SEQUENCE LISTING

110> AMGEN INC.
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120> SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR

130> 6843.51-304

140>
141>

150> US 60/488,681
151> 2003-07-18

160> 194

170> PatentIn Ver. 3.2

210> 1
211> 387
212> DNA
213> Artificial Sequence

220>
223> Description of Artificial Sequence: Synthetic HGF 1.24.1 Light chain V region (Vk, 1-L15)

400> 1
atggacatga gggtgcccgc tcagctcctg gggctcctgc tgctctggtt cccaggttcc 60
gatgcgaca tccagatgac ccagtctcca tcttccgtgt ctgcatctgt aggagacaga 120
tcaccatca cttgtcgggc gagtcagggt attagcagct ggttagcctg gtatcagcag 180
aaaccaggga aagcccctaa cctcctgatc tatgaagcat ccagtttgca aagtggggtc 240
catcaaggt tcggcggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300
agcctgaag attttgcaac ttactattgt caacaggcta acggtttccc gtggacgttc 360
gccaaggga ccaaggtgga aatcaaa 387

210> 2
211> 423
212> DNA
213> Artificial Sequence

220>
223> Description of Artificial Sequence: Synthetic HGF 1.24.1 Heavy chain V region (Vh, H3-11)-huIgG2 C region)

400> 2
atggagtttg ggctgagctg ggttttcctt gttgctatta taaaaggtgt ccagtgtcag 60
gtgcagctgg tggagtctgg gggaggcttg gtcaagcctg gagggtccct gagactctcc 120
gtgcagcct ctggattcac cttcagtgac tactacatga gctggatccg ccaggctcca 180
ggaaaggggc tggagtgggt ttcatacatt agtagtagtg gtagtaccat atactacgca 240
actctgtga agggccgatt caccatctcc agggacaacg ccaagaactc actgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agatgagtat 360
aacagtggct ggtacgtcct ctttgactac tggggccagg gaaccctggt caccgtctct 420
agt 423

<210> 3
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.29.1 Light chain V region (Vk, 4-B3)

<400> 3
atggtgttgc agacccaggt cttcatttct ctgttgctct ggatctctga tgcctacgga 60
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 120
atcaactgca agtccagcca gagtattttt tacagctcca ccaataagaa ctacttagct 180
tggtatcaga agaaaccggg acagcctcct aagctgctca tttactgggc atctacccgg 240
gaatccgggg tccctgaccg gttcagtggc agcgggtctg ggacagattt cactctcacc 300
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact 360
ccgtggacgt tcggccaagg gaccaaggtg gaaatcaaa 399

<210> 4
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.29.1 Heavy chain V region (Vh, 3-33)- huIgG2 C region

<400> 4
atggagtttg ggctgaactg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag 60
gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120
tgtgcagcgt ctggattcac cttcagtagc tatggcatgc actgggtccg ccaggctccg 180
ggcaagggac tggagtgggt ggcagttata tggtatgatg gaagtgataa atactatgca 240
gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agaggactac 360
ggcgagggtt ttgactactg gggccaggga accctggtca ccgtctctag t 411

<210> 5
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.60.1 Light chain V region (Vk, 1-A20)

<400> 5
atggacatga gggtgcccgc tcagctcctg ggactcctgc tgctctggct cccagatacc 60
agatgtgaca tccagatgac ccagtctcca tcctccctgt ctgtatctgt cggagacaga 120
gtcaccatca cttgccgggc gagtcagggc attagcagtt atttagcctg gtatcagcag 180
aaaccaggga aagttcctaa gctcctgatc tatgttgcat ccactttgca atcaggggtc 240

ccgtctcggt tcagtggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300
cagcctgaag atgttgcaac ttattactgt caaaactata acagtgaccc gctcactttc 360
ggcggcggga ccaaggtgga gatcaaa 387

<210> 6
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.60.1 Heavy chain V region (Vh, H1-02)- huIgG2 C region

<400> 6
atggactgga cctggaggat cctcttcttg gtggcagcag ccacaggagc ccactcccag 60
gtgcagctgg tgcagtctgg ggctgaggtg aagaagcctg gggcctcagt gaaggtctcc 120
tgcaaggctt ctggatacac cttcaccggc tactatataa actgggtgcg acaggcccct 180
ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcac aaactatgca 240
cagaagtttc agggcagggt caccatgacc agggacacgt ccatcaccac agcctacatg 300
gagctgagca ggctgagagc tgacgacacg gccgtgtact actgtgcgag agaactggaa 360
ctacgctact acggtatgga cgtctggggc caagggacca cggtcaccgt ctctagt 417

<210> 7
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.61.3 Light chain V region (Vk, 1-018/08)

<400> 7
atggacatga gggtgcccgc tcagctcctg gggctcctgc tgctctggct ctcaggtgcc 60
agatgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccaggc gagtcaggac attagcaact atttaaattg gtatcagcag 180
aaaccaggga cagccctaa actcctgatc tacggtgcat ccgatttgga aacgggggtc 240
ccatcaaggt tcagtggaag tggatctggg acagatttta ctttcgccat cagcagcctg 300
cagcctgaag atattgcaac atattactgt caacagtatg ataatctccc gtacaatttt 360
ggccagggga ccaagctgga gatcaaa 387

<210> 8
<211> 444
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.61.3 Heavy chain V region (Vh, 4-31)- huIgG2 C region

<400> 8
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt cctgtcccag 60
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cacagaccct gtccctcacc 120
tgcactgtct ctggtggctc catcagcagt gatggttact actggagctg gatccgccag 180
cacccaggga agggcctgga gtggattggg tacatctatt acagtgggag cacctactac 240

aacccgtccc tcaagagtcg agtcaccata tcagtagaca cgtctaagaa ccagttctcc 300
ctgaagctga gctctgtgac tgccgcggac acggccgtct attactgtgc gagatcccac 360
cttcattact atgatagtag tggttattac tacggcggtg cttttgatat ctggggccaa 420
gggacaatgg tcaccgtctc tagt 444

<210> 9
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.74.3 Light chain V region (Vk, 1-012/02)

<400> 9
atggacatga gggtgcccgc tcagctcctg gggctcctgc tactctggct ccgaggtgcc 60
agatgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccgggc aagtcagagc attaacagcg atttaaattg gtatcagcag 180
aaaccaggga aagtccctaa gctcctgatc tatgttgcat ccagtttgca aaatggggtc 240
ccatcaaggt tcagtggcag tggatctggg acagatttca ctctcaccat cagcagtctg 300
caacctgaag attttgcaac ttactactgt caacggagtt acagtacccc tcccactttc 360
ggccctggga ccaaagtgga tatcaaa 387

<210> 10
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.74.3 Heavy chain V region (Vh, VG1-02)- huIgG2 C region

