg ccagcggcta cagcatcggc ggctactaca tgaactgggt gcgccaggct      120
cctggacagg gcctggaatg gatggggccg atcaacccca acagcggcga cagcttctac      180
aaccagaaat tcaagggcag ggtgaccatg acccgcgaca ccagcaccag caccgtgtac      240
atggaactga gcagcctgag aagcgaggac accgccgtgt actactgcmc cagagagggc      300
tattacggcg gcagaggcta cgccctggat tactggggcc agggcaccct ggtgaccgtg      360
tcctcc                                           366

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<210>      14
<211>      122
<212>      PRT
<213>      Artificial Sequence

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<220>
<223>      324-B10 VH amino acid sequence

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<400>      14
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
  1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
          20          25          30
Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Arg Ile Asn Pro Asn Ser Gly Asp Ser Phe Tyr Asn Gln Lys Phe

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50

55

60

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 15
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 324-B10 VL nucleotide sequence

<400> 15
gacattcaga tgacccggag ccctagcagc gtgtccgcca gcgtgggcca cagagtgtcc 60
atcacctgtc ggaccagcca ggacatcagc aactacctga actggtatca gcagaagccc 120
gacggcaccg tcaagctgct gatctacaac accagccggc tgacagcgg cgtgccaagc 180
agattcagcg gcagcggctc cggcaccgac ttcacctga ccatcagctc cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcggccag 300
ggtatcaagc tggagatcaa gcgg 324

<210> 16
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 324-B10 VL amino acid sequence

<400> 16
Asp Ile Gln Met Thr Arg Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Ser Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45
Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Ile Lys Leu Glu Ile Lys Arg
100 105

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<210> 17
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 361-C11 VH nucleotide sequence

<400> 17
 caggtgcagc tggtgcagag cggcgccgag gtgaagaaac ctggcgccag cgtgaagggt 60
 tcctgcaagg ccagcggcta cagcatcggc ggctacttca tgaactgggt gcgccaggct 120
 cctggacagg gcctggaatg gatggggccgg atcaacccca acaacggcga cagcttctac 180
 aaccagaaat tcaagggcag ggtgaccatg acccgcgaca ccagcaccag caccgtgtac 240
 atggaactga gcagcctgag aagcgaggac accgccgtgt actactgcgc cagagagggc 300
 tattacggcg gcagaggcta cgccctggat tactggggcc agggcaccct ggtgaccgtg 360
 tcctcc 366

<210> 18
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 361-C11 VH amino acid sequence

<400> 18
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 19
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>

<223> 361-C11 VL nucleotide sequence

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<400>      19
gacattcaga tgacccggag ccctagcagc gtgtccgcca gcgtgggcgg cagagtgtcc      60
atcacctgtc ggaccagcca ggacatcagc aactacctga actggtatca gcagaagccc      120
gacggcaccg tcaagctgct gatctacaac accagccggc tgcacagcgg cgtgccaaagc      180
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagctc cctgcagccc      240
gaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcggccag      300
ggtatcaagc tggagatcaa gcgg                                           324

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<210> 20
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 361-C11 VL amino acid sequence

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

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<210> 21
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 368-G07 VH nucleotide sequence

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<400>      21
caggtgcagc tggtgcagag cggcgccgag gtgaagaaac ctggcgccag cgtgaagggt      60
tcntgcaagg ccagcggcta cagcatcggc ggctacttca tgaactgggt gcgccaggct      120
cctggacagg gcctggaatg gatgggcccg atcaacccca acaacggcga cagcttctac      180
aaccagaaat tcaagggcag ggtgaccatg acccgcgaca ccagcaccag caccgtgtac      240
atggaactga gcagcctgag aagcgaggac accgccgtgt actactgcgc cagagagggc      300

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tattacggcg gcagaggcta cgccctggat tactggggcc agggcaccct ggtgaccgtg 360
tcctcc 366

<210> 22
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 368-G07 VH amino acid sequence

<400> 22
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 23
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 368-G07 VL nucleotide sequence

<400> 23
gacattcaga tgacccggag ccctagcagc gtgtccgcca gcgtgggcga cagagtgtccc 60
atcacctgtc ggaccagcca ggacatcagc aactacctga actggtatca gcagaagccc 120
gacggcaccg tcaagctgct gatctacaac accagccggc tgcacagcgg cgtgccaaagc 180
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagctc cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcggccag 300
ggatatcaagc tggagatcaa gcgg 324

<210> 24
<211> 108
<212> PRT
<213> Artificial Sequence

KR2016011428_Sequence Listing.TXT

<220>

<223> 368-G07 VL amino acid sequence

<400> 24

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

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<210> 25

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> 369-F05 VH nucleotide sequence

<400> 25

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caggtgcagc tggtgcagag cggcgccgag gtgaagaaac ctggcgccag cgtgaagggtg      60
tcctgcaagg ccagcggcta cagcatcggc ggctacttca tgaactgggt gcgccaggct      120
cctggacagg gcctggaatg gatggggccgg atcaacccca acaacggcga cagcttctac      180
aaccagaaat tcaagggcag ggtgaccatg acccgcgaca ccagcaccag caccatgtac      240
atggaactga gcagcctgag aagcgaggac accgccgtgt actactgcgc cagagagggc      300
tattacggcg gcagaggcta cgccctggat tactggggcc agggcaccct ggtgaccgtg      360
tcctcc                                           366

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<210> 26

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> 369-F05 VH amino acid sequence

<400> 26

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1           5           10           15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
          20           25           30

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Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Met Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 27
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 369-F05 VL nucleotide sequenc

<400> 27
 gacattcaga tgacccggag ccctagcagc gtgtccgccg gcgtgggcga cagagtgtcc 60
 atcacctgtc ggaccagcca ggacatcagc aactacctga actggtatca gcagaagccc 120
 gacggcaccg tcaagctgct gatctacaac accagccggc tgcacagcgg cgtgccaaagc 180
 agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagctc cctgcagccc 240
 gaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcggccag 300
 ggtatcaagc tggagatcaa gcgg 324

<210> 28
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 369-F05 VL amino acid sequence

<400> 28
 Asp Ile Gln Met Thr Arg Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Ser Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45
 Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

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

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

<210> 29
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> 361-H05 VH nucleotide sequence

<400> 29
caggtgcagc tgggtgcagag cggcgccgag gtgaagaaac ctggcgccag cgtgaaggtg 60
tcctgcaagg ccagcggcta cagcatcggc ggctacttca tgaactgggt gcgccaggct 120
cctggacagg gcctggaatg gatgggcccg atcaacccca acaacggcga cagcttctac 180
aaccagaaat tcaagggcag ggtgaccacg acccgcgaca ccagcaccag caccgtgtac 240
atggaactga gcagcctgag aagcgaggac accgccgtgt actactgcgc cagagagggc 300
tattacggcg gcagaggcta cgccctggat tactggggcc agggcaccct ggtgactgtg 360
tcctcc 366

<210> 30
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 361-H05 VH amino acid sequence

<400> 30
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 15
1 5 10
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr 30
20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 45
35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe 60
50 55 60
Lys Gly Arg Val Thr Thr Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr 80
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 95
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp 110
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser 120
115 120

<210> 31

KR2016011428_Sequence Listing.TXT

<211> 324
 <212> DNA
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 35 40 45
 Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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 85 90 95
 Thr Phe Gly Gln Gly Ile Lys Leu Glu Ile Lys Arg
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 <212> DNA
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 <223> murine anti-CD43 (mJL-1) IgG Heavy Chain (HC) DNA sequence

