

342-52PCT seq_ST25.txt
SEQUENCE LISTING

<110> Ganymed Pharmaceuticals AG et al.

<120> Antibodies for treatment of cancer

<130> 342-52 PCT

<150> EP 09 014 136.7

<151> 2009-11-11

<150> EP 10 006 956.6

<151> 2010-07-06

<150> US 61/361,618

<151> 2010-07-06

<150> US 61/260,202

<151> 2009-11-11

<160> 53

<170> PatentIn version 3.5

<210> 1

<211> 1369

<212> DNA

<213> Homo sapiens

<400> 1

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<210> 2
 <211> 220
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<400> 2

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 20 25 30

Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val Val Trp Glu
 35 40 45

Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
 50 55 60

Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
 65 70 75 80

Arg Ala Leu Cys Val Ile Ala Leu Leu Val Ala Leu Phe Gly Leu Leu
 85 90 95

Val Tyr Leu Ala Gly Ala Lys Cys Thr Thr Cys Val Glu Glu Lys Asp
 100 105 110

Ser Lys Ala Arg Leu Val Leu Thr Ser Gly Ile Val Phe Val Ile Ser
 115 120 125

Gly Val Leu Thr Leu Ile Pro Val Cys Trp Thr Ala His Ala Ile Ile
 130 135 140

Arg Asp Phe Tyr Asn Pro Leu Val Ala Glu Ala Gln Lys Arg Glu Leu
 145 150 155 160

Gly Ala Ser Leu Tyr Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
 165 170 175

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Gly Gly Gly Leu Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly
180 185 190

Pro Ser His Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser
195 200 205

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

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<212> DNA
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<223> codon-optimized nucleic acid sequence encoding human claudin 6

<400> 3
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gctgggtgaa cggcctggtg tcctgcgccc tgcccatgtg gaaagtgacc gccttcatcg 180
gcaacagcat cgtggtggcc caggctcgtgt gggagggcct gtggatgagc tgtgtggtgc 240
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gctggaccgc ccacgccatc atccgggact tctacaaccc tctggtggcc gagggcccaga 540
agagagagct gggcgccagc ctgtatctgg gatgggcccgc ctcaggactg ctgctgctgg 600
gcggaggcct gctgtgctgt acatgtccta gcggcggtc ccagggccct agccactaca 660
tggcccggta cagcaccagc gccctgccca tcagcagagg cccagcagag taccacacca 720
agaactacgt gtgataggaa ttcgagctct tatggcgcgcc ccaattcgcc ctatagttag 780
tcgtattacg tcgcgctcac tggcc 805

<210> 4
<211> 165
<212> DNA
<213> Artificial

<220>
<223> codon-optimized nucleic acid sequence encoding the predicted extracellular loop 2 (EC2) of human claudin 6

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gctcctgtgg gtcccaggct ctacaggcga cgccgcccag cccagagact tctacaaccc 120

cctggtggcc gaggccaga agctcgagtc tagagggtta attaa

<210> 5
 <211> 38
 <212> PRT
 <213> Artificial

<220>
 <223> predicted 2nd extracellular loop of human claudin 6 containing an
 Ig kappa leader sequence

<220>
 <221> SIGNAL
 <222> (1)..(21)
 <223> Ig kappa leader sequence

<220>
 <221> DOMAIN
 <222> (26)..(38)
 <223> predicted 2nd extracellular loop (EC2) of human claudin 6

<400> 5

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
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Gly Ser Thr Gly Asp Ala Ala Gln Pro Arg Asp Phe Tyr Asn Pro Leu
 20 25 30

Val Ala Glu Ala Gln Lys
 35

<210> 6
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 6

Arg Asp Phe Tyr Asn Pro Leu Val Ala Glu Ala Gln Lys
 1 5 10

<210> 7
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 7

Pro Met Trp Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala
 1 5 10 15

Gln Val Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr
 20 25 30

Gly Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln

35

Asp Leu Gln Ala Ala
50

<210> 8
<211> 220
<212> PRT
<213> Homo sapiens

<220>
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<222> (143)..(143)
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<400> 8

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1 5 10 15

Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp Lys Val
20 25 30

Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val Val Trp Glu
35 40 45

Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
50 55 60

Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
65 70 75 80

Arg Ala Leu Cys Val Ile Ala Leu Leu Val Ala Leu Phe Gly Leu Leu
85 90 95

Val Tyr Leu Ala Gly Ala Lys Cys Thr Thr Cys Val Glu Glu Lys Asp
100 105 110

Ser Lys Ala Arg Leu Val Leu Thr Ser Gly Ile Val Phe Val Ile Ser
115 120 125

Gly Val Leu Thr Leu Ile Pro Val Cys Trp Thr Ala His Ala Val Ile
130 135 140

Arg Asp Phe Tyr Asn Pro Leu Val Ala Glu Ala Gln Lys Arg Glu Leu
145 150 155 160

Gly Ala Ser Leu Tyr Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
165 170 175