<400> 10
atggactgga cctggaggat cctcttcttg gtggcagcag ccacaggagc ccactcccag 60
gtgcagctgg tgcagtctgg ggctgaggtg aagaagcctg gggcctcagt gaaggtctcc 120
tgcaaggctt ctggatacac cttcaccggc tactatatac actgggtgcg acaggcccct 180
ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcac aaactatgca 240
cagaagtttc agggcagggt caccatgacc agggacacgt ccatcagcac agcctacatg 300
gagctgagca ggctgagatc tgacgacacg gccgtgtatt actgtgcgag agaactggaa 360
ctacgctact acggtatgga cgtctggggc caagggacca cggtcaccgt ctctagt 417

<210> 11
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.75.1 Light chain V region (Vk, 1-A30)

<400> 11
atggacatga gggtgcccgc tcagctcctg gggctcctgc tgctctggtt cccaggtgcc 60
aggtgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccgggc aagtcagggc attagaaatg atttaggctg gtttcagcag 180

aaaccaggga aagcccctaa gcgcctgatc tatgctgcat ccagtttgca aagtggggtc 240
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt ctacagcatg atagttaccc gctcactttc 360
ggcggaggga ccaaggtgga gatcaaa 387

<210> 12
<211> 432
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.75.1 Heavy chain V region (Vh, VG4-31)- huIgG2 C region

<400> 12
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt cctgtcccag 60
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cacagaccct gtccctcacc 120
tgcactgtct ctggtggctc catcagcagt ggtggttact actggagctg gatccgccag 180
cacccaggga agggcctgga gtggattggg tacatctatt acagtgggag cacctactac 240
aacccgtccc tcaagagtcg agttaccata tcagtagaca cgtctaagaa ccagttctcc 300
ctgaaggtga gctctgtgac tgccgcggac acggccgtgt attactgtgc gagagaccca 360
ctatggttcg gggagttcga ctactacggt atggacgtct ggggccaagg gaccacggtc 420
accgtctcta gt 432

<210> 13
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.4.4 Light chain V region (Vk, 4-B3)

<400> 13
atggtgttgc agacccaggt cttcatttct ctgttgctct ggatctctgg tgcctacggg 60
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 120
atcaactgca agtccagcca gagtgtttta ttcagctcca acaataagaa ttacttagct 180
tggtatcagc agaaaccagg acagcctcct aagttgctca tttactgggc atctacccgg 240
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 300
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttttagtcct 360
ccgtggacgt tcggccaagg gaccaaggtg gaaatcaaa 399

<210> 14
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.4.4 Heavy chain V region (Vh, VG 4-31)- huIgG2 C region

<400> 14
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatggat cctgtcccag 60
gtgcagctga aggagtcggg cccaggactg gtgaagcctt cacagaccct gtccctcacc 120

tgcactgtct ctggtggctc catcagcagt ggtgtttact actggagctg gatccgccag 180
cacccaggga agggcctgga gtggattggg tacttctatt atagtgggaa cacctaccac 240
aacccgtccc tcaagagtcg agtgaccata tcagtagaca cgtctaagaa ccagttctcc 300
ctgaagctga gctctgtgac tgccgcggac acggccgtgt attactgtgc gagagatcgt 360
agtggctacg atcaccctga tgcttttgat atctggggcc aagggacaat ggtcaccgtc 420
tctagt 426

<210> 15
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.12.1 Light chain V region (Vk, 3-L2/L16)

<400> 15
atggaagccc cagctcagct tctcttcctc ctgctactct ggctcccaga taccactgga 60
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca gagtgttgac agcaacttag cctggtaccg gcagaaacct 180
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 240
aggttcagtg gcagtgggtc tgggactgag ttcactctca ccatcagcag cctgcagtct 300
gaagattttg cagtttatta ctgtcagcag tatattaact ggcctccgat caccttcggc 360
caagggacac gactggagat taaa 384

<210> 16
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.12.1 Heavy chain V region (Vh4-59)- huIgG2 C region

<400> 16
atgaaacacc tgtggttctt ccttctcctg gtggcagctc ccagatgggt cctgtcccag 60
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc 120
tgcactgtct ctggtggctc catcagtatt tactactgga gctggatccg gcagcccccа 180
gggaagggac tggagtggat tgggtatgtc tattacagtg ggagcaccaa ttacaacccc 240
tccctcaaga gtcgagtcac catatcagta gacacgtcca agaaccagtt ctccctgaag 300
ctgaactctg tgaccgctgc ggacacggcc gtgtattact gtgcgagagg gggatacgat 360
ttttggagtg gttattttga ctactggggc cagggaaccc tggtcaccgt ctctagt 417

<210> 17
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.40.1 Light chain V region (Vk, 1A20)

<400> 17
atggacatga gggtgcccgc tcagctcctg gggctcctgc tgctctggtt cccaggtgcc 60

aggtgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccgggc aagtcagggc attagaaatg atttaggctg gtatcagcag 180
aaaccaggga aagcccctaa gcgcctgatc tatgttgcat ccagtttgca aagtggggtc 240
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt ctacaacata atagttaccc gctcactttc 360
ggcggaggga ccaaggtgga gatcaaa 387

<210> 18
<211> 420
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.40.1 Heavy chain V region (Vh, VG 4-31)- huIgG2 C region

<400> 18
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt cctgtcccag 60
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cacagaccct gtccctcacc 120
tgcactgtct ctggtggctc catcagcagt ggtggttact actggagctg gatccgtcag 180
cacccaggga agggcctgga gtggattggg aacatctatt acagtgggat cacctactac 240
aacccgtccc tcaagagtcg agttaccatg tcagtagaca cgtctaagaa ccagttctcc 300
ctgaagctga gttctgtgac tgccgcggac acggccgtgt attactgtgc gagagatccc 360
ctctacggtg actacgggtt cgaccctgg ggccagggaa ccctggtcac cgtctctagt 420

<210> 19
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 3.10.1 Light chain V region (Vk, 3-L2/L16)

<400> 19
atggaagccc cagctcagct tctcttcctc ctgctactct ggctcccaga taccactgga 60
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctcctgggga aagagccacc 120
ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 180
ggccaggctc ccaggctcct catgtatggt gcatccacca gggccactgg tatcccagcc 240
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 300
gaagattttg cagtttatta ctgtcagcag tataataact ggcctccgat caccttcggc 360
caagggacac gactggagat taaa 384

<210> 20
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 3.10.1 Heavy chain V region (Vh, VG 4-34)- huIgG1 C region

<400> 20
atgaaacacc tgtggttctt cctcctcctg gtggcagctc ccagatgggt cctgtcccag 60

gtgcagctac agcagtgggg cgcaggactg ttgaagcctt cggagaccct gtccctcacc 120
tgcgctgtct atggtgggtc cttcagtact tactactgga gctggatccg ccagcccccа 180
gggaaggggc tggagtggat tggggaaatc aatcatagtg gaagcaccaa ctacaacccg 240
tccctcaaga gtcgagtcac catatcagta gacacgtcca agaaccagtt ctccctgaag 300
ctgagctctg tgaccgccgc ggacacggct gtgtattact gtgcgagagg ggggtacgat 360
ttttggagtg gttattatga ctactggggc cagggaaccc tggtcaccgt ctctagt 417

