

SEQUENCE LISTING

<110> Eisai R&D Management

<120> A METHOD FOR PRODUCING ERIBULIN-BASED ANTIBODY-DRUG CONJUGATES

<130> FP20-0574-00

<160> 347

<170> PatentIn version 3.5

<210> 1

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 Heavy chain

<400> 1

Glu 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 Ser Ala Ser Gly Phe Thr Phe Ser Gly Tyr

20 25 30

Gly Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Met Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys

85 90 95

Ala Arg His Gly Asp Asp Pro Ala Trp Phe Ala Tyr Trp Gly Gln Gly

100 105 110

Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe

115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu

130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp

145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu

165

170

175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser

180

185

190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro

195

200

205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys

210

215

220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro

225

230

235

240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser

245

250

255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp

260

265

270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn

275

280

285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val

290

295

300

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

305

310

315

320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys

325

330

335

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

340

345

350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr

355

360

365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu

370

375

380

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

385

390

395

400

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

405

410

415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu

420

425

430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

435

440

445

Lys

<210> 2

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR1

<400> 2

Gly Tyr Gly Leu Ser

1

5

<210> 3

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR2

<400> 3

Met Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 4

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR3

<400> 4

His Gly Asp Asp Pro Ala Trp Phe Ala Tyr

1 5 10

<210> 5

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 Heavy Chain full length pre-protein amino acid sequence

<400> 5

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln

20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe

35 40 45

Ser Gly Tyr Gly Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

50 55 60

Glu Trp Val Ala Met Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Ala

65 70 75 80

Asp Ser Val Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ala Lys Asn

85 90 95

Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val

100

105

110

Tyr Phe Cys Ala Arg His Gly Asp Asp Pro Ala Trp Phe Ala Tyr Trp

115

120

125

Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro

130

135

140

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr

145

150

155

160

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

165

170

175

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro

180

185

190

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr

195

200

205

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn

210

215

220

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser

225 230 235 240

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu

245 250 255

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu

260 265 270

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

275 280 285

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

290 295 300

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

305 310 315 320

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro

340 345 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

355 360 365

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

370 375 380

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

385 390 395 400

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

405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr

420 425 430

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

435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu

450 455 460

Ser Pro Gly Lys

465

<210> 6

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 Light chain

<400> 6

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

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Val Ser Ser Ser Ile Ser Ser Asn

20 25 30

Asn Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp

35 40 45

Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser

50 55 60

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

65 70 75 80

Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro

85 90 95

Tyr Met Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr

100 105 110

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu

115 120 125

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro

130 135 140

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

145 150 155 160

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr

165 170 175

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His

180 185 190

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

195

200

205

Thr Lys Ser Phe Asn Arg Gly Glu Cys

210

215

<210> 7

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR1

<400> 7

Ser Val Ser Ser Ser Ile Ser Ser Asn Asn Leu His

1

5

10

<210> 8

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR2

<400> 8

Gly Thr Ser Asn Leu Ala Ser

1 5

<210> 9

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR3

<400> 9

Gln Gln Trp Ser Ser Tyr Pro Tyr Met Tyr Thr

1 5 10

<210> 10

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 Light Chain full length pre-protein amino acid sequence

<400> 10

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala

20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Val Ser Ser Ser Ile

35 40 45

Ser Ser Asn Asn Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro

50 55 60

Lys Pro Trp Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro Ser

65 70 75 80

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

85 90 95

Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser

100 105 110

Ser Tyr Pro Tyr Met Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile

115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu

165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp

180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr

195 200 205

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

210 215 220

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

225 230 235

<210> 11

<211> 1407

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 HC nt

<400> 11

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactccgag 60

gtccaactgg tggagagcgg tggaggtgtt gtgcaacctg gccggtccct gcgcctgtcc 120

tgctccgcat ctggcttcac cttcagcggc tatgggttgt cttgggtgag acaggcacct 180

ggaaaaggtc ttgagtgggt tgcaatgatt agtagtggtg gtagttatac ctactatgca 240

gacagtgtga agggtagatt tgcaatatcg cgagacaacg ccaagaacac attgttcctg 300

caaatggaca gcctgagacc cgaagacacc ggggtctatt tttgtgcaag acatggggac 360

gatcccgctt gggttcgcta ttggggccaa gggaccccg taccgtctc ctcagcctcc 420

accaagggcc catcgttctt ccccctggca cctcctcca agagcacctc tgggggcaca 480

gcggccctgg gctgcctggt caaggactac ttcccgaac cggtgacggt gtcgtggaac 540

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tctacagtc ctcaggactc 600

tactccctca gcagcgtggt gaccgtgcc tccagcagct tgggcacca gacctacatc 660

tgcaactga atcacaagcc cagcaacacc aaggtggaca agaaagtga gcccaaattc 720

ttgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780

gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 840

acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 900

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 960

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1020

aagtgaagg tctccaacaa agccctcca gcccctatcg agaaaacat ctccaaagcc 1080

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccgga tgagctgacc 1140

aagaaccagg tcagcctgac ctgcctggc aaaggcttct atcccagca catcgccgtg 1200

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1260

tccgacggct ccttcttctt atattcaaag ctcaccgtgg acaagagcag gtggcagcag 1320

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1380

agcctctccc tgtctcccg gaaatga 1407

<210> 12

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 LC nt

<400> 12

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactccgac 60

atccagctga cccagagccc aagcagcctg agcgccagcg tgggtgacag agtgaccatc 120

acctgtagtg tcagctcaag tataagttcc aacaactgc actggtacca gcagaagcca 180

ggtaaggctc caaagccatg gatctacggc acatccaacc tggcttctgg tgtgccaagc 240

agattcagcg gtagcggtag cggtaccgac tacacctca ccatcagcag cctccagcca 300

gaggacatcg ccacctacta ctgccaacag tggagtagtt acccgtagat gtacacgttc 360

ggccaaggga ccaaggtgga aatcaaacga actgtggctg caccatctgt cttcatcttc 420

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600

ctgacgctga gcaaagcaga ctacagaaaa caaaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccg cacaagagc ttcaacaggg gagagtgtta a 711