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Gly Gly Gly Leu Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly
180 185 190

Pro Ser His Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser
195 200 205

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

<210> 9
<211> 217
<212> PRT
<213> Homo sapiens

<400> 9

Met Ala Ser Thr Gly Leu Glu Leu Leu Gly Met Thr Leu Ala Val Leu
1 5 10 15

Gly Trp Leu Gly Thr Leu Val Ser Cys Ala Leu Pro Leu Trp Lys Val
20 25 30

Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val Val Trp Glu
35 40 45

Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
50 55 60

Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
65 70 75 80

Arg Ala Leu Cys Val Ile Ala Leu Leu Leu Ala Leu Leu Gly Leu Leu
85 90 95

Val Ala Ile Thr Gly Ala Gln Cys Thr Thr Cys Val Glu Asp Glu Gly
100 105 110

Ala Lys Ala Arg Ile Val Leu Thr Ala Gly Val Ile Leu Leu Leu Ala
115 120 125

Gly Ile Leu Val Leu Ile Pro Val Cys Trp Thr Ala His Ala Ile Ile
130 135 140

Gln Asp Phe Tyr Asn Pro Leu Val Ala Glu Ala Leu Lys Arg Glu Leu
145 150 155 160

Gly Ala Ser Leu Tyr Leu Gly Trp Ala Ala Ala Ala Leu Leu Met Leu
165 170 175

Gly Gly Gly Leu Leu Cys Cys Thr Cys Pro Pro Pro Gln Val Glu Arg

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180

185

190

Pro Arg Gly Pro Arg Leu Gly Tyr Ser Ile Pro Ser Arg Ser Gly Ala
195 200 205

Ser Gly Leu Asp Lys Arg Asp Tyr Val
210 215

<210> 10
<211> 209
<212> PRT
<213> Homo sapiens

<400> 10

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1 5 10 15

Gly Trp Leu Ala Val Met Leu Cys Cys Ala Leu Pro Met Trp Arg Val
20 25 30

Thr Ala Phe Ile Gly Ser Asn Ile Val Thr Ser Gln Thr Ile Trp Glu
35 40 45

Gly Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
50 55 60

Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
65 70 75 80

Arg Ala Leu Val Ile Ile Ser Ile Ile Val Ala Ala Leu Gly Val Leu
85 90 95

Leu Ser Val Val Gly Gly Lys Cys Thr Asn Cys Leu Glu Asp Glu Ser
100 105 110

Ala Lys Ala Lys Thr Met Ile Val Ala Gly Val Val Phe Leu Leu Ala
115 120 125

Gly Leu Met Val Ile Val Pro Val Ser Trp Thr Ala His Asn Ile Ile
130 135 140

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

Gly Ala Ser Leu Tyr Val Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
165 170 175

Gly Gly Gly Leu Leu Cys Cys Asn Cys Pro Pro Arg Thr Asp Lys Pro
180 185 190

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Tyr Ser Ala Lys Tyr Ser Ala Ala Arg Ser Ala Ala Ala Ser Asn Tyr
195 200 205

Val

<210> 11
<211> 220
<212> PRT
<213> Homo sapiens

<400> 11

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Trp Leu Gly Thr Ile Val Cys Cys Ala Leu Pro Met Trp Arg Val Ser
20 25 30

Ala Phe Ile Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly
35 40 45

Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys
50 55 60

Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg
65 70 75 80

Ala Leu Ile Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val
85 90 95

Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala
100 105 110

Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala
115 120 125

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

Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly
145 150 155 160

Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly
165 170 175

Gly Ala Leu Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr
180 185 190

342-52PCT seq_ST25.txt

Ala Thr Lys Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala
195 200 205

Ser Leu Gly Thr Gly Tyr Asp Arg Lys Asp Tyr Val
210 215 220

<210> 12
<211> 159
<212> DNA
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<220>
<223> codon-optimized nucleic acid sequence encoding the predicted
extracellular loop 1 (EC1) of human claudin 6

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gagggcctgt ggatgagctg cgtggtgcag agcaccggcc agatgcagtg caaggtgtac 120
gacagcctgc tggccctgcc tcaggatctg caggctgct 159