<210> 21
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Human Kappa Constant Region

<400> 21
cgaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 60
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 120
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 180
agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 300
agcttcaaca ggggagagtg ttga 324

<210> 22
<211> 993
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Human IgG1 Constant Region

<400> 22
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 60
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 120
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 240
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 300
aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 360
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 420
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 540
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 600
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 660
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 720
ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 780
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 900
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 960
cagaagagcc tctccctgtc tccgggtaaa tga 993

<210> 23
<211> 981

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Human IgG2 Constant Region

<400> 23
gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 60
agcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 120
tggaactcag gcgctctgac cagcggcgtg cacaccttcc cagctgtcct acagtcctca 180
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcaacttcgg cacccagacc 240
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc 300
aaatgttgtg tcgagtgccc accgtgccca gcaccacctg tggcaggacc gtcagtcttc 360
ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacgtgc 420
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gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc 600
aaggtctcca acaaaggcct cccagccccc atcgagaaaa ccatctccaa aaccaaaggg 660
cagccccgag aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 720
caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 780
gagagcaatg ggcagccgga gaacaactac aagaccacac ctcccatgct ggactccgac 840
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 900
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 960
tccctgtctc cgggtaaatg a 981

<210> 24
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.24.1 Light chain V region (Vk, 1-L15)

<400> 24
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Phe Pro Gly Ser Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

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

Ala Pro Asn Leu Leu Ile Tyr Glu Ala Ser Ser Leu Gln Ser Gly Val
65 70 75 80

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

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

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Ala Asn Gly Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
        115                 120                 125

Lys
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<210> 25
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.24.1
Heavy chain V region (Vh, H3-11)-huIgG2 C region

<400> 25

```
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Ile Lys Gly
  1               5                  10                  15

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

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

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

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

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

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

Tyr Tyr Cys Ala Arg Asp Glu Tyr Asn Ser Gly Trp Tyr Val Leu Phe
        115                 120                 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130                 135                 140
```

<210> 26
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.29.1
Light chain V region (Vk, 4-B3)

<400> 26
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

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

Ile Phe Tyr Ser Ser Thr Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Lys
50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

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

Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr
115 120 125

Lys Val Glu Ile Lys
130

<210> 27
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.29.1 Heavy chain V region (Vh, 3-33)- huIgG2 C region

<400> 27
Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

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

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

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

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Tyr Ala
65 70 75 80

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 28
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.60.1
Light chain V region (Vk, 1-A20)

<400> 28
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Asp Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

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

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

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

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

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

Tyr Asn Ser Asp Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
115 120 125

Lys

<210> 29
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.60.1
Heavy chain V region (Vh, H1-02)- huIgG2 C region

<400> 29
Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

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

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

Thr Gly Tyr Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

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

Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Thr
85 90 95

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

Tyr Tyr Cys Ala Arg Glu Leu Glu Leu Arg Tyr Tyr Gly Met Asp Val
115 120 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
130 135

<210> 30
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.61.3 Light chain V region (Vk, 1-018/08)

<400> 30
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

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

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

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

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Ala
85 90 95

```
Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
            100                 105                 110

Tyr Asp Asn Leu Pro Tyr Asn Phe Gly Gln Gly Thr Lys Leu Glu Ile
        115                 120                 125

Lys
```

<210> 31
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.61.3. Heavy chain V region (Vg, 4-31)- huIgG2 C region

<400> 31

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

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

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

Ser Ser Asp Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr
65                  70                  75                  80

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
                85                  90                  95

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

Val Tyr Tyr Cys Ala Arg Ser His Leu His Tyr Tyr Asp Ser Ser Gly
        115                 120                 125

Tyr Tyr Tyr Gly Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
    130                 135                 140

Thr Val Ser Ser
145
```

<210> 32
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.74.3
Light chain V region (Vk, 1-012/02)

<400> 32
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

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

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

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

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

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

Ser Tyr Ser Thr Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
115 120 125

Lys

<210> 33
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.74.3
Heavy chain V region(Vh, VG1-02)-huIgG2 C region

<400> 33
Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

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

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

Thr Gly Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

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

```
Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Glu Leu Glu Leu Arg Tyr Tyr Gly Met Asp Val
        115                 120                 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
    130                 135
```

<210> 34
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.75.1 Light chain V region (Vk, 1-A30)

<400> 34

```
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
  1               5                  10                  15

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

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

Gln Gly Ile Arg Asn Asp Leu Gly Trp Phe Gln Gln Lys Pro Gly Lys
    50                  55                  60

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

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
                85                  90                  95

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

His Asp Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
        115                 120                 125

Lys
```

<210> 35
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 1.75.1
Heavy chain V region (Vh, VG4-31)-huIgG2 C region

<400> 35

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

<210> 36
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.4.4
Light chain V region (Vk, 4-B3)

<400> 36

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

```
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65                  70                  75                  80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

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

Tyr Cys Gln Gln Tyr Phe Ser Pro Pro Trp Thr Phe Gly Gln Gly Thr
        115                 120                 125

Lys Val Glu Ile Lys
    130
```

<210> 37
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.4.4 Heavy chain V region (Vh, VG 4-31)-huIgG2 C region

<400> 37

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

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

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

Ser Ser Gly Val Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Ile Gly Tyr Phe Tyr Tyr Ser Gly Asn Thr Tyr His
 65                  70                  75                  80

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
                85                  90                  95

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

Val Tyr Tyr Cys Ala Arg Asp Arg Ser Gly Tyr Asp His Pro Asp Ala
        115                 120                 125

Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
    130                 135                 140
```

<210> 38
<211> 128

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.12.1
Light chain V region (Vk, 3-L2/L16)

<400> 38
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

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

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

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

Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala
65 70 75 80

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

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

Asn Trp Pro Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
115 120 125

<210> 39
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.12.1
Heavy chain V region (Vg, 4-59)- huIgG2 C region

<400> 39
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

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

```
Glu Trp Ile Gly Tyr Val Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro
 65                  70                  75                  80

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

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

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

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130                 135
```

<210> 40
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.40.1 Light chain V region (Vk, 1A20)

<400> 40

```
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
  1               5                  10                  15

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

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

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

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

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
                85                  90                  95

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

His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
        115                 120                 125

Lys
```

<210> 41
<211> 140

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 2.40.1
Heavy chain V region (Vh, VG 4-31)-huIgG2 C region

<400> 41
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

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

Ser Ser Gly Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys
50 55 60

Gly Leu Glu Trp Ile Gly Asn Ile Tyr Tyr Ser Gly Ile Thr Tyr Tyr
65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys
85 90 95

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

Val Tyr Tyr Cys Ala Arg Asp Pro Leu Tyr Gly Asp Tyr Gly Phe Asp
115 120 125

Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

<210> 42
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 3.10.1
Light chain V region (Vk, 3-L2/L16)

<400> 42
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

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

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

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

```
Arg Leu Leu Met Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala
 65                  70                  75                  80

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

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

Asn Trp Pro Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
        115                 120                 125
```