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35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
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Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr 190
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser 220
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 240
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 255
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His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 285
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 300
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 320
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 335
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln 350
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val 365
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val 380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro 400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr 415
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<220>
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<220>
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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
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agcacggtgg gctaattgtt ccatgggtag catatactac ccaaatatct ggatagcata	2460
tgctatccta atctatatct gggtagcata ggctatccta atctatatct gggtagcata	2520
tgctatccta atctatatct gggtagtata tgctatccta atttatatct gggtagcata	2580
ggctatccta atctatatct gggtagcata tgctatccta atctatatct gggtagtata	2640
tgctatccta atctgtatcc gggtagcata tgctatccta atagagatta gggtagtata	2700
tgctatccta atttatatct gggtagcata tactacccaa atatctggat agcatatgct	2760
atcctaattc atatctgggt agcatatgct atcctaattc atatctgggt agcataggct	2820
atcctaattc atatctgggt agcatatgct atcctaattc atatctgggt agtatatgct	2880
atcctaattt atatctgggt agcataggct atcctaattc atatctgggt agcatatgct	2940
atcctaattc atatctgggt agtatatgct atcctaattc gtatccgggt agcatatgct	3000
atcctcatga taagctgtca aacatgagaa ttaattcttg aagacgaaag ggcctcgtga	3060

KR2016011428_Sequence Listing.TXT

tacgcctatt tttataggtt aatgtcatga taataatggt ttcttagacg tcagggtggca	3120
cttttcgggg aaatgtgcgc ggaacccta tttgtttatt tttctaaata cattcaaata	3180
tgtatccgct catgagacaa taaccctgat aaatgcttca ataatattga aaaaggaaga	3240
gtatgagtat tcaacatttc cgtgtcgccc ttattccctt ttttgcggca ttttgccttc	3300
ctgtttttgc tcaccagaa acgctggtga aagtaaaaga tgctgaagat cagttgggtg	3360
cacgagtggg ttacatcgaa ctggatctca acagcggtaa gatccttgag agttttcgcc	3420
ccgaagaacg ttttccaatg atgagcactt ttaaagtctt gctatgtggc gcggtattat	3480
cccgtgttga cgccgggcaa gagcaactcg gtcgccgat acactattct cagaatgact	3540
tggttgagta ctcaccagtc acagaaaagc atcttacgga tggcatgaca gtaagagaat	3600
tatgcagtgc tgccataacc atgagtata acactgcggc caacttactt ctgacaacga	3660
tcggaggacc gaaggagcta accgcttttt tgcacaacat gggggatcat gtaactcgcc	3720
ttgatcgttg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt gacaccacga	3780
tgctgcagc aatggcaaca acgttgcgca aactattaac tggcgaacta cttactctag	3840
cttcccggca acaattaata gactggatgg aggcggataa agttgcagga ccacttctgc	3900
gctcggccct tccggctggc tggtttattg ctgataaatc tggagccggt gagcgtgggt	3960
ctcgcggtat cattgcagca ctggggccag atggtaagcc ctcccgtatc gtagttatct	4020
acacgacggg gagtcaggca actatggatg aacgaaatag acagatcgct gagataggtg	4080
cctcactgat taagcattgg taactgtcag accaagttta ctcatatata ctttagattg	4140
atttaaaact tcatttttaa tttaaaagga tctaggtgaa gatccttttt gataatctca	4200
tgacaaaat cccttaacgt gagttttcgt tccactgagc gtcagacccc gtagaaaaga	4260
tcaaaggatc ttcttgagat cttttttttc tgcgcgtaat ctgctgcttg caaacaaaaa	4320
aaccaccgct accagcgggt gtttgtttgc cggatcaaga gctaccaact ctttttccga	4380
aggtaactgg cttcagcaga ggcagatac caaatactgt tcttctagtg tagccgtagt	4440
taggccacca cttcaagaac tctgtagcac cgcctacata cctcgtcttg ctaatcctgt	4500
taccagtggc tgctgccagt ggcgataagt cgtgtcttac cgggttggac tcaagacgat	4560
agttaccgga taaggcgcag cggtcgggct gaacgggggg ttcgtgcaca cagcccagct	4620
tggagcgaac gacctacacc gaactgagat acctacagcg tgagctatga gaaagcgcca	4680
cgcttcccga agggagaaa ggcgacaggt atccggtaag cggcagggtc ggaacaggag	4740
agcgcacgag ggagcttcca gggggaaacg cctgggtatct ttatagtcct gtcgggtttc	4800
gccacctctg acttgagcgt cgatttttgt gatgctcgtc aggggggagg agcctatgga	4860
aaaacgccag caacgcggcc tttttacggt tcctggcctt ttgctggcct tttgctcaca	4920
tgttctttcc tgcgttatcc cctgattctg tggataaccg tattaccgcc tttgagttag	4980
ctgataccgc tcgccgcagc cgaacgaccg agcgcagcga gtcagtgagc gaggaagc	5038

KR2016011428_Sequence Listing.TXT

<211> 1356
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Sh741JLH IgG HC DNA sequence

<400> 39
 caggtgcagc tggtgcagag cggcagcgag ctgaagaagc ccggcgccag cgtcaagggtg 60
 tcctgcaagg ccagcggcta caccttcacc ggctacttca tgaactgggt gcggcaggcc 120
 cctgggcagg gactggagtg gatggggccgc atcaacccca acaacggcga cagcttctac 180
 aaccagggct tcaccggccg cttcgtgttc agcctggaca ccagcgtgtc caccgcctac 240
 ctgcagatca gcagcctgaa ggccgaggac accgccgtgt actactgcgc cagggagggc 300
 tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtgaccgtg 360
 tccagcgcta gcaccaaggg cccatcggtc tttcccctgg caccctcctc caagagcacc 420
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccg gc tgtcctacag 540
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagagagtt 660
 gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 720
 gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg 780
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggtgaat 960
 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1020
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200
 cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc 1260
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320
 tacacgcaga agagcctctc cctgtctccg ggtaaa 1356

<210> 40
 <211> 452
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Sh741JLH IgG HC amino acid sequence

<400> 40
 Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
 1 5 10 15

KR2016011428_Sequence Listing.TXT

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Gly Phe
 50 55 60
 Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 225 230 235 240
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

KR2016011428_Sequence Listing.TXT

370
 385 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 390 395 400
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445
 Ser Pro Gly Lys
 450

<210> 41
 <211> 1356
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Sh145JLH IgG HC DNA sequence

<400> 41
 cagatgcagc tgggtgcagag cggcgccgag gtgaagaaaa ccggcagcag cgtcaagggtg 60
 tcctgcaagg ccagcggcta caccttcacc ggctacttca tgaactgggt gcgccaggcc 120
 cccggccagg ccctggagtg gatggggccgc atcaacccca acaacggcga cagcttctac 180
 aaccagaagt tccaggaccg cgtcaccatc acccgcgacc gcagcatgag caccgcctac 240
 atggagctgt ccagcctgag cagcgaggac accgcatgt actactgagc cagggaagggc 300
 tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtgaccgtg 360
 tccagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 420
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagagagtt 660
 gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 720
 gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg 780
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960
 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1020
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

KR2016011428_Sequence Listing.TXT

cccgtgctgg actccgacgg ctcttcttc ctctacagca agctcaccgt ggacaagagc 1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320
tacacgcaga agagcctctc cctgtctccg ggtaaa 1356

<210> 42
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Sh145JLH IgG HC amino acid sequence

<400> 42
Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Thr Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Ala Leu Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Gln Asp Arg Val Thr Ile Thr Arg Asp Arg Ser Met Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
210 215 220
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235 240
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260 265 270

KR2016011428_Sequence Listing.TXT

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
 450

<210> 43
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sh146JLH IgG HC DNA sequence

<400> 43
 cagggtgcagc tgggtgcagag cggcgccgag gtgaagaagc ccggcgccag cgtcaagggtg 60
 tcctgcaagg ccagcggcta cacccttcaac ggctacttca tgaactgggt gaggcaggcc 120
 cctgggcagg gactggagtg gatgggcccgc atcaacccca acaacggcga cagcttctac 180
 aaccagaagt tccagggccg cgtcaccatg acccgcgaca ccagcaccag caccgtgtac 240
 atggagctgt ccagcctgcg cagcgaggac accgccgtgt actactgcgc cagggagggc 300
 tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtgaccgtg 360
 tccagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 420
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt 660