<210> 13
<211> 106
<212> PRT
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<220>
<223> predicted 1st extracellular loop of human claudin 6 containing an
Ig kappa leader sequence

<220>
<221> Signal
<222> (1)..(21)
<223> Ig kappa leader sequence

<220>
<221> Domain
<222> (26)..(78)
<223> predicted 1st extracellular loop (EC1) of human claudin 6

<400> 13

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1 5 10 15

Gly Ser Thr Gly Asp Ala Ala Gln Pro Pro Met Trp Lys Val Thr Ala
20 25 30

Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val Val Trp Glu Gly Leu
35 40 45

Trp Met Ser Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys Val
50 55 60

342-52PCT seq_ST25.txt

Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Leu Glu
65 70 75 80

Ser Arg Gly Pro Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
85 90 95

Met His Thr Gly His His His His His His
100 105

<210> 14
<211> 13
<212> PRT
<213> Homo sapiens

<400> 14

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1 5 10

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

<400> 15

Met Trp Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala
1 5 10 15

<210> 16
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide

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<210> 17
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 17
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<210> 18
<211> 43
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<223> Oligonucleotide

<400> 18
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<210> 19
<211> 43
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<223> Oligonucleotide

<400> 19
gagagggccc ttggtggagg ctgaggagac tgtgagagtg gtg 43

<210> 20
<211> 43
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<210> 22
<211> 33
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<213> Artificial Sequence

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<223> Oligonucleotide

<400> 22
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<210> 23
<211> 33
<212> DNA
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<223> Oligonucleotide

<400> 23
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<210> 24
<211> 993
<212> DNA
<213> Homo sapiens

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tggaacagcg gagccctgac ctccggcgtg cacaccttcc ccgccgtgct gcagagcagc 180
ggcctgtaca gcctgagcag cgtggtgacc gtgcccagca gcagcctggg caccagacc 240
tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagag agtggagccc 300
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cccagcgtgt tcctgttccc cccaagccc aaggacaccc tgatgatcag caggaccccc 420
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gaatacaagt gcaaggtctc caacaaggcc ctgccagccc ccatcgaaaa gaccatcagc 660
aaggccaagg gccagccacg ggagccccag gtgtacaccc tgccccccag ccgggaggag 720
atgaccaaga accaggtgtc cctgacctgt ctggtgaagg gcttctaccc cagcgacatc 780
gccgtggagt gggagagcaa cggccagccc gagaacaact acaagaccac cccccagtg 840
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cagaagtccc tgagcctgag ccccggaag tag 993

<210> 25
<211> 330
<212> PRT
<213> Homo sapiens

<400> 25
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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

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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
 Arg 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 Glu Glu
 225 230 235 240
 Met 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

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

<210> 26
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 26
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 ggcaccgcca gcgtggtgtg cctgctgaac aacttctacc cccgggaggg caaggtgcag 120
 tggaaggtgg acaacgccct gcagagcggc aacagccagg agagcgtcac cgagcaggac 180
 agcaaggact ccacctacag cctgagcagc accctgaccc tgagcaaggc cgactacgag 240
 aagcacaagg tgtacgctg cgaggtgacc caccagggcc tgtccagccc cgtgaccaag 300
 agcttcaaca ggggcgagtg ctag 324

<210> 27
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 27

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> 28
 <211> 32
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Oligonucleotide

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<222> (31)..(32)
<223> any nucleotide

<400> 28
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<210> 29
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<223> Oligonucleotide

<400> 29
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<210> 30
<211> 26
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<220>
<223> Oligonucleotide

<400> 30
ctgctcactg gatggtggga agatgg 26

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 31
acaggggcca gtggatagac cgatg 25

<210> 32
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<212> DNA
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<400> 32
gtaatacgac tcactatagg gcaagcagtg gatatcaacgc agagt 45

<210> 33
<211> 22

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<212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 33
 gtaatacgac tcactatagg gc

22

<210> 34
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 <213> Artificial Sequence

<220>
 <223> Antibody VH sequence

<400> 34

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

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

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
 35 40 45

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

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

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

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

Leu Thr Val Ser Ser
 115

<210> 35
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<220>
 <223> Antibody VL sequence

<400> 35

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

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

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Val Tyr
35 40 45

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

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ile Tyr Pro Pro Trp
85 90 95

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

<210> 36
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH sequence

<400> 36

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

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

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45

Gly Leu Ile Asn Pro Tyr Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe
50 55 60