<210> 43
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic HGF 3.10.1 Heavy chain V region (Vh, VG 4-34)-huIgG1 C region

```
<400> 43
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1               5                  10                  15

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

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

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

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

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

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
            100                 105                 110

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

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130                 135
```

<210> 44
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Human Kappa Constant Region

<400> 44
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 45
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Human IgG1 Constant Region

<400> 45
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

```
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 46
<211> 326
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Human IgG2 Constant Region

<400> 46

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1               5                  10                  15

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130                 135                 140

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275                 280                 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    290                 295                 300
```

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

<210> 47
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic t-cell epitope peptide

<400> 47
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Lys
1 5 10 15

Lys Cys

<210> 48
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (18)..(23)
<223> a, t, c or g

<400> 48
ggccggatag gcctccannn nnnt 24

<210> 49
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 49
ggacactgac atggactgaa ggagta 26

<210> 50
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 50
ggggtcaggc tggaactgag g 21

<210> 51
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 51
acaacaaagc ttctagacca ccatggaagc cccagctcag cttctctt 48

<210> 52
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 52
cttgtcgact caacactctc ccctgttgaa gctc 34

<210> 53
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 53
ggacactgac atggactgaa ggagta 26

<210> 54
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 54
agcagaagct tctagaccac catgaaacac ctgtggttct tcctcctc 48

<210> 55
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 55
gtggaggcac tagagacggt gaccagggtt cc 32

<210> 56
<211> 1043
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic pI/hCh1 heavy chain nucleotide sequence

<400> 56
tctagaccac cgccatgggt gaaaattgaa tcgtctctag tgcctccacc aagggcccat 60
cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg gccctgggct 120
gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca ggcgccctga 180
ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac tccctcagca 240
gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc aacgtgaatc 300
acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt gacaaaactc 360
acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc ttcctcttcc 420
ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg 480
tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac ggcgtggagg 540
tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca 600
gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag tgcaaggtct 660
ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa gggcagcccc 720
gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag aaccaggtca 780
gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag tgggagagca 840
atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc gacggctcct 900
tcttcctcta tagcaagctc accgtggaca agagcaggtg gcagcagggg aacgtcttct 960
catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc ctctccctgt 1020
ctccgggtaa atgataagtc gac 1043

<210> 57
<211> 540
<212> DNA
<213> Gallus gallus

<220>
<221> CDS
<222> (2)..(520)

<400> 57
c ccc acc atg gtg cac gca acc tcc ccg ctg ctg ctg ctg ctg ctg ctc 49
Pro Thr Met Val His Ala Thr Ser Pro Leu Leu Leu Leu Leu Leu Leu
1 5 10 15

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agc ctg gct ctg gtg gct ccc ggc ctc tct gcc aga aag tgc tcg ctg   97
Ser Leu Ala Leu Val Ala Pro Gly Leu Ser Ala Arg Lys Cys Ser Leu
                20                  25                  30

act ggg aaa tgg acc aac gat ctg ggc tcc aac atg acc atc ggg gct  145
Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser Asn Met Thr Ile Gly Ala
            35                  40                  45

gtg aac agc aaa ggt gaa ttc aca ggc acc tac acc aca gcc gta aca  193
Val Asn Ser Lys Gly Glu Phe Thr Gly Thr Tyr Thr Thr Ala Val Thr
        50                  55                  60

gcc aca tca aat gag atc aaa gag tca cca ctg cat ggg aca caa aac  241
Ala Thr Ser Asn Glu Ile Lys Glu Ser Pro Leu His Gly Thr Gln Asn
    65                  70                  75                  80

acc atc aac aag agg acc cag ccc acc ttt ggc ttc act gtc aat tgg  289
Thr Ile Asn Lys Arg Thr Gln Pro Thr Phe Gly Phe Thr Val Asn Trp
                85                  90                  95

aag ttt tca gag tcc acc act gtc ttc acg ggc cag tgc ttc ata gac  337
Lys Phe Ser Glu Ser Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp
            100                 105                 110

agg aac ggg aag gag gtc ctg aag acc atg tgg ctg ctg cgg tca agt  385
Arg Asn Gly Lys Glu Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser
        115                 120                 125

gtt aat gac att ggt gat gac tgg aaa gct acc agg gtc ggc atc aac  433
Val Asn Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn
    130                 135                 140

atc ttc act cgc ctg cgc aca cag aag gag cag ctg cta gca agc ttg  481
Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu Gln Leu Leu Ala Ser Leu
145                 150                 155                 160

cta gcg gcc gct cga ggc cgg caa ggc cgg atc cag aca tgataagata   530
Leu Ala Ala Ala Arg Gly Arg Gln Gly Arg Ile Gln Thr
                165                 170

cattgatgag                                                      540
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<210> 58
<211> 540
<212> DNA
<213> Gallus gallus

<400> 58
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aagcttgcta gcagctgctc cttctgtgtg cgcaggcgag tgaagatgtt gatgccgacc 120
ctggtagctt tccagtcatc accaatgtca ttaacacttg accgcagcag ccacatggtc 180
ttcaggacct ccttcccgtt cctgtctatg aagcactggc ccgtgaagac agtggtggac 240
tctgaaaact tccaattgac agtgaagcca aaggtgggct gggtcctctt gttgatggtg 300
ttttgtgtcc catgcagtgg tgactctttg atctcatttg atgtggctgt tacggctgtg 360
gtgtaggtgc ctgtgaattc acctttgctg ttcacagccc cgatggtcat gttggagccc 420
agatcgttgg tccatttccc agtcagcgag cactttctgg cagagaggcc gggagccacc 480
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agagccaggc tgagcagcag cagcagcagc agcggggagg ttgcgtgcac catggtgggg 540

<210> 59
<211> 173
<212> PRT
<213> Gallus gallus

<400> 59
Pro Thr Met Val His Ala Thr Ser Pro Leu Leu Leu Leu Leu Leu Leu
1 5 10 15

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

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

Val Asn Ser Lys Gly Glu Phe Thr Gly Thr Tyr Thr Thr Ala Val Thr
50 55 60

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

Thr Ile Asn Lys Arg Thr Gln Pro Thr Phe Gly Phe Thr Val Asn Trp
85 90 95

Lys Phe Ser Glu Ser Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp
100 105 110

Arg Asn Gly Lys Glu Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser
115 120 125

Val Asn Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn
130 135 140

Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu Gln Leu Leu Ala Ser Leu
145 150 155 160

Leu Ala Ala Ala Arg Gly Arg Gln Gly Arg Ile Gln Thr
165 170

<210> 60
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 60
Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 61
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 61
Lys Ser Ser Gln Ser Ile Phe Tyr Ser Ser Thr Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 62
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 62
Arg Ala Ser Gln Gly Ile Ser Ser Tyr Leu Ala
1 5 10

<210> 63
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 63
Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 64
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 64
Arg Ala Ser Gln Ser Ile Asn Ser Asp Leu Asn
1 5 10

<210> 65
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 65
Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Gly
1 5 10