<210> 13

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR1; IMGT

<400> 13

Gly Phe Thr Phe Ser Gly Tyr Gly

1 5

<210> 14

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR2; IMGT

<400> 14

Ile Ser Ser Gly Gly Ser Tyr Thr

1 5

<210> 15

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR3; IMGT

<400> 15

Ala Arg His Gly Asp Asp Pro Ala Trp Phe Ala Tyr

1 5 10

<210> 16

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR1; IMGT

<400> 16

Ser Ser Ile Ser Ser Asn Asn

1 5

<210> 17

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR2; IMGT

<400> 17

Gly Thr Ser

1

<210> 18

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR3; IMGT

<400> 18

Gln Gln Trp Ser Ser Tyr Pro Tyr Met Tyr Thr

1 5 10

<210> 19

<211> 257

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Gln Arg Met Thr Thr Gln Leu Leu Leu Leu Val Trp Val

1 5 10 15

Ala Val Val Gly Glu Ala Gln Thr Arg Ile Ala Trp Ala Arg Thr Glu

20 25 30

Leu Leu Asn Val Cys Met Asn Ala Lys His His Lys Glu Lys Pro Gly
35 40 45

Pro Glu Asp Lys Leu His Glu Gln Cys Arg Pro Trp Arg Lys Asn Ala
50 55 60

Cys Cys Ser Thr Asn Thr Ser Gln Glu Ala His Lys Asp Val Ser Tyr
65 70 75 80

Leu Tyr Arg Phe Asn Trp Asn His Cys Gly Glu Met Ala Pro Ala Cys
85 90 95

Lys Arg His Phe Ile Gln Asp Thr Cys Leu Tyr Glu Cys Ser Pro Asn
100 105 110

Leu Gly Pro Trp Ile Gln Gln Val Asp Gln Ser Trp Arg Lys Glu Arg
115 120 125

Val Leu Asn Val Pro Leu Cys Lys Glu Asp Cys Glu Gln Trp Trp Glu
130 135 140

Asp Cys Arg Thr Ser Tyr Thr Cys Lys Ser Asn Trp His Lys Gly Trp
145 150 155 160

Asn Trp Thr Ser Gly Phe Asn Lys Cys Ala Val Gly Ala Ala Cys Gln

165

170

175

Pro Phe His Phe Tyr Phe Pro Thr Pro Thr Val Leu Cys Asn Glu Ile

180

185

190

Trp Thr His Ser Tyr Lys Val Ser Asn Tyr Ser Arg Gly Ser Gly Arg

195

200

205

Cys Ile Gln Met Trp Phe Asp Pro Ala Gln Gly Asn Pro Asn Glu Glu

210

215

220

Val Ala Arg Phe Tyr Ala Ala Ala Met Ser Gly Ala Gly Pro Trp Ala

225

230

235

240

Ala Trp Pro Phe Leu Leu Ser Leu Ala Leu Met Leu Leu Trp Leu Leu

245

250

255

Ser

<210> 20

<211> 982

<212> DNA

<213> Homo sapiens

<400> 20

catccttgg tgccactgac cacagctctt tcttcaggga cagacatggc tcagcggatg 60

acaacacagc tgctgctcct tctagtgtgg gtggctgtag taggggaggc tcagacaagg 120

attgcatggg ccaggactga gcttctcaat gtctgcatga acgccaagca ccacaaggaa 180

aagccaggcc ccgaggacaa gttgcatgag cagtgtcgac cctggaggaa gaatgcctgc 240

tgttctacca acaccagcca ggaagcccat aaggatgttt cctacctata tagattcaac 300

tggaaccact gtggagagat ggcacctgcc tgcaaacggc atttcatcca ggacacctgc 360

ctctacgagt gctccccaa cttggggccc tggatccagc aggtggatca gagctggcgc 420

aaagagcggg tactgaacgt gccctgtgc aaagaggact gtgagcaatg gtgggaagat 480

gtcgcacct cctacacctg caagagcaac tggcacaagg gctggaactg gacttcaggg 540

tttaacaagt gcgcagtggg agctgcctgc caacctttcc atttctactt cccacaccc 600

actgttctgt gcaatgaaat ctggactcac tcctacaagg tcagcaacta cagccgaggg 660

agtggccgct gcatccagat gtggttcgac ccagcccagg gcaaccccaa tgaggaggtg 720

gcgaggttct atgctgcagc catgagtggg gctgggccct gggcagcctg gcctttcctg 780

cttagcctgg ccctaagtct gctgtggctg ctcagctgac ctccttttac cttctgatac 840

ctggaaatcc ctgccctgtt cagccccaca gctcccaact atttggttcc tgctccatgg 900

tcgggcctct gacagccact ttgaataaac cagacaccgc acatgtgtct tgagaattat 960

ttggaaaaaa aaaaaaaaaa aa 982

<210> 21

<211> 1255

<212> PRT

<213> Homo sapiens

<400> 21

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu

1 5 10 15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys

20 25 30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His

35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr

50 55 60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65 70 75 80

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

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
 100 105 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
 115 120 125

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

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145 150 155 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
 165 170 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
 180 185 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser

195 200 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys

210 215 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys

225 230 235 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu

245 250 255

His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val

260 265 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg

275 280 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu

290 295 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln

305 310 315 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys

325 330 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu

340 345 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys

355 360 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp

370 375 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe

385 390 395 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro

405 410 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg

420 425 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu

435 440 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly

450 455 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val

465 470 475 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr

485 490 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His

500 505 510

Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys

515 520 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys

530 535 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys

545 550 555 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys

565

570

575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp

580

585

590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu

595

600

605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln

610

615

620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys

625

630

635

640

Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser

645

650

655

Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly

660

665

670

Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg

675

680

685

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

690 695 700

Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu

705 710 715 720

Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys

725 730 735

Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile

740 745 750

Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu

755 760 765

Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg

770 775 780

Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu

785 790 795 800

Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg

805 810 815

Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly

820 825 830

Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala

835 840 845

Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe

850 855 860

Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp

865 870 875 880

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg

885 890 895

Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val

900 905 910

Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala

915 920 925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro

930 935 940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met

945 950 955 960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe

965 970 975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu

980 985 990

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu

995 1000 1005

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr

1010 1015 1020

Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly

1025 1030 1035

Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg

1040 1045 1050

Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu
1055 1060 1065

Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
1070 1075 1080

Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu
1085 1090 1095

Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser
1100 1105 1110

Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val
1115 1120 1125

Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
1130 1135 1140

Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro
1145 1150 1155

Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro Lys Thr Leu
1160 1165 1170

Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly

1175 1180 1185

Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala

1190 1195 1200

Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp

1205 1210 1215

Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro

1220 1225 1230

Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr

1235 1240 1245

Leu Gly Leu Asp Val Pro Val

1250 1255

<210> 22

<211> 3768

<212> DNA

<213> Homo sapiens

<400> 22

atggagctgg cggccttgtag cgcctggggg ctctctctcg ccctcttgcc ccccgagacc 60

gcgagcacc aagtgtgac cggcacagac atgaagctgc ggctccctgc cagtcccgag 120

accacactgg acatgctccg ccacctctac cagggtgcc aggtggtgca gggaaacctg 180

gaactcacct acctccac caatgccagc ctgtccttc tgcaggatat ccaggagggtg 240

cagggtacg tgctcatgc tcacaacaa gtgaggcagg tccactgca gaggctgcgg 300

attgtgcgag gcaccagct cttgaggac aactatgcc tggccgtgct agacaatgga 360

gaccgctga acaataccac ccctgtcac ggggcctccc caggaggcct gcgggagctg 420

cagcttcgaa gcctcacaga gatcttgaaa ggaggggtct tgatccagcg gaacccccag 480

ctctgctacc aggacacgat ttgtggaag gacatcttc acaagaacaa ccagctggct 540

ctcacactga tagacacaa ccgtctcgg gcctgccacc cctgttctcc gatgtgtaag 600

ggctccgct gctggggaga gaggctgag gattgtcaga gcctgacgc cactgtctgt 660

gccggtggct gtcccgtg caaggggcca ctgccactg actgctgcca tgagcagtg 720

gctgccggct gcacgggcc caagcactct gactgcctgg cctgcctca cttcaaccac 780

agtggcatct gtgagctga ctgccagcc ctggtcacct acaacacaga cacgtttgag 840

tcatgcca atccgaggg ccggtatata ttcggcgcca gctgtgtgac tgcctgtccc 900

tacaactacc tttctacgga cgtgggatcc tgcaccctcg tctgcccct gcacaaccaa 960

gaggtgacag cagaggatgg aacacagcgg tgtgagaagt gcagcaagcc ctgtgcccga 1020

gtgtgctatg gtctgggcat ggagcacttg cgagaggtga gggcagttac cagtccaat 1080

atccaggagt ttgctggctg caagaagatc ttggggagcc tggcatttct gccggagagc 1140

tttgatgggg acccagcctc caaactgcc ccgctccagc cagagcagct ccaagtgtt 1200

gagactctgg aagagatcac aggttaccta tacatctcag catggccgga cagcctgcct 1260

gacctcagcg tcttcagaa cctgcaagta atccggggac gaattctgca caatggcgcc 1320

tactcgctga ccctgcaagg gctgggcatc agctggctgg ggctgcgctc actgagggaa 1380

ctgggcagtg gactggccct catccaccat aacaccacc tctgcttctg gcacacggtg 1440

ccctgggacc agctctttcg gaaccgcac caagctctgc tccacactgc caaccggcca 1500

gaggacgagt gtgtggcgga gggcctggcc tgccaccagc tgtgcgcccg agggcactgc 1560

tggggtccag ggcccacca gtgtgtcaac tgcagccagt tccttcgggg ccaggagtgc 1620

gtggaggaat gccgagtact gcaggggctc cccaggagat atgtgaatgc caggcactgt 1680

ttgccgtgcc accctgagtg tcagccccag aatggctcag tgacctgtt tggaccggag 1740

gctgaccagt gtgtggcctg tgcccactat aaggaccctc ccttctcgt ggcccgtgc 1800

cccagcgtg tgaaacctga cctctctac atgcccattt ggaagtttcc agatgaggag 1860

ggcgcatgcc agccttgccc catcaactgc acccactcct gtgtggacct ggatgacaag 1920
 ggctgccccg ccgagcagag agccagccct ctgacgtcca tcatctctgc ggtggttggc 1980
 attctgctgg tcgtggtctt gggggtggtc ttgggatcc tcatcaagcg acggcagcag 2040
 aagatccgga agtacacgat gcggagactg ctgcaggaaa cggagctggt ggagccgctg 2100
 acacctagcg gagcgatgcc caaccaggcg cagatgcgga tcctgaaaga gacggagctg 2160
 aggaaggtga aggtgcttgg atctggcgct ttggcacag tctacaaggg catctggatc 2220
 cctgatgggg agaatgtgaa aattccagtg gccatcaaag tgttgaggga aaacacatcc 2280
 cccaaagcca acaaagaaat cttagacgaa gcatactga tggctggtgt gggctcccca 2340
 tatgtctccc gccttctggg catctgcctg acatccacgg tgcagctggt gacacagctt 2400
 atgccctatg gctgcctctt agaccatgtc cgggaaaacc gcggacgcct gggctcccag 2460
 gacctgctga actggtgtat gcagattgcc aaggggatga gctacctgga ggatgtgcgg 2520
 ctctacaca gggacttggc cgctcggaac gtgctggtca agagtcccaa ccatgtcaaa 2580
 attacagact tcgggctggc tcggctgctg gacattgacg agacagagta ccatgcagat 2640
 gggggcaagg tgccatcaa gtggatggcg ctggagtcca ttctccgccg gcggttcacc 2700
 caccagatg atgtgtggag ttatggtgtg actgtgtggg agctgatgac ttttggggcc 2760

aaaccttacg atgggatccc agcccgagg atccctgacc tgctggaaaa gggggagcgg 2820

ctgccccagc ccccatctg caccattgat gtctacatga tcatggtaa atgttgatg 2880

attgactctg aatgtcgcc aagattccgg gagggtgt ctgaatttc ccgcatggc 2940

agggacccc agcgcttgt ggtcatccag aatgaggact tgggccagc cagtccttg 3000

gacagcacct tctaccgctc actgctggag gacgatgaca tgggggacct ggtggatgct 3060

gaggagtatc tggtagccca gcagggttc ttctgtccag accctgccc gggcgctggg 3120

ggcatggtcc accacaggca ccgagctca tctaccagga gtggcggtgg ggacctgaca 3180

ctagggtgg agccctctga agaggaggcc cccaggtctc cactggcacc ctccgaaggg 3240

gctggctccg atgtattga tggtagctg ggaatggggg cagccaaggg gctgcaaagc 3300

ctccccacac atgacccag ccctctacag cggtagctg aggacccac agtaccctg 3360

ccctctgaga ctgatggcta cggtgcccc ctgacctga gccccagcc tgaatatgtg 3420

aaccagccag atgttcggcc ccagcccct tcgcccagaggccctct gcctgctgcc 3480

cgacctgctg gtgacctct ggaaaggccc aagactctct cccaggga gaatggggtc 3540

gtcaaagacg ttttgcctt tgggggtgcc gtggagaacc ccgagtactt gacacccag 3600

ggaggagctg cccctcagcc ccacctct cctgcctca gccagcctt cgacaacctc 3660

tattactggg accaggacc accagagcgg ggggtccac ccagcacctt caaagggaca 3720

cctacggcag agaaccaga gtacctgggt ctggacgtgc cagtgatga

3768

<210> 23

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 Heavy chain (Table 2)