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

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

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

Leu Thr Val Ser Ser
115

<210> 37
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VL sequence

<400> 37

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

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

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Cys Ile Tyr
35 40 45

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

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Asn Tyr Pro Pro Trp
85 90 95

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

<210> 38
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH sequence

<400> 38

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

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

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45

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Gly Leu Ile Asn Pro Tyr Asn Gly Gly Ile Ile Tyr Asn Gln Lys Phe
50 55 60

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

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

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

Leu Thr Val Ser Ser
115

<210> 39
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VL sequence

<400> 39

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

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

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
35 40 45

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

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Pro Trp
85 90 95

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

<210> 40
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> Antibody VH sequence

<400> 40

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

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

Thr Leu Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
 35 40 45

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

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

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

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

Leu Thr Val Ser Ser
 115

<210> 41

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Antibody VL sequence

<400> 41

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

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Met
 20 25 30

His Trp Phe Gln Leu Lys Pro Gly Thr Ser Pro Lys Leu Leu Ile Tyr
 35 40 45

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

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Asn Asn Tyr Pro Pro Trp
85 90 95

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

<210> 42
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH CDR3 sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Any amino acid, preferably Leu or Phe, more preferably Leu

<400> 42

Xaa Gly Xaa Val Xaa
1 5

<210> 43
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH CDR3 sequence

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>

<221> MISC_FEATURE
 <222> (6)..(6)
 <223> Any amino acid, preferably Leu or Phe, more preferably Leu
 <400> 43

Asp Xaa Gly Xaa Val Xaa
 1 5

<210> 44
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Antibody VH CDR3 sequence

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> Any amino acid, preferably Leu or Phe, more preferably Leu

<400> 44

Xaa Gly Xaa Val Xaa Asp
 1 5

<210> 45
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Antibody VH CDR3 sequence

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>

<221> MISC_FEATURE
 <222> (6)..(6)
 <223> Any amino acid, preferably Leu or Phe, more preferably Leu
 <400> 45

Asp Xaa Gly Xaa Val Xaa Asp
 1 5

<210> 46
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Antibody VH CDR3 sequence

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
 <221> MISC_FEATURE
 <222> (8)..(8)
 <223> Any amino acid, preferably Leu or Phe, more preferably Leu

<400> 46

Ala Arg Asp Xaa Gly Xaa Val Xaa Asp Tyr
 1 5 10

<210> 47
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Antibody VH CDR1 sequence

<400> 47

Gly Tyr Ser Phe Thr Gly Tyr Thr
 1 5

<210> 48
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Antibody VH CDR2 sequence

<220>
 <221> MISC_FEATURE
 <222> (8)..(8)
 <223> Any amino acid, preferably Thr, Ser or Ile, most preferably Thr
 <400> 48

Ile Asn Pro Tyr Asn Gly Gly Xaa
 1 5

<210> 49
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Antibody VL CDR3 sequence

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> Any amino acid, preferably Ser or Asn, most preferably Ser

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Any amino acid, preferably Tyr, Ser, Ile, Asn or Thr, more preferably Tyr, Ser, or Asn, most preferably Asn

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Any amino acid, preferably Ser or Tyr, more preferably Tyr

<400> 49

Arg Xaa Xaa Xaa Pro
 1 5

<210> 50
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Antibody VL CDR3 sequence

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Any amino acid, preferably Ser or Asn, most preferably Ser

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Any amino acid, preferably Tyr, Ser, Ile, Asn or Thr, more preferably Tyr, Ser, or Asn, most preferably Asn

<220>

<221> MISC_FEATURE
 <222> (5)..(5)
 <223> Any amino acid, preferably Ser or Tyr, more preferably Tyr
 <400> 50

Gln Arg Xaa Xaa Xaa Pro Pro
 1 5

<210> 51
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Antibody VL CDR3 sequence

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Any amino acid, preferably Ser or Asn, most preferably Ser

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> Any amino acid, preferably Tyr, Ser, Ile, Asn or Thr, more preferably Tyr, Ser, or Asn, most preferably Asn

<220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> Any amino acid, preferably Ser or Tyr, more preferably Tyr

<400> 51

Gln Gln Arg Xaa Xaa Xaa Pro Pro Trp Thr
 1 5 10

<210> 52
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Antibody VL CDR1 sequence

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Any amino acid, preferably Ser or Asn, most preferably Ser

<400> 52

Ser Ser Val Xaa Tyr
 1 5

<210> 53
 <211> 3
 <212> PRT

<213> Artificial Sequence

<220>

<223> Antibody VL CDR2 sequence

<400> 53

Ser Thr Ser

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