<210> 66
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 66
Lys Ser Ser Gln Ser Val Leu Phe Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 67
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 67
Arg Ala Ser Gln Ser Val Asp Ser Asn Leu Ala
1 5 10

<210> 68
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 68
Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Gly
1 5 10

<210> 69
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 69
Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 70
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 70
Glu Ala Ser Ser Leu Gln Ser
1 5

<210> 71
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 71
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 72
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 72
Val Ala Ser Thr Leu Gln Ser
1 5

<210> 73
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 73
Gly Ala Ser Asp Leu Glu Thr
1 5

<210> 74
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 74
Val Ala Ser Ser Leu Gln Asn
1 5

<210> 75
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 75
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 76
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 76
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 77
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 77
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 78
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 78
Val Ala Ser Ser Leu Gln Ser
1 5

<210> 79
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 79
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 80
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain

variable region CDR peptide

<400> 80
Gln Gln Ala Asn Gly Phe Pro Trp Thr
1 5

<210> 81
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 81
Gln Gln Tyr Tyr Ser Thr Pro Trp Thr
1 5

<210> 82
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 82
Gln Asn Tyr Asn Ser Asp Pro Leu Thr
1 5

<210> 83
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 83
Gln Gln Tyr Asp Asn Leu Pro Tyr Asn
1 5

<210> 84
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 84
Gln Arg Ser Tyr Ser Thr Pro Pro Thr
1 5

<210> 85
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 85
Leu Gln His Asp Ser Tyr Pro Leu Thr
1 5

<210> 86
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 86
Gln Gln Tyr Phe Ser Pro Pro Trp Thr
1 5

<210> 87
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 87
Gln Gln Tyr Ile Asn Trp Pro Pro Ile Thr
1 5 10

<210> 88
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 88
Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 89
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic light chain variable region CDR peptide

<400> 89
Gln Gln Tyr Asn Asn Trp Pro Pro Ile Thr
1 5 10

<210> 90
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 90
Asp Tyr Tyr Met Ser
1 5

<210> 91
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 91
Ser Tyr Gly Met His
1 5

<210> 92
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 92
Gly Tyr Tyr Ile Asn
1 5

<210> 93
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 93
Ser Asp Gly Tyr Tyr Trp Ser
1 5

<210> 94
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 94
Gly Tyr Tyr Ile His
1 5

<210> 95
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 95
Ser Gly Gly Tyr Tyr Trp Ser
1 5

<210> 96
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 96
Ser Gly Val Tyr Tyr Trp Ser
1 5

<210> 97
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 97
Ile Tyr Tyr Trp Ser
1 5

<210> 98
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 98
Ser Gly Gly Tyr Tyr Trp Ser
1 5

<210> 99
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 99
Thr Tyr Tyr Trp Ser
1 5

<210> 100
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 100
Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 101
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 101
Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 102
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 102
Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 103
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 103
Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 104
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 104
Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 105
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 105
Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 106
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 106
Tyr Phe Tyr Tyr Ser Gly Asn Thr Tyr His Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 107
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 107
Tyr Val Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

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

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 108
Asn Ile Tyr Tyr Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 109
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 109
Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 110
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 110
Asp Glu Tyr Asn Ser Gly Trp Tyr Val Leu Phe Asp Tyr
1 5 10

<210> 111
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 111
Glu Asp Tyr Gly Glu Gly Phe Asp Tyr
1 5

<210> 112
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 112
Glu Leu Glu Leu Arg Tyr Tyr Gly Met Asp Val
1 5 10

<210> 113
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 113
Ser His Leu His Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Gly Gly Ala
1 5 10 15

Phe Asp Ile

<210> 114
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 114
Glu Leu Glu Leu Arg Tyr Tyr Gly Met Asp Val
1 5 10

<210> 115
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 115
Asp Pro Leu Trp Phe Gly Glu Phe Asp Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 116
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 116
Asp Arg Ser Gly Tyr Asp His Pro Asp Ala Phe Asp Ile
1 5 10

<210> 117
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 117
Gly Gly Tyr Asp Phe Trp Ser Gly Tyr Phe Asp Tyr
1 5 10

<210> 118
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 118
Asp Pro Leu Tyr Gly Asp Tyr Gly Phe Asp Pro
1 5 10

<210> 119
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic heavy chain variable region CDR peptide

<400> 119
Gly Gly Tyr Asp Phe Trp Ser Gly Tyr Tyr Asp Tyr
1 5 10

<210> 120
<211> 279
<212> PRT
<213> Homo sapiens

<400> 120
Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro
1 5 10 15

Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp
20 25 30

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

Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr
50 55 60

Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val
65 70 75 80

Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu
85 90 95

Ala Trp Leu Gly Ile His Asp Val His Gly Arg Gly Asp Glu Lys Cys
100 105 110

Lys Gln Val Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly Ser
115 120 125

Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp Phe
130 135 140

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

Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr
165 170 175

Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys
180 185 190

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

Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr
210 215 220

Gly Gly Pro Leu Val Cys Glu Gln His Lys Met Arg Met Val Leu Gly
225 230 235 240

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Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile
                245                 250                 255

Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile Leu
            260                 265                 270

Thr Tyr Lys Val Pro Gln Ser
        275
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<210> 121
<211> 278
<212> PRT
<213> Mus musculus

<400> 121

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Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro
  1               5                  10                  15

Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp
            20                  25                  30

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

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

Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val
65                  70                  75                  80

Leu Thr Ala Arg Gln Cys Phe Pro Ala Arg Asn Lys Asp Leu Lys Asp
                85                  90                  95

Tyr Glu Ala Trp Leu Gly Ile His Asp Val His Glu Arg Gly Glu Glu
            100                 105                 110

Lys Arg Lys Gln Ile Leu Asn Ile Ser Gln Leu Val Tyr Gly Pro Glu
        115                 120                 125

Gly Ser Asp Leu Val Leu Leu Lys Leu Ala Arg Pro Ala Ile Leu Asp
    130                 135                 140

Asn Phe Val Ser Thr Ile Asp Leu Pro Ser Tyr Gly Cys Thr Ile Pro
145                 150                 155                 160

Glu Lys Thr Thr Cys Ser Ile Tyr Gly Trp Gly Tyr Thr Gly Leu Ile
                165                 170                 175

Asn Ala Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn
            180                 185                 190

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

Glu Leu Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly
    210                 215                 220
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Asp Tyr Gly Gly Pro Leu Ile Cys Glu Gln His Lys Met Arg Met Val
225                 230                 235                 240

Leu Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro
                245                 250                 255

Gly Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Val
            260                 265                 270

Ile Leu Thr Tyr Lys Leu
        275
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<210> 122
<211> 278
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<220>
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<222> (53)..(53)
<223> Undetermined consensus residue; variable amino acid

<220>
<221> MOD_RES
<222> (55)..(55)
<223> Undetermined consensus residue; variable amino acid

<220>
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<222> (91)..(92)
<223> Undetermined consensus residue; variable amino acid

<220>
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<222> (108)..(108)
<223> Undetermined consensus residue; variable amino acid