KR2016011428_Sequence Listing.TXT

gagcccaa	at	ctt	gtg	acaa	aact	cacaca	tgccc	accgt	gccc	agcacc	tgaact	cctg	720	
ggggg	accgt	cagt	cttc	ctt	ccccca	aaacca	agg	acacc	ctcat	gat	ctccc	gg	780	
accct	gagg	tcac	atgc	gt	gg	tggtg	gac	gtg	agcc	acg	aagacc	ctga	840	
aact	ggtac	g	tg	gac	ggc	gt	ggag	gtcat	aat	gcc	aaga	caaag	ccgc	900
taca	acag	ca	cgt	acc	gtgt	gg	tcag	cgtc	ctc	acc	gtcc	tgc	acc	960
ggca	agg	agt	aca	agt	gcaa	gg	tct	cca	aac	aa	agcc	ctcc	cag	1020
atct	ccaa	ag	caa	agg	gca	gccc	gaga	aa	ccac	aggt	gt	acacc	ctg	1080
gat	gag	ctga	cca	aga	acca	gg	tcag	cctg	ac	ctg	cctg	g	tcaa	1140
gac	atc	gccg	tg	gag	tg	gga	gag	caat	ggg	cag	ccg	gaga	aca	1200
ccc	gtg	ctg	g	act	ccg	acg	gtc	ctt	cttc	ct	tac	agca	ag	1260
agg	tg	gcag	c	agg	gga	acgt	ctt	ct	cat	gc	tcc	gtg	atg	1320
tac	acg	caga	ag	ag	cct	ctc	cct	gt	ctcc	g	g	taaa		1356

<210> 44
 <211> 452
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> sh146JLH IgG HC amino acid sequence

<400>	44
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Gly Tyr	20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe	50 55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr	65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys	85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp	100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	115 120 125
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr	130 135 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr	145 150 155 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro	165 170 175

KR2016011428_Sequence Listing.TXT

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
210 215 220
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235 240
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260 265 270
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
290 295 300
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
325 330 335
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
355 360 365
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
405 410 415
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445
Ser Pro Gly Lys
450

<210> 45
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Sh434JLH IgG HC DNA sequence

<400> 45
caggtgcagc tgcaggagag cggccccggc ctggtgaagc ccagccagac cctgagcctg

KR2016011428_Sequence Listing.TXT

acctgcgccg tctacggagg aagcttcagc ggctacttca tgaactggat caggcagccc	120
cccggcaagg gcctggagtg gatcggccgc atcaaccca acaacggcga cttcagctac	180
aaccagagcc tgaagagccg cgtgaccatc agcgtggaca ccagcaagaa ccagttcagc	240
ctgaagctgt ccagcgtgac cgccgccgac accgccgtgt actactgcgc cagggagggc	300
tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtgaccgtg	360
tccagcgcta gcaccaaggc cccatcggtc ttccccctgg caccctcctc caagagcacc	420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag	540
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	600
cagacctaca tctgcaacgt gaatcacaa cccagcaaca ccaaggtgga caagagagtt	660
gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	720
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg	780
acccttgagg tcacatgcgt ggtgggtggac gtgagccacg aagaccctga ggtcaagttc	840
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	900
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	960
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	1080
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1140
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1200
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc	1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	1320
tacacgcaga agagcctctc cctgtctccg ggtaaa	1356

<210> 46
 <211> 452
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Sh434JLH IgG HC amino acid sequence

<400> 46
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
 20 25 30
 Phe Met Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Asn Pro Asn Asn Gly Asp Phe Ser Tyr Asn Gln Ser Leu
 50 55 60
 Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser

KR2016011428_Sequence Listing.TXT

65		70		75		80
Leu	Lys	Leu	Ser	Ser	Val	Thr
			85			Ala
						Ala
						Asp
						Thr
						Ala
						Val
						Tyr
						Tyr
						Cys
						95
Ala	Arg	Glu	Gly	Tyr	Tyr	Gly
			100			Gly
						Arg
						105
						Gly
						Tyr
						Ala
						Leu
						Asp
						110
Gly	Gln	Gly	Thr	Leu	Val	Thr
			115			Val
						120
						Ser
						Ser
						Ala
						Ser
						Thr
						125
						Lys
						Gly
						Gly
						Thr
Ser	Val	Phe	Pro	Leu	Ala	Pro
						135
						Ser
						Ser
						Lys
						Ser
						Thr
						140
						Ser
						Gly
						Gly
						Thr
Ala	Ala	Leu	Gly	Cys	Leu	Val
						150
						Lys
						Asp
						Tyr
						Phe
						155
						Pro
						Glu
						Pro
						Val
						Thr
						160
Val	Ser	Trp	Asn	Ser	Gly	Ala
						165
						Leu
						Thr
						170
						Ser
						Gly
						Val
						His
						Thr
						Phe
						175
						Pro
Ala	Val	Leu	Gln	Ser	Ser	Gly
						180
						Leu
						Tyr
						185
						Ser
						Leu
						Ser
						Ser
						Val
						190
Val	Pro	Ser	Ser	Ser	Leu	Gly
						200
						Gln
						Thr
						Tyr
						Ile
						Cys
						205
						Asn
						Val
						Asn
His	Lys	Pro	Ser	Asn	Thr	Lys
						215
						Val
						Asp
						Lys
						Arg
						Val
						220
						Glu
						Pro
						Lys
						Ser
Cys	Asp	Lys	Thr	His	Thr	Cys
						230
						Pro
						Pro
						Cys
						235
						Ala
						Pro
						Glu
						Leu
						240
Gly	Gly	Pro	Ser	Val	Phe	Leu
						245
						Phe
						Pro
						250
						Lys
						Pro
						Lys
						Asp
						Thr
						255
						Leu
Met	Ile	Ser	Arg	Thr	Pro	Glu
						260
						Val
						Thr
						265
						Cys
						Val
						Val
						Val
						Asp
						270
						Val
						Ser
His	Glu	Asp	Pro	Glu	Val	Lys
						280
						Phe
						Asn
						Trp
						Tyr
						Val
						Asp
						285
						Gly
						Val
						Glu
Val	His	Asn	Ala	Lys	Thr	Lys
						295
						Pro
						Arg
						Glu
						Glu
						Gln
						300
						Tyr
						Asn
						Ser
						Thr
Tyr	Arg	Val	Val	Ser	Val	Leu
						310
						Thr
						Val
						Leu
						His
						315
						Gln
						Asp
						Trp
						Leu
						Asn
						320
Gly	Lys	Glu	Tyr	Lys	Cys	Lys
						325
						Val
						Ser
						Asn
						330
						Lys
						Ala
						Leu
						Pro
						Ala
						335
						Pro
Ile	Glu	Lys	Thr	Ile	Ser	Lys
						340
						Ala
						Lys
						345
						Gly
						Gln
						Pro
						Arg
						Glu
						350
						Pro
						Gln
Val	Tyr	Thr	Leu	Pro	Pro	Ser
						360
						Arg
						Asp
						Glu
						Leu
						Thr
						Lys
						365
						Asn
						Gln
						Val
Ser	Leu	Thr	Cys	Leu	Val	Lys
						375
						Gly
						Phe
						Tyr
						Pro
						Ser
						380
						Asp
						Ile
						Ala
						Val
Glu	Trp	Glu	Ser	Asn	Gly	Gln
						390
						Pro
						Glu
						Asn
						Asn
						395
						Tyr
						Lys
						Thr
						Thr
						Pro
						400
Pro	Val	Leu	Asp	Ser	Asp	Gly
						405
						Ser
						Phe
						Phe
						410
						Leu
						Tyr
						Ser
						Lys
						Leu
						415
						Thr
Val	Asp	Lys	Ser	Arg	Trp	Gln
						420
						Gln
						Gly
						425
						Asn
						Val
						Phe
						Ser
						Cys
						430
						Ser
						Val

KR2016011428_Sequence Listing.TXT

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

Ser Pro Gly Lys
450

<210> 47
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Sh112JLL IgG LC DNA sequence