<400> 23

Glu 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 Ser Ala Ser Gly Phe Thr Phe Ser Gly Tyr

20 25 30

Gly Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Met Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys

85 90 95

Ala Arg His Gly Asp Asp Pro Ala Trp Phe Ala Tyr Trp Gly Gln Gly

100 105 110

Thr Pro Val Thr Val Ser Ser

115

<210> 24

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-003 Light chain (Table 2)

<400> 24

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

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Val Ser Ser Ser Ile Ser Ser Asn

20 25 30

Asn Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp

35 40 45

Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser

50 55 60

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

65 70 75 80

Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro

85 90 95

Tyr Met Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 25

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 Heavy chain (Table 2)

<400> 25

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala

1 5 10 15

Ser Val 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 Ser Leu Glu Trp Ile

35 40 45

Gly Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe

50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Asp Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr Trp Gly Ser Gly

100 105 110

Thr Pro Val Thr Val Ser Ser

115

<210> 26

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 Light chain (Table 2)

<400> 26

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

1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met

20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr

35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Gly Arg Phe Ser Gly Ser

50 55 60

Gly Ser Gly Asn Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Glu

65 70 75 80

Asp Asp Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Lys His Pro Leu Thr
85 90 95

Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
100 105

<210> 27

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab Heavy chain

<400> 27

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 28

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab Light chain

<400> 28

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 Asp Val Asn Thr Ala

20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Arg 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 His Tyr Thr Thr Pro Pro

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 29

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi Heavy chain

<400> 29

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

1 5 10 15

Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Ser Leu Ser Ser Asp Ala

20 25 30

Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile Gly

35 40 45

Ile Ile Asn Gly Gly Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly

50 55 60

Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu Lys Ile Thr

65 70 75 80

Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Gly Ile

85 90 95

Gln His Gly Gly Gly Asn Ser Asp Tyr Tyr Tyr Tyr Gly Met Asp Leu

100 105 110

Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 30

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi Light chain

<400> 30

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

1 5 10 15

Asp Thr Val Thr Ile Lys Cys Gln Ala Ser Gln Ser Ile Ser Ser Val

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile

35 40 45

Tyr Leu Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Arg Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Asp Leu Glu Cys

65 70 75 80

Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Thr Asn Tyr Gly Thr Ser Ser

85 90 95

Ser Asn Tyr Gly Phe Ala Phe Gly Gly Gly Thr Glu Val Val Val Lys

100 105 110

<210> 31

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu Heavy chain

<400> 31

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Ser Leu Ser Ser Asp

20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile

35 40 45

Gly Ile Ile Asn Gly Gly Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys

50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Ile Gln His Gly Gly Gly Asn Ser Asp Tyr Tyr Tyr Tyr Gly

100 105 110

Met Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120 125

<210> 32

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu Light chain

<400> 32

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 Gln Ser Ile Ser Ser Val

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Leu Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Cys

65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Thr Asn Tyr Gly Thr Ser Ser

85 90 95

Ser Asn Tyr Gly Phe Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 33

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi Heavy chain

<400> 33

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

1 5 10 15

Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Asn Asn Tyr Ala

20 25 30

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly

35 40 45

Ser Ile Ser Thr Gly Gly Leu Ala Phe Tyr Ala Asn Trp Ala Lys Gly

50 55 60

Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu Lys Met Thr

65 70 75 80

Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Gly Arg Asn Gly

85

90

95

Gly Gly Ser Tyr Ile Phe Tyr Tyr Phe Asp Leu Trp Gly Gln Gly Thr

100

105

110

Leu Val Thr Val Ser Ser

115

<210> 34

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi Light chain

<400> 34

Ala Phe Glu Leu Thr Gln Thr Pro Ser Ser Val Glu Ala Ala Val Gly

1

5

10

15

Gly Thr Ile Thr Ile Lys Cys Gln Ala Ser Gln Ser Ile Ser Ser Tyr

20

25

30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile

35 40 45

Tyr Ser Ala Ser Thr Leu Ala Ser Gly Val Ser Ser Arg Phe Lys Gly

50 55 60

Ser Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Asp Leu Glu Cys

65 70 75 80

Ala Asp Ala Ala Thr Tyr Phe Cys Gln Ser Tyr Tyr Asp Ile Gly Thr

85 90 95

Ser Thr Phe Gly Gly Gly Thr Glu Val Val Val Lys

100 105

<210> 35

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu Heavy chain

<400> 35

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Asn Asn Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Ser Ile Ser Thr Gly Gly Leu Ala Phe Tyr Ala Asn Trp Ala Lys

50 55 60

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

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asn Gly Gly Gly Ser Tyr Ile Phe Tyr Tyr Phe Asp Leu Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 36

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu Light chain

<400> 36

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 Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ser Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Cys

65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Ser Tyr Tyr Asp Ile Gly Thr

85 90 95

Ser Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100

105

<210> 37

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi Heavy chain

<400> 37

Gln Ser Val Lys Glu Ser Gly Gly Arg Leu Val Thr Pro Gly Thr Pro

1

5

10

15

Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Ser Tyr Ala

20

25

30

Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile Gly

35

40

45

Thr Ile Asn Ile Gly Gly Arg Val Tyr Tyr Ala Ser Trp Ala Lys Gly

50

55

60

Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu Lys Ala Pro

65 70 75 80

Ser Leu Thr Ala Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Tyr Tyr

85 90 95

Asn Gly Gly Ser Tyr Asp Ile Trp Gly Pro Gly Thr Leu Val Thr Val

100 105 110

Ser Leu

<210> 38

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi Light chain

<400> 38

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

1 5 10 15

Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Ser Ile Tyr Arg Val

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile

35 40 45

Tyr Asp Thr Ser Thr Leu Ala Ser Gly Ala Pro Ser Arg Phe Lys Gly

50 55 60

Ser Gly Tyr Gly Thr Glu Phe Thr Leu Thr Ile Ser Gly Val Gln Cys

65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gly Gly Tyr Tyr Ala Asp Ser