<220>
<221> MOD_RES
<222> (114)..(114)
<223> Undetermined consensus residue; variable amino acid

<220>
<221> MOD_RES
<222> (145)..(145)
<223> Undetermined consensus residue; variable amino acid

<220>
<221> MOD_RES
<222> (154)..(154)
<223> Undetermined consensus residue; variable amino acid

<220>
<221> MOD_RES
<222> (178)..(178)
<223> Undetermined consensus residue; variable amino acid

<220>
<221> MOD_RES
<222> (200)..(200)
<223> Undetermined consensus residue; variable amino acid

<400> 122

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Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro
 1               5                  10                  15

Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp
            20                  25                  30

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

Gly Ile Pro Thr Xaa Thr Xaa Ile Gly Trp Met Val Ser Leu Lys Tyr
    50                  55                  60

Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val
65                  70                  75                  80

Leu Thr Ala Arg Gln Cys Phe Pro Ala Arg Xaa Xaa Asp Leu Lys Asp
                85                  90                  95

Tyr Glu Ala Trp Leu Gly Ile His Asp Val His Xaa Arg Gly Asp Glu
            100                 105                 110

Lys Xaa Lys Gln Ile Leu Asn Ile Ser Gln Leu Val Tyr Gly Pro Glu
        115                 120                 125

Gly Ser Asp Leu Val Leu Leu Lys Leu Ala Arg Pro Ala Ile Leu Asp
    130                 135                 140

Xaa Phe Val Ser Thr Ile Asp Leu Pro Xaa Tyr Gly Cys Thr Ile Pro
145                 150                 155                 160

Glu Lys Thr Ser Cys Ser Ile Tyr Gly Trp Gly Tyr Thr Gly Leu Ile
                165                 170                 175

Asn Xaa Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn
            180                 185                 190

Glu Lys Cys Ser Gln His His Xaa Gly Lys Val Thr Leu Asn Glu Ser
        195                 200                 205

Glu Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly
    210                 215                 220

Asp Tyr Gly Gly Pro Leu Ile Cys Glu Gln His Lys Met Arg Met Val
225                 230                 235                 240
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Leu Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro
245 250 255

Gly Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile
260 265 270

Ile Leu Thr Tyr Lys Leu
275

<210> 123
<211> 77
<212> PRT
<213> Homo sapiens

<400> 123
Gly Trp Met Val Ser Leu Arg Tyr Arg Asn Lys His Ile Cys Gly Gly
1 5 10 15

Ser Leu Ile Lys Glu Ser Trp Val Leu Thr Ala Arg Gln Cys Phe Pro
20 25 30

Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp Leu Gly Ile His Asp Val
35 40 45

His Gly Arg Gly Asp Glu Lys Cys Lys Gln Val Leu Asn Val Ser Gln
50 55 60

Leu Val Tyr Gly Pro Glu Gly Ser Asp Leu Val Leu Met
65 70 75

<210> 124
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 124
atgcgtctcc cttgatgatg ctggctgcat ttc 33

<210> 125
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 125
atgcgtctct caagggaagg tgactctgaa tga 33

<210> 126
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 126
atgcgtctct aactaggtaa atcaatcgta ctaaca 36

<210> 127
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 127
atgcgtctct agttatggat gcacaattcc tgaaa 35

<210> 128
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 128
atgcgtctca ttatccagg acagcaggcc tg 32

<210> 129
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 129
atgcgtctca taatttgtt agtacgattg atttacc 37

<210> 130
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 130
atgcgtctcg cgtttctcat ctcctcttcc gt 32

<210> 131
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 131
atgcgtctca aacgcaaaca ggttctcaat gttt 34

<210> 132
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 132
atgcgtctcc tttcgtggac atcatgaatt ccaa 34

<210> 133
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 133
atgcgtctcc gaaagaggag atgagaaatg caaa 34

<210> 134
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 134
gagcagctgc tagcaagctt gcta 24

<210> 135
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 135
atgcgtctca gagacttgaa agactatgaa gcttg 35

<210> 136
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 136
atgcgtctcg tctctggctg gaaaacattg tctt 34

<210> 137
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 137
atgcgtctca acaaagactt gaaagattat gaagcttg 38

<210> 138
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 138
atgcgtctct ttgtttcgag aagggaaaca ctgtcg 36

<210> 139

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

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 139
atgcgtctca agcttgccag gcctgctgt 29

<210> 140
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 140
atgcgtctca agcttcagta aaaccaagtc tga 33

<210> 141
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 141
atgcgtctca agcttgctcg acctgcaatc 30

<210> 142
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 142
atgcgtctca agcttcatta aaaccagatc tga 33

<210> 143
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 143
atgcgtctca agcttgccag gcctgctgt 29

<210> 144
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 144
atgcgtctca agcttcagta aaaccaagtc tga 33

<210> 145
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 145
atgcgtctca agcttgctcg acctgcaatc 30

<210> 146
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 146
atgcgtctca agcttcatta aaaccagatc tga 33

<210> 147
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 147
atgcgtctct aggatggatg gttagtttga gat 33

<210> 148
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 148
atgcgtctca tcctactgtt gtttgtgttg gaat 34

<210> 149
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 149
atgcgtctct aggatggatg gttagtttga aata 34

<210> 150
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 150
atgcgtctca tcctatgttt gttcgtgttg g 31

<210> 151
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 151
atgcgtctca tgcatccaag gtcaaggaga ag 32

<210> 152
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 152
atgcgtctca tgcattcagt tgtttccata gg 32

<210> 153
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 153
atgcgtctca tgcatgacct gcaatgggga g 31

<210> 154
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 154
atgcgtctca tgcattcaac ttctgaacac tga 33

<210> 155
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 155
atgcgtctca tgcatcattg gtaaaggacg c 31

<210> 156
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 156
atgcgtctca tgcagtttct aatatagtct ttgttttc 38

<210> 157
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 157
atgggatccc tatgactgtg gtaccttata tg 32

<210> 158
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 158
atgcggccgc acaaaggaaa agaagaaata caattc 36

<210> 159
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 159
cgggatcctt acaacttgta tgtcaaaatt ac 32

<210> 160
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 160
atgatggcgg ccgctcagaa gaaaagaaga aatacacttc 40

<210> 161
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 161
Val Val Asn Gly Ile Pro Thr Arg His Gly Arg
1 5 10

<210> 162
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 162
Gly Ile Pro Thr Arg Thr His Gly Arg
1 5

<210> 163
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 163
Val Asn Thr Leu Asp Gln
1 5

<210> 164
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 164
Val Val Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser
1 5 10 15

Leu Arg Tyr Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu
20 25 30

Ser Trp Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys
35 40 45

Asp Tyr Glu Ala Trp Leu Gly Ile His Asp Val His Gly Arg
50 55 60

<210> 165
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 165
Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr
1 5 10 15

Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val
20 25 30

Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu
35 40 45

Ala Trp Leu Gly Ile His Asp Val His Gly Arg
50 55

<210> 166
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Light chain CDR1 consensus sequence (CDR1a)