<400> 47
gacatccaga tgacccagag ccccagcagc gtgtccgcca gcgtgggcga ccgcgtgacc 60
atcacctgcc gcaccagcca ggacatcagc aactacctga actggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacaac accagccgcc tgcacagcgg cgtgccctcc 180
agattctccg gcagcggatc tggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcggccag 300
ggcaccaagc tggagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcga 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagttcac cggtgacaaa gagcttcaac aggggagagt gt 642

<210> 48
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Sh112JLL IgG LC amino acid sequence

<400> 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
85 90 95

KR2016011428_Sequence Listing.TXT

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 49
<211> 751
<212> DNA
<213> Artificial Sequence

<220>
<223> murine anti-CD43 (mJL1) scFv DNA sequence

<400> 49
ccatggccga gggttcagctg cagcagctctg gtcctgagct ggtgaagcct ggggcttcag 60
tgaagatttc ctgcaaggcc tctggttact caattggtgg ctactttatg aactgggtga 120
agcagagcca cggcaagagc cctgagtggg ttgggcgtat taatcctaac aatggtgatt 180
ctttctacaa ccagaaattc aagggcacgg ccacattgac tgttgaccgc tcttctgaca 240
cagtcacat ggaggtcctg agcctgacat ctgaggactc tgcagtctat tattgtggcc 300
gcgaagggtta ctacgggtggg cgaggggtatg ctttggacta ctgggggtcaa ggcacctcgg 360
tcaccgtctc ctacggcggc ggagctagcg ggggaggagg atccggaggc gggggatctg 420
atatccagat gacacagact acatcctccc tgtctgcctc tctgggcgac cgcgtcacca 480
tcagctgccg gacaagtcag gacattagca attatttgaa ctggtatcag cagaaaccag 540
atggtactgt taaactcctg atctataaca catcacgctt gcactcaggc gtcccatcac 600
ggttcagtg cagcgggtct ggtacagatt attccctcac cattcgcaac ctggaacaaa 660
aagatattgc cacttacttt tgccaacaga gcaatatgtt tccgtacacg ttcggggggg 720
ggaccaagct ggaaatcaag cgggcggccg c 751

<210> 50
<211> 247
<212> PRT
<213> Artificial Sequence

<220>

<223> murine anti-CD43 (mJL1) scFv amino acid sequence

<400> 50
Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro
1 5 10 15
Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly
20 25 30
Gly Tyr Phe Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Pro Glu
35 40 45
Trp Ile Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln
50 55 60
Lys Phe Lys Gly Thr Ala Thr Leu Thr Val Asp Arg Ser Ser Asp Thr
65 70 75 80
Val His Met Glu Val Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
85 90 95
Tyr Cys Gly Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp
100 105 110
Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Ala
115 120 125
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
130 135 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145 150 155 160
Ser Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
165 170 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Asn Thr Ser Arg
180 185 190
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Asp Tyr Ser Leu Thr Ile Arg Asn Leu Glu Gln Lys Asp Ile Ala Thr
210 215 220
Tyr Phe Cys Gln Gln Ser Asn Met Phe Pro Tyr Thr Phe Gly Gly Gly
225 230 235 240
Thr Lys Leu Glu Ile Lys Arg
245

<210> 51
<211> 751
<212> DNA
<213> Artificial sequence

<220>
<223> Sh741-112 scFv DNA sequence

<400> 51
ccatggccca ggtgcagctg gtgcagagcg gcagcgagct gaagaagccc ggcgccagcg 60
tcaaggtgtc ctgcaaggcc agcggctaca ctttcaccgg ctacttcattg aactgggtgc 120
gccaggcccc tgggcaggga ctggagtgga tgggccgcat caacccaac aacggcgaca 180

KR2016011428_Sequence Listing.TXT

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gcttctacaa ccagggcttc accggccgct tcgtgttcag cctggacacc agcgtgtcca      240
ccgcctacct gcagatcagc agcctgaagg ccgaggacac cgccgtgtac tactgcgcca      300
gggaggggcta ctacggaggg agaggggtacg ccctggacta ctggggccag ggcaccctgg      360
tgaccgtgtc ctccggcggc ggaggatccg gaggcggggg atctggggga ggagctagcg      420
acatccagat gacccagagc ccttcttctg tctccgccag cgtgggcgac cgcgtgacca      480
tcacctgccg caccagccag gacatcagca actacctgaa ctggtatcag cagaagcccg      540
gcaaggcccc caagctgctg atctacaaca ccagcaggct ccactctgga gtccccagcc      600
gcttctccgg ctccgggtct ggaaccgact tcaccctgac catcagctcc ctgcagcccg      660
aggacttcgc cacctactac tgccagcaga gcaacatgtt cccctacacc ttcgggcagg      720
ggaccaagct ggagatcaag cgggcggccg c                                     751

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<210> 52
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> sh741-112 scFv amino acid sequence

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<400> 52
Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
 1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
          20          25          30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Gly Phe
          50          55          60
Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
          65          70          75          80
Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
          100          105          110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
          115          120          125
Gly Gly Gly Ser Gly Gly Gly Ala Ser Asp Ile Gln Met Thr Gln Ser
          130          135          140
Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
          145          150          155          160
Arg Thr Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys
          165          170          175
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asn Thr Ser Arg Leu His
          180          185          190

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KR2016011428_Sequence Listing.TXT

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Thr Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Ser Asn Met Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys Arg
245

<210> 53
<211> 751
<212> DNA
<213> Artificial Sequence

<220>
<223> Sh145-112 scFv DNA sequence

<400> 53
ccatggccca gatgcagctg gtgcagagcg gcgccgaggt gaagaaaacc ggcagcagcg 60
tcaaggtgtc ctgcaaggcc agcggctaca ccttcaccgg ctacttcatg aactgggtgc 120
gccaggcccc cggccaggcc ctggagtggg tgggccgcat caacccaac aacggcgaca 180
gcttctacaa ccagaagttc caggaccgcg tcaccatcac ccgcgaccgc agcatgagca 240
ccgcctacat ggagctgtcc agcctgcgca gcgaggacac cgccatgtac tactgcgcca 300
gggagggcta ctacggcggc agaggctacg ccctggacta ctggggccag ggcaccctgg 360
tgaccgtgtc ctccggcggc ggaggatccg gaggcggggg atctggggga ggagctagcg 420
acatccagat gaccagagc ctttcttctg tctccgccag cgtgggagc cgcgtagca 480
tcacctgccg caccagccag gacatcagca actacctgaa ctggtatcag cagaagcccg 540
gcaaggcccc caagctgctg atctacaaca ccagcaggct ccactctgga gtccccagcc 600
gcttctccgg ctccgggtct ggaaccgact tcaccctgac catcagctcc ctgcagcccc 660
aggacttcgc cacctactac tgccagcaga gcaacatgtt cccctacacc ttcgggcagg 720
ggaccaagct ggagatcaag cgggcggccg c 751

<210> 54
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Sh145-112 scFv amino acid sequence

<400> 54
Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Thr Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Ala Leu Glu Trp Met
35 40 45

KR2016011428_Sequence Listing.TXT

Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Gln Asp Arg Val Thr Ile Thr Arg Asp Arg Ser Met Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125
Gly Gly Gly Ser Gly Gly Gly Ala Ser Asp Ile Gln Met Thr Gln Ser
130 135 140
Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160
Arg Thr Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys
165 170 175
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asn Thr Ser Arg Leu His
180 185 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Ser Asn Met Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240
Leu Glu Ile Lys Arg
245

<210> 55
<211> 751
<212> DNA
<213> Artificial Sequence
<220>
<223> Sh146-112 scFv DNA sequence

<400> 55
ccatggccca ggtgcagctg gtgcagagcg gcgccgaggt gaagaagccc ggcgccagcg 60
tcaaggtgtc ctgcaaggcc agcggctaca ctttcaacgg ctacttcatg aactgggtga 120
ggcaggcccc tgggcaggga ctggagtgga tgggccgcat caaccccaac aacggcgaca 180
gcttctacaa ccagaagttc cagggccgcg tcaccatgac ccgcgacacc agcaccagca 240
ccgtgtacat ggagctgtcc agcctgcgca gcgaggacac cgccgtgtac tactgcgcca 300
gggaggggcta ctacggcggc agaggctacg ccctggacta ctgggggtcaa ggcaccctgg 360
tgaccgtgtc cagcggcggc ggaggatccg gaggcggggg atctggggga ggagctagcg 420
acatccagat gaccagagc ctttcttctg tctccgccag cgtgggcgac cgcgtgacca 480
tcacctgccg caccagccag gacatcagca actacctgaa ctggtatcag cagaagcccg 540