85 90 95

Tyr Gly Ile Ala Phe Gly Gly Gly Thr Glu Val Val Val Lys

100 105 110

<210> 39

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu Heavy chain

<400> 39

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Ile Asp Leu Ser Ser Tyr

20 25 30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile

35 40 45

Gly Thr Ile Asn Ile Gly Gly Arg Val Tyr Tyr Ala Ser Trp Ala Lys

50 55 60

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

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Tyr Tyr Asn Gly Gly Ser Tyr Asp Ile Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 40

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu Light chain

<400> 40

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

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Glu Ser Ile Tyr Arg Val

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Asp Thr Ser Thr Leu Ala 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 Cys

65 70 75 80

Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gly Gly Tyr Tyr Ala Asp Ser

85 90 95

Tyr Gly Ile Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 41

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi Heavy chain

<400> 41

Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Lys Pro Asp Glu Ser

1 5 10 15

Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser Ser Tyr Ala

20 25 30

Met Ile Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Ile Gly

35 40 45

Thr Ile Ser Thr Gly Gly Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly

50 55 60

Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu Lys Ile Thr

65 70 75 80

Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Gly Gly

85 90 95

Tyr Ala Ala Ser Ser Ala Tyr Tyr Leu Pro Tyr Tyr Phe Asp Leu Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 42

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi Light chain

<400> 42

Ala Ala Val Leu Thr Gln Thr Pro Ser Pro Val Ser Ala Ala Val Gly

1 5 10 15

Gly Thr Val Thr Ile Ser Cys Gln Ser Ser Gln Ser Val Tyr Asn Asn

20 25 30

Asn Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu

35 40 45

Leu Ile Tyr Leu Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe

50 55 60

Ser Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Gly Val

65 70 75 80

Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Gly Cys Asp Asp

85 90 95

Asp Ala Asp Thr Phe Ala Phe Gly Gly Gly Thr Glu Val Val Val Lys

100 105 110

<210> 43

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu Heavy chain

<400> 43

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Ser Tyr

20 25 30

Ala Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Thr Ile Ser Thr Gly Gly Ile Thr Tyr Tyr Ala Ser Trp Ala Lys

50 55 60

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

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Gly Tyr Ala Ala Ser Ser Ala Tyr Tyr Leu Pro Tyr Tyr Phe
100 105 110

Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 44

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu Light chain

<400> 44

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 Ser Ser Gln Ser Val Tyr Asn Asn
20 25 30

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

Leu Ile Tyr Leu Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe

50 55 60

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu

65 70 75 80

Gln Cys Glu Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Gly Cys Asp Asp

85 90 95

Asp Ala Asp Thr Phe Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 45

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 Heavy chain (Table 3)

<400> 45

gaggtccaac tgggtggagag cgggtggaggt gttgtgcaac ctggccggtc cctgcgcctg 60

tcctgctccg catctggctt caccttcagc ggctatgggt tgtcttgggt gagacaggca 120

cctggaaaag gtcttgagtg ggttgcaatg attagtagtg gtggtagtta tacctactat 180

gcagacagtg tgaaggtag atttgaata tcgcgagaca acgccaagaa cacattgttc 240

ctgcaaattg acagcctgag acccgaagac accgggtct attttgtgc aagacatggg 300

gacgatcccg cctggttcgc ttattggggc caagggaccc cggtcaccgt ctctca 357

<210> 46

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 Light chain (Table 3)

<400> 46

gacatccagc tgaccagag cccaagcagc ctgagcgcca gcgtgggtga cagagtgacc 60

atcacctgta gtgtcagctc aagtataagt tccaacaact tgactggta ccagcagaag 120

ccaggtaagg ctccaaagcc atggatctac ggcacatcca acctggcttc tgggtgcca 180

agcagattca gcggtagcgg tagcggtagc gactacacct tcaccatcag cagcctccag 240

ccagaggaca tcgccaccta ctactgcca cagtggagta gttaccgta catgtacacg 300

ttcggccaag ggaccaaggt ggaaatcaaa 330

<210> 47

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 Heavy chain (Table 3)

<400> 47

caggtagaac tgcagcagtc tgggcctgag ctggagaagc ctggcgcttc agtgaagata 60

tcctgcaagg cttctgttta ctattcact ggctacacca tgaactgggt gaagcagagc 120

catggaaaga gccttgagtg gattggactt attactcctt acaatggtgc ttctagctac 180

aaccagaagt tcaggggcaa ggccacatta actgtagaca agtcatccag cacagcctac 240

atggacctcc tcagtctgac atctgaagac tctgcagtct atttctgtgc aaggggggggt 300

tacgacggga ggggttttga ctactgggga tccgggaccc cggtcacctg ctctca 357

<210> 48

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 Light chain (Table 3)

<400> 48

gacatcgagc tcactcagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60

atgacctgca gtgccagctc aagtgttaagt tacatgcact ggtaccagca gaagtcaggc 120

acctccccc aaagatggat ttatgacaca tccaaactgg cttctggagt cccaggtcgc 180

ttcagtggca gtgggtctgg aaactcttac tcttcacaa tcagcagcgt ggaggctgaa 240

gatgatgcaa cttattactg ccagcagtgg agtaagcacc ctctcacgtt cggatccggg 300

accaaggtgg aatcaaa 318

<210> 49

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi Heavy chain (Table 3)

<400> 49

cagtcggtgg aggagtccgg gggtgcctg gtcacgcctg ggacaccct gacactcacc 60

tgcaccgtct ctggaatctc cctcagtagc gatgcaataa gctgggtccg ccaggctcca 120

gggaaggggc tcgaatacat cggaatcatt aatggtggtg gtaacacata ctacgcgagc 180

tgggcgaaag gccgattcac catctcaaa acctcgacca cgttggtatct gaaaatcacc 240

agtccgacaa ccgaggacac ggccacctat ttctgtgcca gaggcattca acatggtggt 300

ggtaatagt attattatta ttacggcatg gacctctggg gccagggcac cctggtcact 360

gtctcttca

369

<210> 50

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi Light chain (Table 3)