<220>
<221> MOD_RES
<222> (1)
<223> lysine, arginine, or glutamine

<220>
<221> MOD_RES
<222> (2)
<223> serine or alanine

<220>
<221> MOD_RES
<222> (5)
<223> serine, glycine, or aspartic acid

<220>
<221> MOD_RES
<222> (6)
<223> valine or isoleucine or is not present

<220>
<221> MOD_RES
<222> (7)
<223> leucine or phenylalanine or is not present

<220>
<221> MOD_RES
<222> (8)
<223> phenylalanine, tyrosine or is not present

<220>
<221> MOD_RES
<222> (9)..(10)
<223> serine or not present

<220>
<221> MOD_RES
<222> (11)
<223> asparagine, threonine, or not present

<220>
<221> MOD_RES
<222> (12)
<223> asparagine, isoleucine, or valine

<220>
<221> MOD_RES
<222> (13)
<223> lysine, arginine, asparagine, or aspartic acid

<220>
<221> MOD_RES
<222> (14)
<223> asparagine or serine

<220>
<221> MOD_RES
<222> (15)
<223> tyrosine, aspartic acid, tryptophan, or asparagine

<220>
<221> MOD_RES
<222> (17)
<223> alanine, glycine, or asparagine

<400> 166
Xaa Xaa Ser Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu
1 5 10 15

Xaa

<210> 167
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Light chain CDR2 consensus sequence (CDR2a)

<220>
<221> MOD_RES
<222> (1)
<223> tryptophan, alanine, valine, glutamic acid, or glycine

<220>
<221> MOD_RES
<222> (4)
<223> threonine, serine, or aspartic acid

<220>
<221> MOD_RES
<222> (5)
<223> arginine or leucine

<220>
<221> MOD_RES
<222> (6)
<223> glutamic acid, glutamine, or alanine

<220>
<221> MOD_RES
<222> (7)
<223> serine, asparagine, or threonine

<400> 167
Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 168
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Light chain CDR3 consensus sequence (CDR3a)

<220>
<221> MOD_RES
<222> (1)
<223> glutamine or leucine

<220>
<221> MOD_RES

<222> (2)
<223> glutamine, asparagine, or arginine

<220>
<221> MOD_RES
<222> (3)
<223> tyrosine, histidine, alanine, or serine

<220>
<221> MOD_RES
<222> (4)
<223> phenylalanine, tyrosine, aspartic acid, asparagine,
or isoleucine

<220>
<221> MOD_RES
<222> (5)
<223> serine, glycine, or asparagine

<220>
<221> MOD_RES
<222> (6)
<223> proline, tyrosine, threonine, phenylalanine, aspartic acid,
leucine, or tryptophan

<220>
<221> MOD_RES
<222> (8)
<223> proline or is not present

<220>
<221> MOD_RES
<222> (9)
<223> tryptophan, leucine, proline, tyrosine, or isoleucine

<220>
<221> MOD_RES
<222> (10)
<223> threonine or asparagine

<400> 168
Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa
1 5 10

<210> 169
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Heavy chain CDR1
consensus sequence (CDR1b)

<220>
<221> MOD_RES

<222> (1)
<223> serine or is not present

<220>
<221> MOD_RES
<222> (2)
<223> aspartic acid or glycine, or is not present

<220>
<221> MOD_RES
<222> (3)
<223> aspartic acid, glycine, serine, valine, threonine, or isoleucine

<220>
<221> MOD_RES
<222> (5)
<223> tyrosine or glycine

<220>
<221> MOD_RES
<222> (6)
<223> isoleucine, methionine, or tryptophan

<220>
<221> MOD_RES
<222> (7)
<223> histidine, asparagine, or serine

<400> 169
Xaa Xaa Xaa Tyr Xaa Xaa Xaa
1 5

<210> 170
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Heavy chain CDR2 consensus sequence (CDR2b)

<220>
<221> MOD_RES
<222> (1)
<223> tryptophan, tyrosine, valine, asparagine, or glutamic acid

<220>
<221> MOD_RES
<222> (2)
<223> isoleucine, phenylalanine, or valine

<220>
<221> MOD_RES
<222> (3)
<223> asparagine, serine, tryptophan, or tyrosine

<220>
<221> MOD_RES
<222> (4)
<223> proline, serine, tyrosine, or histidine

<220>
<221> MOD_RES
<222> (5)
<223> asparagine, serine, or aspartic acid

<220>
<221> MOD_RES
<222> (6)
<223> serine or glycine

<220>
<221> MOD_RES
<222> (7)
<223> glycine or serine, or is not present

<220>
<221> MOD_RES
<222> (8)
<223> glycine, threonine, aspartic acid, serine, isoleucine, or asparagine

<220>
<221> MOD_RES
<222> (9)
<223> threonine, isoleucine, or lysine

<220>
<221> MOD_RES
<222> (10)
<223> asparagine or tyrosine

<220>
<221> MOD_RES
<222> (11)
<223> tyrosine or histidine

<220>
<221> MOD_RES
<222> (12)
<223> alanine or asparagine

<220>
<221> MOD_RES
<222> (13)
<223> glutamine, aspartic acid, or proline

<220>
<221> MOD_RES
<222> (14)
<223> lysine or serine

<220>
<221> MOD_RES
<222> (15)
<223> phenylalanine, valine, or leucine

<220>
<221> MOD_RES
<222> (16)
<223> glutamine or lysine

<220>
<221> MOD_RES
<222> (17)
<223> glycine or serine

<400> 170
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa

<210> 171
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Heavy chain CDR3 consensus sequence (CDR3b)

<220>
<221> MOD_RES
<222> (1)
<223> glutamic acid, aspartic acid, serine, or glycine, or is not present

<220>
<221> MOD_RES
<222> (2)
<223> leucine, glutamic acid, aspartic acid, histidine, proline, or glycine, or is not present

<220>
<221> MOD_RES
<222> (3)
<223> glutamic acid, tyrosine, or leucine, or is not present

<220>
<221> MOD_RES
<222> (4)
<223> leucine, asparagine, glycine, histidine, tyrosine, or tryptophan, or is not present

<220>
<221> MOD_RES

<222> (5)
<223> arginine, serine, glutamic acid, tyrosine, glycine, or phenylalanine, or is not present

<220>
<221> MOD_RES
<222> (6)
<223> glycine or is not present

<220>
<221> MOD_RES
<222> (7)
<223> tryptophan or tyrosine, or is not present

<220>
<221> MOD_RES
<222> (8)
<223> aspartic acid or is not present

<220>
<221> MOD_RES
<222> (9)
<223> serine or arginine, or is not present

<220>
<221> MOD_RES
<222> (10)
<223> serine or is not present

<220>
<221> MOD_RES
<222> (11)
<223> glycine or tyrosine, or is not present

<220>
<221> MOD_RES
<222> (12)
<223> tyrosine, glutamic acid, or aspartic acid, or is not present