KR2016011428_Sequence Listing.TXT

gcaaggcccc caagctgctg atctacaaca ccagcaggct ccactctgga gtccccagcc	600
gcttctccgg ctccgggtct ggaaccgact tcaccctgac catcagctcc ctgcagcccc	660
aggacttcgc cacctactac tgccagcaga gcaacatgtt ccctacacc ttcgggcagg	720
gtacaaagct ggagatcaag cgggcggccg c	751

<210> 56
 <211> 247
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> sh146-112 scFv amino acid sequence

<400> 56
 Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
 1 5 10 15
 Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn
 20 25 30
 Gly Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 35 40 45
 Trp Met Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln
 50 55 60
 Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr
 65 70 75 80
 Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp
 100 105 110
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ser Asp Ile Gln Met Thr
 130 135 140
 Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile
 145 150 155 160
 Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
 165 170 175
 Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asn Thr Ser Arg
 180 185 190
 Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220
 Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr Thr Phe Gly Gln Gly
 225 230 235 240
 Thr Lys Leu Glu Ile Lys Arg
 245

KR2016011428_Sequence Listing.TXT

<210> 57
<211> 751
<212> DNA
<213> Artificial Sequence

<220>
<223> Sh434-112 scFv DNA sequence

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<400> 57
ccatggccca ggtgcagctg caggagagcg gccccggcct ggtgaagccc agccagaccc      60
tgagcctgac ctgcgccgtc tacggaggaa gcttcagcgg ctacttcatg aactggatca      120
ggcagccccc cggcaagggc ctggagtgga tcggccgcat caaccccaac aacggcgact      180
tcagctacaa ccagagcctg aagagccgcg tgaccatcag cgtggacacc agcaagaacc      240
agttcagcct gaagctgtcc agcgtgaccg ccgccgacac cgccgtgtac tactgcgcca      300
gggaggggcta ctacggcggc agaggctacg ccctggacta ctggggccag ggcaccctgg      360
tgaccgtgtc cagcggcggc ggaggatccg gaggcggggg atctggggga ggagctagcg      420
acatccagat gaccagagc ctttcttctg tctccgccag cgtgggcgac cgcgtgacca      480
tcacctgccg caccagccag gacatcagca actacctgaa ctggtatcag cagaagccccg      540
gcaaggcccc caagctgctg atctacaaca ccagcaggct ccactctgga gtccccagcc      600
gcttctccgg ctccgggtct ggaaccgact tcacctgac catcagctcc ctgcagccccg      660
aggacttcgc cacctactac tgccagcaga gcaacatgtt cccctacacc ttcgggcagg      720
gtacaaagct ggagatcaag cgggcggccg c                                     751
    
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<210> 58
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Sh434-112 scFv amino acid sequence

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<400> 58
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1          5          10          15
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
          20          25          30
Phe Met Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
          35          40          45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Phe Ser Tyr Asn Gln Ser Leu
          50          55          60
Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
          65          70          75          80
Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
          100          105          110
    
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KR2016011428_Sequence Listing.TXT

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125
Gly Gly Gly Ser Gly Gly Gly Ala Ser Asp Ile Gln Met Thr Gln Ser
130 135 140
Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160
Arg Thr Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys
165 170 175
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asn Thr Ser Arg Leu His
180 185 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Ser Asn Met Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240
Leu Glu Ile Lys Arg
245

<210> 59
<211> 1356
<212> DNA
<213> Artificial Sequence
<220>
<223> Sh741JLHP45 IgG HC DNA sequence

<400> 59
cagggtgcagc tgggtgcagag cggcagcgcg ctgaagaagc ccggcgccag cgtcaagggtg 60
tcctgcaagg ccagcggcta caccttcacc ggctacttca tgaactgggt gcgccaggcc 120
cccggacagg ggcccagagt gatgggcccgc atcaacccca acaacggcga cagcttctac 180
aaccagggct tcaccggccg cttcgtgttc agcctggaca ccagcgtgtc caccgcctac 240
ctgcagatca gcagcctgaa ggccgaggac accgccgtgt actactgcgc cagggagggc 300
tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtgaccgtg 360
tccagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag 540
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtga caagagagtt 660
gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 720
gggggaccgt cagtcttct cttccccca aaaccaagg acaccctcat gatctcccg 780
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caagccgcg ggaggagcag 900

KR2016011428_Sequence Listing.TXT

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	960
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	1080
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1140
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1200
cccgtgctgg actccgacgg ctctttcttc ctctacagca agctcaccgt ggacaagagc	1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	1320
tacacgcaga agagcctctc cctgtctccg ggtaaa	1356

<210> 60
 <211> 452
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Sh741JLHP45 IgG HC amino acid sequence, wherein the 45th amino acid residue is substituted with P

<400> 60
 Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Pro Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Gly Phe
 50 55 60
 Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
 450

<210> 61
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sh145JLHP45 IgG HC DNA sequence

<400> 61
 cagatgcagc tgggtgcagag cggcgccgag gtgaagaaaa ccggcagcag cggtcaagggtg 60
 tcctgcaagg ccagcggcta caccttcacc ggctacttca tgaactgggt gaggcaggcc 120
 cctggacagg ccccgagtg gatgggccgc atcaacccca acaacggcga cagcttctac 180
 aaccagaagt tccaggaccg cgtcaccatc acccgcgacc gcagcatgag caccgcctac 240
 atggagctgt ccagcctgcg cagcaggagc accgcatgt actactgcgc cagggagggc 300

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tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtgaccgtg	360
tccagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctcttc caagagcacc	420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag	540
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	600
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtga caagagagtt	660
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	720
gggggaccgt cagtcttctt cttcccccca aaaccaaggg acaccctcat gatctcccgg	780
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	840
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	900
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	960
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	1080
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1140
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1200
cccgtgctgg actccgacgg ctcttctctt ctctacagca agctcaccgt ggacaagagc	1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	1320
tacacgcaga agagcctctc cctgtctccg ggtaaa	1356

<210> 62
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> sh145JLHP45 IgG HC variant (residue 45 is substituted with P)
 amino acid sequence

<400> 62
Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Thr Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Ala Pro Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Gln Asp Arg Val Thr Ile Thr Arg Asp Arg Ser Met Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp

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100		105		110											
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
		115					120					125			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
	130					135					140				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
145					150					155					160
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
			165						170					175	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
		180						185					190		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
	195						200					205			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser
210						215					220				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
225					230					235					240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
			245						250					255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
		260						265					270		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
	275						280					285			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
	290					295					300				
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
305					310					315					320
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
				325					330					335	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
		340						345					350		
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
	355						360					365			
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
	370					375					380				
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
385					390					395					400
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr
			405						410					415	
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
		420						425					430		
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
	435					440						445			
Ser	Pro	Gly	Lys												
450															

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<210> 63
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sh112JLV44 IgG LC variant DNA sequence

<400> 63
 gacatccaga tgaccagag cccagcagc gtgtccgcca gcgtgggcga ccgcgtgacc 60
 atcacctgcc gcaccagcca ggacatcagc aactacctga actggtatca gcagaagccc 120
 ggcaaggccg tgaagctgct gatctacaac accagccgcc tgcacagcgg cgtgccctcc 180
 agattctccg gcagcggatc tggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
 gaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcggccag 300
 ggcaccaagc tggagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagttcac cggtgacaaa gagcttcaac aggggagagt gt 642

<210> 64
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sh112JLV44 IgG LC variant (residue 44 is substituted with V)
 amino acid sequence

<400> 64
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Val Lys Leu Leu Ile
 35 40 45
 Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

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Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 65
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence CDhRZ7VHKb (Conv. Humanized variants IgG)