<400> 50

gaagtgttga tgaccagac tccatcctcc gtgtctgcag ctgtgggaga cacagtcacc 60

atcaagtgcc aggcagtc gagcattagt agtgtcttgt cctggatatca gcagaaacca 120

gggcagcctc ccaagctcct gatctatctg gcatccactc tggcatctgg ggtcccatcg 180

cggttcagcg gcagtagatc tgggacagag ttactctca ccatcagcga cctggagtgt 240

gacgatgctg ccactacta ctgtcaaacc aattatggta ctagtagtag taattatggt 300

tttgctttcg gcggaggagac cgaggtggtc gtcaaa 336

<210> 51

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu Heavy chain (Table 3)

<400> 51

gaagtccaac tggaggaaag cgggggagga ctggtgcagc cgggcggatc cctccggctg 60

tcatgtgctg catcggaat ttcctctcc tccgacgca ttagctgggt cagacaggcc 120

cccgaaagg ggctggagta catcggatc atcaacggcg gcggaaacac ctactacgcc 180

tcctgggcca agggccgctt caccatctcg cggcataatt ccaagaacac tctgtacttg 240

caaatgaact ccctgagggc caggacacc gccgtgtact actgcgcgcg cggcatccag 300

cacggtggtg gaaacagcga ctactactac tatgggatgg atctgtgggg ccagggaact 360

cttgtgaccg tgtcgtca 378

<210> 52

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu Light chain (Table 3)

<400> 52

gacattcaga tgaccagtc cccaagctcg ctgtccgcct ccgtgggcga ccgcgtgacc 60

atcacgtgcc aggcgtccca gtcaattagc agcgtgctct cctggtacca acagaagccg 120

gggaaagcac ccaagctgct gatctacttg gcctccactc tggcctcggg agtgccttca 180

cggttctccg gatcgggatc tggctactgat ttcaccctca ccatctcgag ccttcagtgc 240

gaggacatcg ctacttacta ttgtcaaacc aactacggaa cctccagctc caactacggc 300

tttccttcg gtggcgggac caaggtcgaa atcaaa 336

<210> 53

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi Heavy chain (Table 3)

<400> 53

cagtcggtgg aggagtccgg gggtcgctg gtcacgcctg ggacaccctc gacactcacc 60

tgacacgtct ctggattctc cctcaataac tatgcaatga gctgggtccg ccagggtcca 120

gggaaggggc tggaatggat cgatccatt agtactgggt gtctcgcatc ctacgcgaac 180

tgggcaaaag gccgattcac catctccaga acctcgacca cgggtgatct gaaaatgacc 240

agtctgacaa ccgaggacac ggccacctat ttctgtggca gaaatgggtg tggtagttat 300

atcttctatt atcttgactt gtggggccaa ggcaccctcg tcactgtctc ttca 354

<210> 54

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi Light chain (Table 3)

<400> 54

gcattcgaat tgaccagac tccatcctcc gtggaggcag ctgtgggagg cacaatcacc 60

atcaagtgcc aggccagtca gagcattagt agttacttat cctggtatca gcagaaacca 120

gggcagcctc ccaagctcct gatctattct gcatccactc tggcatctgg ggtctcatcg 180

cggttcaaag gcagtggatc tgggacagag tacactctca ccatcagcga cctggagtgt 240

gccgatgctg ccacttactt ctgtcaaagc tattatgata ttggtactag tactttcggc 300

ggagggaccg aggtggtcgt caaa 324

<210> 55

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu Heavy chain (Table 3)

<400> 55

gaagtgcagc tgggtggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg 60

tcttgtgccg cctccggctt ctccctgaac aactacgcca tgtcctgggt gcgacaggcc 120

cctggcaaag gcctggaatg gatcggctcc atcagcacag gcggcctggc cttctacgcc 180

aattgggccca agggccggtt caccatcagc cgggacaact ccaagaacac cctgtacctc 240

cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgccag aaacggcgga 300

ggctcctaca tcttctacta cttcgacctg tggggccagg gcaccctcgt gacagtgtca 360

tct 363

<210> 56

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu Light chain (Table 3)

<400> 56

gatattcaga tgaccagtc cccctccagc ctgtccgctt ctgtggcgca cagagtgacc 60

atcacctgtc aggcctcca gtccatctcc tctacctgt cctggatatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactct gcctccacac tggcctccgg cgtgccctct 180

agattctccg gctctggctc tggcaccgac ttaccctga ccatcagctc cctccagtgc 240

gaggatgccg ccacctacta ctgccagtcc tactacgaca tcggcacctc caccttcggc 300

ggaggcacca aggtggaaat caaa 324

<210> 57

<211> 342

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi Heavy chain (Table 3)

<400> 57

cagtcagtga aggagtccgg gggtcgcctg gtcacgcctg ggacaccctc gacactcacc 60

tgcacagtct ctggaatcga cctcagtagc tatgcaatgg gctggttccg ccaggctcca 120

gggaaggggc tggaatacat cggaaccatt aatattggtg gtcgcgtata ttacgcgagc 180

tgggcaaaag gccgattcac catctccaga acctcgacca cggatgatct gaaagcgccc 240

agtctgacag ccgaggacac ggccacctat ttctgtgcca gatattataa tgggtgtagt 300

tatgacatct ggggcccagg caccctggtc accgtctctt ta 342

<210> 58

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi Light chain (Table 3)

<400> 58

gatgttgga tgaccagac tccagcctcc gcgtctgaac ctgtgggagg cacagtcacc 60

atcaagtgcc aggccagtga gagcatttat cgcgtattgg cctggatatca gcagaaacca 120

gggcagcctc ccaagctcct gatctatgat acatccactc tggcatctgg ggcccatcg 180

cggttcaaag gcagtggata tgggacagag ttcactctca ccatcagcgg cgtgcagtgt 240

gaagatgctg ccacttacta ctgtcaaggc ggttattatg ctgatagtta tggatttgct 300

ttcggcggag ggaccgaggt ggtgggtcaaa 330

<210> 59

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu Heavy chain (Table 3)

<400> 59

caggtgcagc tgggtggaatc tggcggagga ctggtgcagc ctggcggctc tctgagactg 60

tcctgttccg cctccggaat cgacctgtcc tcctacgcta tgggctgggt gcgacaggct 120

cctggcaagg gcctggagta catcggcacc atcaacatcg gcggcagagt gtactacgcc 180

tcctgggcca agggccggtt caccatctcc agagacaact ccaagaacac cctgtacctc 240

cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgcgcccg gtactacaac 300

ggcggctcct acgatatctg gggccagggc acactcgtga ccgtgtcctc t 351

<210> 60

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu Light chain (Table 3)