<220>
<221> MOD_RES
<222> (13)
<223> tyrosine, phenylalanine, or aspartic acid, or is not present

<220>
<221> MOD_RES
<222> (14)
<223> tyrosine, aspartic acid, histidine, or tryptophan, or is not present

<220>
<221> MOD_RES
<222> (15)
<223> tyrosine, glycine, aspartic acid, proline, or serine, or is not present

<220>
<221> MOD_RES
<222> (16)
<223> glycine, valine, tyrosine, or aspartic acid, or is not present

<220>
<221> MOD_RES
<222> (17)
<223> leucine, alanine, glycine, or tyrosine, or is not present

<220>
<221> MOD_RES
<222> (18)
<223> methionine, phenylalanine, or tyrosine

<220>
<221> MOD_RES
<222> (20)
<223> valine, tyrosine, isoleucine, or proline

<400> 171
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Asp Xaa
20

<210> 172
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 172
Val Val Asn Gly Ile Pro Thr Arg Thr Asn
1 5 10

<210> 173
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic kappa light chain protein sequence

<400> 173
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

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

Tyr Phe Ser Pro Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

Lys
```

<210> 174
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic kappa light chain protein sequence

<400> 174

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Ile Phe Tyr Ser
            20                  25                  30

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

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

Tyr Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

Lys
```

<210> 175
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic kappa light chain protein sequence

<400> 175
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Gly Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

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

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

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

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

<210> 176
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic kappa light chain protein sequence

<400> 176
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

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


<210> 177
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic kappa light
      chain protein sequence

<400> 177
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 Ala Ser Gln Gly Ile Ser Ser Trp
            20                  25                  30

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

Tyr Glu Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Gly 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 Ala Asn Gly Phe Pro Trp
                85                  90                  95

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


<210> 178
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic kappa light
      chain protein sequence

<400> 178
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Val Gly
  1               5                  10                  15

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

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

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

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

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

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

<210> 179
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic kappa light chain protein sequence

<400> 179

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

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

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

Tyr Val Ala Ser Ser Leu Gln Asn 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 Arg Ser Tyr Ser Thr Pro Pro
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105
```

<210> 180
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic kappa light chain protein sequence

<400> 180

```
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 Gln Ala Ser Asp Gln Ile Ser Asn Tyr
20 25 30

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

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

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

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

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

<210> 181
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic kappa light chain protein sequence

<400> 181
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

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

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

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

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

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

<210> 182
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic kappa light chain protein sequence

<400> 182
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

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

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

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

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

<210> 183
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic kappa light chain consensus sequence

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Undetermined consensus residue; variable amino acid

<220>
<221> MOD_RES
<222> (29)..(34)
<223> Undetermined consensus residue; variable amino acid

<220>
<221> MOD_RES
<222> (36)..(38)
<223> Undetermined consensus residue; variable amino acid

<220>
<221> MOD_RES
<222> (56)..(56)
<223> Undetermined consensus residue; variable amino acid

:220>
:221> MOD_RES
:222> (98)..(98)
:223> Undetermined consensus residue; variable amino acid

:220>
:221> MOD_RES
:222> (100)..(100)
:223> Undetermined consensus residue; variable amino acid

:220>
:221> MOD_RES
:222> (102)..(103)
:223> Undetermined consensus residue; variable amino acid

<400> 183
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Xaa Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Xaa Xaa Xaa Xaa
20 25 30

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

Ala Pro Lys Leu Leu Ile Tyr Xaa Ala Ser Thr Leu Gln Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

Tyr Xaa Ser Xaa Pro Xaa Xaa Thr Phe Gly Gln Gly Thr Lys Val Glu
100 105 110

Ile Lys

<210> 184
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic gamma heavy chain protein sequence

<400> 184
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 Thr Gly Tyr
20 25 30

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

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

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

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

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

Gly Thr Thr Val Thr Val
        115
```

<210> 185
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic gamma heavy chain protein sequence

<400> 185

```
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 Thr Gly Tyr
            20                  25                  30

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

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

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

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

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

Gly Thr Thr Val Thr Val
        115
```

<210> 186
<211> 120

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic gamma heavy chain protein sequence

<400> 186
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

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

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

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

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

Gly Gln Gly Thr Leu Val Thr Val
115 120

<210> 187
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic gamma heavy chain protein sequence

<400> 187
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

Ala Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val
        115
```

<210> 188
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic gamma heavy chain protein sequence

<400> 188

```
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 Thr Val Ser Gly Gly Ser Ile Ser Ser Asp
            20                  25                  30

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

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Ser His Leu His Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr
            100                 105                 110

Gly Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val
        115                 120                 125
```

<210> 189
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic gamma heavy chain protein sequence

<400> 189
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 Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

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

Trp Ile Gly Asn Ile Tyr Tyr Ser Gly Ile Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Pro Leu Tyr Gly Asp Tyr Gly Phe Asp Pro Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val
115

<210> 190
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic gamma heavy chain protein sequence

<400> 190
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 Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

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

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Val Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Pro Leu Trp Phe Gly Glu Phe Asp Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
115 120

<210> 191
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic gamma heavy chain protein sequence

<400> 191
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Val Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Phe Tyr Tyr Ser Gly Asn Thr Tyr His Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

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

Trp Gly Gln Gly Thr Met Val Thr Val
115 120

<210> 192
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic gamma heavy chain protein sequence

<400> 192
Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                 85                  90                  95

Arg Gly Gly Tyr Asp Phe Trp Ser Gly Tyr Tyr Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val
        115
```

<210> 193
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic gamma heavy chain protein sequence

<400> 193

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ile Tyr
            20                  25                  30

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

Gly Tyr Val Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
      50                  55                  60

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

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

Arg Gly Gly Tyr Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val
        115
```

<210> 194
<211> 128

:212> PRT
:213> Artificial Sequence

:220>
:223> Description of Artificial Sequence: Synthetic gamma heavy chain consensus sequence

:220>
:221> MOD_RES
:222> (16)..(16)
:223> Undetermined consensus residue; variable amino acid

:220>
:221> MOD_RES
:222> (31)..(32)
:223> Undetermined consensus residue; variable amino acid

:220>
:221> MOD_RES
:222> (42)..(42)
:223> Undetermined consensus residue; variable amino acid

:220>
:221> MOD_RES
:222> (58)..(58)
:223> Undetermined consensus residue; variable amino acid

:220>
:221> MOD_RES
:222> (102)..(112)
:223> Undetermined consensus residue; variable amino acid

:220>
:221> MOD_RES
:222> (114)..(114)
:223> Undetermined consensus residue; variable amino acid

:220>
:221> MOD_RES
:222> (116)..(116)
:223> Undetermined consensus residue; variable amino acid

:400> 194
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Xaa
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Xaa Xaa
20 25 30

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

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Xaa Ser Thr Tyr Tyr Asn Pro
50 55 60

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

```
he Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
                85                  90                  95

yr Cys Ala Arg Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            100                 105                 110

yr Xaa Gly Xaa Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
        115                 120                 125
```