<400> 65
gaggtgcagc tgggtccagag cggcgccgag gtcaagaagc ctggcgccac cgtcaagatc 60
agctgcaagg ccagcggcta caccttcagc ggctacttca tgaactgggt ccgccaggcc 120
ccaggcaagg gactggagtg gatgggccgc atcaacccca acaacggcga cagcttctac 180
aaccagaagt tcaagggccg cgtcaccatc accgcccaca ccagcaccga caccggctac 240
ctggagctgt ccagcctgag aagcgaggac accgcccgtgt actactgtgc cgccgagggc 300
tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtgtccgtg 360
agcagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgccttacag 540
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt 660
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 720
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg 780
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840
aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 900
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140

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gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200
cccgtgctgg actccgacgg ctctttcttc ctctacagca agctcaccgt ggacaagagc 1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320
tacacgcaga agagcctctc cctgtctccg ggtaaa 1356

<210> 66
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence CDhRZ7VHKb (Conv. Humanized variants IgG)

<400> 66
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Gly Tyr
20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Gly Tyr
65 70 75 80
Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Ser Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
210 215 220
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235 240
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

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260

265

270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445
 Ser Pro Gly Lys
 450

<210> 67
 <211> 1356
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> DNA sequence CDhRZ7VH_KbR73 (Conv. Humanized variants IgG)

<400> 67
 gaggtgcagc tggtccagag cggcgccgag gtcaagaagc ctggcgccac cgtcaagatc 60
 agctgcaagg ccagcggcta caccttcagc ggctacttca tgaactgggt ccgccaggcc 120
 ccaggcaagg gactggagtg gatgggcccgc atcaacccca acaacggcga cagcttctac 180
 aaccagaagt tcaagggccg cgtcaccatc accgccgacc gcagcaccga caccggctac 240
 ctggagctgt ccagcctgag aagcgaggac accgccgtgt actactgtgc cgccgagggc 300
 tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtgtccgtg 360
 agcagcgcta gcaccaaggg cccatcggtc tttcccctgg caccctctc caagagcacc 420
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag 540
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600

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cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt	660
gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	720
gggggaccgt cagtcttcct cttcccccca aaaccaaggg acaccctcat gatctcccgg	780
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	840
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	900
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	960
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	1080
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1140
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1200
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc	1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	1320
tacacgcaga agagcctctc cctgtctccg ggtaaa	1356

<210> 68
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence CDhRZ7VH_KbR73 (Conv. Humanized variants IgG)

<400> 68
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Gly Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Ile Thr Ala Asp Arg Ser Thr Asp Thr Gly Tyr
 65 70 75 80
 Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Ser Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160

KR2016011428_Sequence Listing.TXT

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
450

<210> 69

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA sequence CDhL7IVHkb (Conv. Humanized variants IgG)

<400> 69

KR2016011428_Sequence Listing.TXT

gaggtgcagc tggtcgagag cggcgggggc ctggtgcagc ctggcggcag cctgcgccctg	60
agctgcgccg ccagcggcctt caccttcacc ggctacttca tgaactgggt ccgccaggcc	120
ccagggaaag gcctggagtg ggtggccccg atcaacccca acaacggcga cagcttctac	180
aaccagaagt tcaagggccg cttcacccctg agcgtggacc gcagcaagaa caccctgtac	240
ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgc cagagagggc	300
tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtcacccgtg	360
tccagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctcttc caagagcacc	420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag	540
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	600
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagagagtt	660
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	720
gggggaccgt cagtcttctt cttcccccca aaaccaagg acaccctcat gatctcccgg	780
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	840
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	900
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctgggtgaat	960
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	1080
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1140
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1200
cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc	1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	1320
tacacgcaga agagcctctc cctgtctccg ggtaaa	1356

<210> 70
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence CDhL7IVHkb (Conv. Humanized variants IgG)

<400> 70
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Gly Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
 50 55 60

KR2016011428_Sequence Listing.TXT

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 225 230 235 240
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

KR2016011428_Sequence Listing.TXT

420 425 430
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445
 Ser Pro Gly Lys
 450

<210> 71
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence CDhRZ7VHAM (Conv. Humanized variants IgG)

<400> 71
 gaggtgcagc tgggtccagag cggcgccgag gtcaagaagc ctggcgccac cgtcaagatc 60
 agctgcaagg ccagcggcta cagcatcggc ggctacttca tgaactgggt ccgccaggcc 120
 ccaggcaagg gactggagtg gatgggcccgc atcaacccca acaacggcga cagcttctac 180
 aaccagaagt tcaagggccg cgtcaccatc accgcccaca ccagcaccga caccggctac 240
 ctggagctgt ccagcctgag aagcgaggac accgcccgtgt actactgtgc cgccgagggc 300
 tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtgtccgtg 360
 agcagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 420
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagagagtt 660
 gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 720
 gggggaccgt cagtcttctt cttcccccca aaacccaagg acaccctcat gatctcccg 780
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960
 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1020
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200
 cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320
 tacacgcaga agagcctctc cctgtctccg ggtaaa 1356

<210> 72
 <211> 452

KR2016011428_Sequence Listing.TXT

<212> PRT
 <213> Artificial Sequence
 <220>
 <223> Amino acid sequence CDhRZ7VHAM (Conv. Humanized variants IgG)

<400> 72
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Gly Tyr
 65 70 75 80
 Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Ser Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 225 230 235 240
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

KR2016011428_Sequence Listing.TXT

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

<210> 73
 <211> 1356
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> DNA sequence CDHRZ7VHAMR73 (Conv. Humanized variants IgG)

<400> 73
 gaggtgcagc tggtccagag cggcgccgag gtcaagaagc ctggcgccac cgtcaagatc 60
 agctgcaagg ccagcggcta ctccatcggc ggctacttca tgaactgggt ccgccaggcc 120
 ccaggcaagg gactggagtg gatggggccgc atcaacccca acaacggcga cagcttctac 180
 aaccagaagt tcaagggccg cgtcaccatc accgccgacc gcagcaccga caccggctac 240
 ctggagctgt ccagcctgag aagcgaggac accgccgtgt actactgtgc cgccgagggc 300
 tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtgtccgtg 360
 agcagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctcttc caagagcacc 420
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag 540
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600
 cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaagggtga caagagagtt 660
 gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 720
 gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg 780
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

KR2016011428_Sequence Listing.TXT

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	960
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	1080
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1140
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1200
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc	1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	1320
tacacgcaga agagcctctc cctgtctccg ggtaaa	1356

<210> 74
 <211> 452
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Amino acid sequence CDhRZ7VHAMR73 (Conv. Humanized variants IgG)

<400> 74
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Ile Thr Ala Asp Arg Ser Thr Asp Thr Gly Tyr
 65 70 75 80
 Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Ser Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220

KR2016011428_Sequence Listing.TXT

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 225 230 235 240
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445
 Ser Pro Gly Lys
 450

<210> 75
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence CDhL7IVHAM (Conv. Humanized variants IgG)

<400> 75	
gaggtgcagc tggtcgagag cggcgggggc ctggtgcagc ctggcggcag cctgcgcctg	60
agctgcgccg ccagcggcta ctccatcggc ggctacttca tgaactgggt ccgccaggcc	120
ccagggaaag gcctggagtg ggtggcccgc atcaacccca acaacggcga cagcttctac	180
aaccagaagt tcaagggccg cttcaccctg agcgtggacc gcagcaagaa caccctgtac	240
ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgc cagagagggc	300
tactacggcg gcagaggcta cgccctggac tactggggcc agggcaccct ggtcaccgtg	360

KR2016011428_Sequence Listing.TXT

tccagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc	420
tctggggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag	540
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttggggcacc	600
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtga caagagagtt	660
gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	720
gggggaccgt cagtcttcct cttcccccca aaaccaagg acacctcat gatctcccgg	780
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	840
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	900
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	960
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acacctgcc cccatcccgg	1080
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1140
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1200
cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc	1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	1320
tacacgcaga agagcctctc cctgtctccg ggtaaa	1356

<210> 76
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence CDhL7IVHAM (Conv. Humanized variants IgG)