<400> 60

gatatccaga tgaccagtc cccctccacc ctgtctgcct ctgtgggcga cagagtgacc 60

atcacctgtc aggctccga gtccatctac cgggtgctgg cctggatatca gcagaagcct 120

ggcaaggccc ccaagctgct gatctacgac accagcacac tggcctccgg cgtgccctct 180

agatttccg gctctggctc tggcaccgag ttaccctga ccatctccag cctccagtgc 240

gacgacgccg ccacctacta ttgtcagggc ggctactacg ccgactccta cggaatcgct 300

ttcggcggag gcaccaaggt ggaaatcaaa 330

<210> 61

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi Heavy chain (Table 3)

<400> 61

cagtcggtgg aggagtccgg cggtcgcctg gtaaagcctg acgaatccct gacactcacc 60

tgacacgcct ctgattctc cctcagtagt tatgcaatga tctgggtccg ccaggctcca 120

ggggaggggc tggaatggat cggaaccatt agtactggtg gtatcacata ctacgcgagc 180

tgggcgaaag gccgattcac catctccaaa acctcgacca cgggtgatct gaaaatcacc 240

agtccgacaa ccgaggacac ggccacctat ttctgtgcca gagggggata tgctgctagt 300

agtgttatt atctccgta ctactttgac ttgtggggcc aaggggacct ggtcacgcgc 360

tcctca

366

<210> 62

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi Light chain (Table 3)

<400> 62

gcagccgtgc tgaccagac accatcacc gtgtctgcag ctgtgggagg cacagtcacc 60

atcagttgcc agtccagtca gagtgtttat aataataaca acttagcctg gtttcagcag 120

aaaccgggc agcctccaa gcttctgac tatctggcat ccactctggc atctggggtc 180

ccatcacggt tcagcggcag tggatctggg acacagttca ctctacccat cagcggcgtg 240

cagtgtagc atgctgccac ttattactgt ctaggtggtt gtgatgatga tgctgatact 300

tttgctttcg gcggaggac tgaggtggtg gtcaaa 336

<210> 63

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu Heavy chain (Table 3)

<400> 63

gaagtgcagc tgggtggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg 60

tcttgtagc cctccggctt ctccctgtcc tctacgcta tgatctgggt gcgacaggcc 120

cctggcaagg gcctggaatg gatcggcacc atctctaccg gcggaattac ctactacgcc 180

tcctgggccca agggccggtt caccatctcc agagacaact ccaagaacac cctgtacctc 240

cagatgaact ccctgcgggc cgaggacacc gccgtgtact attgtgctag aggcggctac 300

gccgccagct ccgcttacta cctgccctac tacttcgacc tgtggggcca gggcacctc 360

gtgacagtgt catct 375

<210> 64

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu Light chain (Table 3)

<400> 64

gatattcaga tgaccagtc cccctccagc ctgtccgctt ctgtgggcga cagagtgacc 60

atcacctgtc agtcctcca gtccgtgtat aacaacaaca acctggcctg gtatcagcag 120

aaaccggca aggtgccaa gctgctgac tacctggcct ccacactggc ctctggcgtg 180

ccctctagat tctccggctc tggctctggc accgacttta ccctgacat cagctccctc 240

cagtgcgagg atgccgccac ctactattgc ctgggcggct gcgacgacga cgccgatacc 300

tttgcttttg gcggaggcac caagtgga atcaaa 336

<210> 65

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR1 (Table 4)

<400> 65

Gly Tyr Thr Met Asn

1 5

<210> 66

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR2 (Table 4)

<400> 66

Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe Arg

1 5 10 15

Gly

<210> 67

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR3 (Table 4)

<400> 67

Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr

1 5 10

<210> 68

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR1 (Table 4)

<400> 68

Ser Ala Ser Ser Ser Val Ser Tyr Met His

1 5 10

<210> 69

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR2 (Table 4)

<400> 69

Asp Thr Ser Lys Leu Ala Ser

1 5

<210> 70

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR3 (Table 4)

<400> 70

Gln Gln Trp Ser Lys His Pro Leu Thr

1 5

<210> 71

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab HC CDR1 (Table 4)

<400> 71

Asp Thr Tyr Ile His

1 5

<210> 72

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab HC CDR2 (Table 4)

<400> 72

Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 73

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab HC CDR3 (Table 4)

<400> 73

Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr

1 5 10

<210> 74

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab LC CDR1 (Table 4)

<400> 74

Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala

1 5 10

<210> 75

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab LC CDR2 (Table 4)

<400> 75

Ser Ala Ser Phe Leu Tyr Ser

1 5

<210> 76

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab LC CDR3 (Table 4)

<400> 76

Gln Gln His Tyr Thr Thr Pro Pro Thr

1 5

<210> 77

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR1 (Table 4)

<400> 77

Ser Asp Ala Ile Ser

1 5

<210> 78

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR2 (Table 4)

<400> 78

Ile Ile Asn Gly Gly Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly

1 5 10 15

<210> 79

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR3 (Table 4)

<400> 79

Gly Ile Gln His Gly Gly Gly Asn Ser Asp Tyr Tyr Tyr Tyr Gly Met

1 5 10 15

Asp Leu

<210> 80

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR1 (Table 4)

<400> 80

Gln Ala Ser Gln Ser Ile Ser Ser Val Leu Ser

1 5 10

<210> 81

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR2 (Table 4)

<400> 81

Leu Ala Ser Thr Leu Ala Ser

1 5

<210> 82

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR3 (Table 4)

<400> 82

Gln Thr Asn Tyr Gly Thr Ser Ser Ser Asn Tyr Gly Phe Ala

1 5 10

<210> 83

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR1 (Table 4)

<400> 83

Ser Asp Ala Ile Ser

1 5

<210> 84

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR2 (Table 4)

<400> 84

Ile Ile Asn Gly Gly Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly

1 5 10 15

<210> 85

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR3 (Table 4)

<400> 85

Gly Ile Gln His Gly Gly Gly Asn Ser Asp Tyr Tyr Tyr Tyr Gly Met

1 5 10 15

Asp Leu

<210> 86

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR1 (Table 4)