<400> 76
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro

KR2016011428_Sequence Listing.TXT

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115                               120                               125
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130                               135                               140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                               150                               155                               160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165                               170                               175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180                               185                               190
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195                               200                               205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
210                               215                               220
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                               230                               235                               240
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245                               250                               255
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260                               265                               270
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
275                               280                               285
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
290                               295                               300
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                               310                               315                               320
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
325                               330                               335
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340                               345                               350
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
355                               360                               365
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370                               375                               380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                               390                               395                               400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
405                               410                               415
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420                               425                               430
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435                               440                               445
Ser Pro Gly Lys
450

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<210> 77
<211> 642

KR2016011428_Sequence Listing.TXT

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> DNA sequence CDhRZ7Vk (light chain variant)

<400> 77
 gacatccaga tgacccagag ccccagcagc gtgtccgcca gcgtgggcga ccgcgtgacc 60
 atcacctgcc gcaccagcca ggacatcagc aactacctga actggtatca gcagaagccc 120
 ggcaaggccc ccaagctgct gatctacaac accagccgcc tgcacagcgg cgtgccctcc 180
 agattctccg gcagcggatc tggcaccgac ttcagcctga ccatcaatag cctgcagccc 240
 gaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcggcggc 300
 ggcaccaagg tggagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagttcac cggtgacaaa gagcttcaac aggggagagt gt 642

<210> 78
 <211> 214
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Amino acid sequence CDhRZ7Vk (light chain variant)

<400> 78
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Asn Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

KR2016011428_Sequence Listing.TXT

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 79
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence CDhRZ7VkFS (light chain variant)

<400> 79
 gacatccaga tgaccagag cccagcagc gtgtccgcca gcgtgggcga ccgcgtgacc 60
 atcacctgcc gcaccagcca ggacatcagc aactacctga actggtatca gcagaagccc 120
 ggcaaggccc ccaagctgct gatctacaac accagccgcc tgcacagcgg cgtgccctcc 180
 agattctccg gcagcggatc tggcaccgac ttcagcctga ccatccgcag cctgcagccc 240
 aaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcggcggc 300
 ggcaccaagg tggagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagttcac cggtgacaaa gagcttcaac aggggagagt gt 642

<210> 80
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence CDhRZ7VkFS (light chain variant)

<400> 80
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

KR2016011428_Sequence Listing.TXT

Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Arg Ser Leu Gln Pro
65 70 75 80
Lys Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 81
<211> 642
<212> DNA
<213> Artificial sequence

<220>
<223> DNA sequence CDHL7IVk (light chain variant)

<400> 81
gacatccaga tgaccagag cccagcagc ctgtccgcca gcgtgggcga ccgcgtgacc 60
atcacctgcc gcaccagcca ggacatcagc aactacctga actggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacaac accagccgcc tgcacagcgg cgtgccctcc 180
agattctccg gcagcggatc tggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag agcaacatgt tcccctacac cttcggccag 300
ggcaccaagg tggagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagttcac cggtgacaaa gagcttcaac aggggagagt gt 642

<210> 82

KR2016011428_Sequence Listing.TXT

<211> 214
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Amino acid sequence CDhL7IVk (light chain variant)

<400> 82
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 83
 <211> 122
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> sh146-112 heavy chain variable region (VH)

<400> 83
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Gly Tyr
 20 25 30

KR2016011428_Sequence_Listing.TXT

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 84
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 36-10 Q6R heavy chain variable region (VH)

<400> 84
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Arg Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 85
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 153-28 heavy chain variable region (VH)

<400> 85
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
Page 65

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20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 86
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 324-B10 heavy chain variable region (VH)

<400> 86
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
20 25 30
Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Asn Ser Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Arg Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 87
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 361-C11 heavy chain variable region (VH)

<400> 87
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

KR2016011428_Sequence Listing.TXT

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 88
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 368-G07 heavy chain variable region (VH)

<400> 88
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
20 25 30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 89
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 369-F05 heavy chain variable region (VH)

<400> 89

KR2016011428_Sequence Listing.TXT

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Met Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 90
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 361-H05 heavy chain variable region (VH)

<400> 90
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Thr Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 91
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Quikchange mutant heavy chain variable region (VH)

KR2016011428_Sequence Listing.TXT

```

<400>      91
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1              5              10              15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile Gly Gly Tyr
              20              25              30
Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
              35              40              45
Gly Arg Ile Asn Pro Asn Ser Gly Asp Ser Phe Tyr Asn Gln Lys Phe
              50              55              60
Lys Gly Arg Val Thr Thr Thr Arg Asp Arg Ser Thr Ser Thr Met Tyr
              65              70              75              80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
              85              90              95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
              100              105              110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
              115              120

```

```

<210>      92
<211>      122
<212>      PRT
<213>      Artificial sequence

<220>
<223>      45-37 VH heavy chain variable region (VH)

```

```

<400>      92
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1              5              10              15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Gly Tyr
              20              25              30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Arg Met
              35              40              45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
              50              55              60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
              65              70              75              80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
              85              90              95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
              100              105              110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
              115              120

```

```

<210>      93
<211>      122
<212>      PRT
<213>      Artificial sequence

<220>

```

<223> 257-10 heavy chain variable region (VH)

```

<400>      93
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Gly Tyr
          20          25          30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Arg Trp Met
          35          40          45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
          50          55          60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
          65          70          75          80
Met Glu Pro Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
          100          105          110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
          115          120

```

```

<210>      94
<211>      122
<212>      PRT
<213>      Artificial Sequence

```

<220>
<223> 456-D10 heavy chain variable region (VH)

```

<400>      94
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Gly Tyr
          20          25          30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Arg Met
          35          40          45
Gly Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe
          50          55          60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
          65          70          75          80
Met Glu Leu Pro Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Arg Glu Gly Tyr Tyr Gly Gly Arg Gly Tyr Ala Leu Asp Tyr Trp
          100          105          110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
          115          120

```

```

<210>      95
<211>      108
<212>      PRT
<213>      Artificial Sequence

```

KR2016011428_Sequence Listing.TXT

<220>

<223> sh146-112 light chain variable region (VL)

<400>

```

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

```

<210> 96

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 36-10 Q6R light chain variable region (VL)

<400>

```

      96
Asp Ile Gln Met Thr Arg Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
      20           25           30
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
      35           40           45
Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
      50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
      65           70           75           80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
      85           90           95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
      100           105

```

<210> 97

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 153-28 light chain variable region (VL)

KR2016011428_Sequence Listing.TXT

```

<400>      97
Asp Ile Gln Met Thr Arg Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1          5          10          15
Asp Arg Val Ser Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
          20          25          30
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
          35          40          45
Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
          65          70          75          80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
          85          90          95
Thr Phe Gly Gln Gly Ile Lys Leu Glu Ile Lys Arg
          100          105

```

```

<210>      98
<211>      108
<212>      PRT
<213>      Artificial Sequence

<220>
<223>      324-B10 light chain variable region (VL)

```

```

<400>      98
Asp Ile Gln Met Thr Arg Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1          5          10          15
Asp Arg Val Ser Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
          20          25          30
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
          35          40          45
Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
          65          70          75          80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
          85          90          95
Thr Phe Gly Gln Gly Ile Lys Leu Glu Ile Lys Arg
          100          105

```

```

<210>      99
<211>      108
<212>      PRT
<213>      Artificial Sequence

<220>
<223>      361-C11 light chain variable region (VL)

```

```

<400>      99
Asp Ile Gln Met Thr Arg Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1          5          10          15

```

KR2016011428_Sequence Listing.TXT

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

<210> 100
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 368-G07 light chain variable region (VL)

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

<210> 101
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 369-F05 light chain variable region (VL)

<400> 101
Asp Ile Gln Met Thr Arg Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Ser Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
20 25 30

KR2016011428_Sequence Listing.TXT

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45
 Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Ile Lys Leu Glu Ile Lys Arg
 100 105

<210> 102
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 361-H05 light chain variable region (VL)

<400> 102
 Asp Ile Gln Met Thr Arg Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Ser Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45
 Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Ile Lys Leu Glu Ile Lys Arg
 100 105

<210> 103
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Quikchange mutant light chain variable region (VL)

<400> 103
 Asp Ile Gln Met Thr Arg Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
 Gly Arg Val Pro Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45
 Tyr Asn Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly

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50

55

60

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

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

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

<210> 104

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 45-37 light chain variable region (VL)

<400> 104

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

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

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

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

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

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

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

<210> 105

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 257-10 light chain variable region (VL)

<400> 105

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

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

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

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

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

KR2016011428_Sequence Listing.TXT

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

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

<210> 106
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 456-D10 light chain variable region (VL)

<400> 106
Asp Thr Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

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

<210> 107
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable region (VL) variant (deglycosylated)

<400> 107
Asp Thr Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

KR2016011428_Sequence Listing.TXT

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

<210> 108
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable region (VL) variant (deglycosylated)

<400> 108
Asp Thr Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Gln Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 109
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable region (VL) variant (deglycosylated)

<400> 109
Asp Thr Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Met Phe Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

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<210>      110
<211>      5
<212>      PRT
<213>      Artificial Sequence

<220>
<221>      MOD_RES
<222>      (3)
<223>      Xaa is Phe (F) or Tyr (Y)

<220>
<223>      CDRH1 of anti-CD43 antibody or antigen-binding fragment

<400>      110
Gly Tyr Xaa Met Asn
  1             5

<210>      111
<211>      5
<212>      PRT
<213>      Artificial Sequence

<220>
<223>      CDRH1 of anti-CD43 antibody or antigen-binding fragment

<400>      111
Gly Tyr Phe Met Asn
  1             5

<210>      112
<211>      5
<212>      PRT
<213>      Artificial Sequence

<220>
<223>      CDRH1 of anti-CD43 antibody or antigen-binding fragment

<400>      112
Gly Tyr Tyr Met Asn
  1             5

<210>      113
<211>      17
<212>      PRT
<213>      Artificial Sequence

<220>
<221>      MOD_RES
<222>      (6)
<223>      Xaa is Asn (N) or Ser (S)

<220>
<221>      MOD_RES
<222>      (16)
<223>      Xaa is Gln (Q) or Lys (K)

<220>
<223>      CDRH2 of anti-CD43 antibody or antigen-binding fragment

<400>      113
Arg Ile Asn Pro Asn Xaa Gly Asp Ser Phe Tyr Asn Gln Lys Phe Xaa

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1	5	10	15
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Gly

<210> 114
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRH2 of anti-CD43 antibody or antigen-binding fragment

<400> 114
 Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 115
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRH2 of anti-CD43 antibody or antigen-binding fragment

<400> 115
 Arg Ile Asn Pro Asn Ser Gly Asp Ser Phe Tyr Asn Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 116
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRH2 of anti-CD43 antibody or antigen-binding fragment

<400> 116
 Arg Ile Asn Pro Asn Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe Lys
 1 5 10 15

Gly

<210> 117
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRH2 of anti-CD43 antibody or antigen-binding fragment

<400> 117
 Arg Ile Asn Pro Asn Ser Gly Asp Ser Phe Tyr Asn Gln Lys Phe Lys

Asn Thr Ser Arg Leu His Ser
1 5

<210> 122
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of anti-CD43 antibody or antigen-binding fragment

<400> 122
Asn Thr Ala Arg Leu His Ser
1 5

<210> 123
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of anti-CD43 antibody or antigen-binding fragment

<400> 123
Gln Thr Ser Arg Leu His Ser
1 5

<210> 124
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of anti-CD43 antibody or antigen-binding fragment

<400> 124
Ala Thr Ser Arg Leu His Ser
1 5

<210> 125
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3 of anti-CD43 antibody or antigen-binding fragment

<400> 125
Gln Gln Ser Asn Met Phe Pro Tyr
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<210> 126
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (4)

<223> Xaa is Gly (G) or Ala (A)

<220>

<223> linker

<400> 126

Gly Gly Gly Xaa Ser
1 5

<210> 127

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 127

Gly Gly Gly Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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<210> 128

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 128

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ser
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<210> 129

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> epitope containing peptide, DN2

<400> 129

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<210> 130

<211> 400

<212> PRT

<213> Artificial Sequence

<220>

<223> human CD43

<400> 130

Met Ala Thr Leu Leu Leu Leu Gly Val Leu Val Val Ser Pro Asp
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Ala Leu Gly Ser Thr Thr Ala Val Gln Thr Pro Thr Ser Gly Glu Pro

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20

25

30

Leu Val Ser Thr Ser Glu Pro Leu Ser Ser Lys Met Tyr Thr Thr Ser
35 40 45
Ile Thr Ser Asp Pro Lys Ala Asp Ser Thr Gly Asp Gln Thr Ser Ala
50 55 60
Leu Pro Pro Ser Thr Ser Ile Asn Glu Gly Ser Pro Leu Trp Thr Ser
65 70 75 80
Ile Gly Ala Ser Thr Gly Ser Pro Leu Pro Glu Pro Thr Thr Tyr Gln
85 90 95
Glu Val Ser Ile Lys Met Ser Ser Val Pro Gln Glu Thr Pro His Ala
100 105 110
Thr Ser His Pro Ala Val Pro Ile Thr Ala Asn Ser Leu Gly Ser His
115 120 125
Thr Val Thr Gly Gly Thr Ile Thr Thr Asn Ser Pro Glu Thr Ser Ser
130 135 140
Arg Thr Ser Gly Ala Pro Val Thr Thr Ala Ala Ser Ser Leu Glu Thr
145 150 155 160
Ser Arg Gly Thr Ser Gly Pro Pro Leu Thr Met Ala Thr Val Ser Leu
165 170 175
Glu Thr Ser Lys Gly Thr Ser Gly Pro Pro Val Thr Met Ala Thr Asp
180 185 190
Ser Leu Glu Thr Ser Thr Gly Thr Thr Gly Pro Pro Val Thr Met Thr
195 200 205
Thr Gly Ser Leu Glu Pro Ser Ser Gly Ala Ser Gly Pro Gln Val Ser
210 215 220
Ser Val Lys Leu Ser Thr Met Met Ser Pro Thr Thr Ser Thr Asn Ala
225 230 235 240
Ser Thr Val Pro Phe Arg Asn Pro Asp Glu Asn Ser Arg Gly Met Leu
245 250 255
Pro Val Ala Val Leu Val Ala Leu Leu Ala Val Ile Val Leu Val Ala
260 265 270
Leu Leu Leu Leu Trp Arg Arg Arg Gln Lys Arg Arg Thr Gly Ala Leu
275 280 285
Val Leu Ser Arg Gly Gly Lys Arg Asn Gly Val Val Asp Ala Trp Ala
290 295 300
Gly Pro Ala Gln Val Pro Glu Glu Gly Ala Val Thr Val Thr Val Gly
305 310 315 320
Gly Ser Gly Gly Asp Lys Gly Ser Gly Phe Pro Asp Gly Glu Gly Ser
325 330 335
Ser Arg Arg Pro Thr Leu Thr Thr Phe Phe Gly Arg Arg Lys Ser Arg
340 345 350
Gln Gly Ser Leu Ala Met Glu Glu Leu Lys Ser Gly Ser Gly Pro Ser
355 360 365
Leu Lys Gly Glu Glu Glu Pro Leu Val Ala Ser Glu Asp Gly Ala Val
370 375 380

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Asp Ala Pro Ala Pro Asp Glu Pro Glu Gly Gly Asp Gly Ala Ala Pro
385 390 395 400

<210> 131
<211> 6
<212> PRT
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<220>
<223> epitope

<400> 131
Pro Leu Trp Thr Ser Ile
1 5

<210> 132
<211> 7
<212> PRT
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<220>
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<400> 132
Ser Pro Leu Trp Thr Ser Ile
1 5

<210> 133
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 133
Gly Ser Pro Leu Trp Thr Ser Ile
1 5

<210> 134
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> epitope

<400> 134
Glu Gly Ser Pro Leu Trp Thr Ser Ile
1 5