<400> 86

Gln Ala Ser Gln Ser Ile Ser Ser Val Leu Ser

1 5 10

<210> 87

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR2 (Table 4)

<400> 87

Leu Ala Ser Thr Leu Ala Ser

1 5

<210> 88

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR3 (Table 4)

<400> 88

Gln Thr Asn Tyr Gly Thr Ser Ser Ser Asn Tyr Gly Phe Ala

1 5 10

<210> 89

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR1 (Table 4)

<400> 89

Asn Tyr Ala Met Ser

1 5

<210> 90

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR2 (Table 4)

<400> 90

Ser Ile Ser Thr Gly Gly Leu Ala Phe Tyr Ala Asn Trp Ala Lys Gly

1 5 10 15

<210> 91

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR3 (Table 4)

<400> 91

Asn Gly Gly Gly Ser Tyr Ile Phe Tyr Tyr Phe Asp Leu

1 5 10

<210> 92

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR1 (Table 4)

<400> 92

Gln Ala Ser Gln Ser Ile Ser Ser Tyr Leu Ser

1 5 10

<210> 93

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR2 (Table 4)

<400> 93

Ser Ala Ser Thr Leu Ala Ser

1 5

<210> 94

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR3 (Table 4)

<400> 94

Gln Ser Tyr Tyr Asp Ile Gly Thr Ser Thr

1 5 10

<210> 95

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR1 (Table 4)

<400> 95

Asn Tyr Ala Met Ser

1 5

<210> 96

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR2 (Table 4)

<400> 96

Ser Ile Ser Thr Gly Gly Leu Ala Phe Tyr Ala Asn Trp Ala Lys Gly

1 5 10 15

<210> 97

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR3 (Table 4)

<400> 97

Asn Gly Gly Gly Ser Tyr Ile Phe Tyr Tyr Phe Asp Leu

1 5 10

<210> 98

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR1 (Table 4)

<400> 98

Gln Ala Ser Gln Ser Ile Ser Ser Tyr Leu Ser

1 5 10

<210> 99

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR2 (Table 4)

<400> 99

Ser Ala Ser Thr Leu Ala Ser

1 5

<210> 100

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR3 (Table 4)

<400> 100

Gln Ser Tyr Tyr Asp Ile Gly Thr Ser Thr

1 5 10

<210> 101

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR1 (Table 4)

<400> 101

Ser Tyr Ala Met Gly

1 5

<210> 102

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR2 (Table 4)

<400> 102

Thr Ile Asn Ile Gly Gly Arg Val Tyr Tyr Ala Ser Trp Ala Lys Gly

1 5 10 15

<210> 103

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR3 (Table 4)

<400> 103

Tyr Tyr Asn Gly Gly Ser Tyr Asp Ile

1 5

<210> 104

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR1 (Table 4)

<400> 104

Gln Ala Ser Glu Ser Ile Tyr Arg Val Leu Ala

1 5 10

<210> 105

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR2 (Table 4)

<400> 105

Asp Thr Ser Thr Leu Ala Ser

1 5

<210> 106

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR3 (Table 4)

<400> 106

Gln Gly Gly Tyr Tyr Ala Asp Ser Tyr Gly Ile Ala

1 5 10

<210> 107

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR1 (Table 4)

<400> 107

Ser Tyr Ala Met Gly

1 5

<210> 108

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR2 (Table 4)

<400> 108

Thr Ile Asn Ile Gly Gly Arg Val Tyr Tyr Ala Ser Trp Ala Lys Gly

1 5 10 15

<210> 109

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR3 (Table 4)

<400> 109

Tyr Tyr Asn Gly Gly Ser Tyr Asp Ile

1 5

<210> 110

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR1 (Table 4)

<400> 110

Gln Ala Ser Glu Ser Ile Tyr Arg Val Leu Ala

1 5 10

<210> 111

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR2 (Table 4)

<400> 111

Asp Thr Ser Thr Leu Ala Ser

1 5

<210> 112

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR3 (Table 4)

<400> 112

Gln Gly Gly Tyr Tyr Ala Asp Ser Tyr Gly Ile Ala

1 5 10

<210> 113

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR1 (Table 4)

<400> 113

Ser Tyr Ala Met Ile

1 5

<210> 114

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR2 (Table 4)

<400> 114

Thr Ile Ser Thr Gly Gly Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly

1 5 10 15

<210> 115

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR3 (Table 4)

<400> 115

Gly Gly Tyr Ala Ala Ser Ser Ala Tyr Tyr Leu Pro Tyr Tyr Phe Asp

1 5 10 15

Leu

<210> 116

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR1 (Table 4)

<400> 116

Gln Ser Ser Gln Ser Val Tyr Asn Asn Asn Asn Leu Ala

1 5 10

<210> 117

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR2 (Table 4)

<400> 117

Leu Ala Ser Thr Leu Ala Ser

1 5

<210> 118

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR3 (Table 4)

<400> 118

Leu Gly Gly Cys Asp Asp Asp Ala Asp Thr Phe Ala

1 5 10

<210> 119

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR1 (Table 4)

<400> 119

Ser Tyr Ala Met Ile

1 5

<210> 120

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR2 (Table 4)

<400> 120

Thr Ile Ser Thr Gly Gly Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly

1 5 10 15

<210> 121

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR3 (Table 4)

<400> 121

Gly Gly Tyr Ala Ala Ser Ser Ala Tyr Tyr Leu Pro Tyr Tyr Phe Asp

1 5 10 15

Leu

<210> 122

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR1 (Table 4)

<400> 122

Gln Ser Ser Gln Ser Val Tyr Asn Asn Asn Asn Leu Ala

1 5 10

<210> 123

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR2 (Table 4)

<400> 123

Leu Ala Ser Thr Leu Ala Ser

1 5

<210> 124

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR3 (Table 4)

<400> 124

Leu Gly Gly Cys Asp Asp Asp Ala Asp Thr Phe Ala

1 5 10

<210> 125

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR1 (Table 5)

<400> 125

ggctatgggt tgtct 15

<210> 126

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR2 (Table 5)

<400> 126

atgattagta gtggtgtag ttatacctac tatgcagaca gtgtgaaggg t 51

<210> 127

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR3 (Table 5)

<400> 127

catggggacg atcccgctg gttcgcttat 30

<210> 128

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR1 (Table 5)

<400> 128

agtgtagct caagtataag ttccaacaac ttgcac 36

<210> 129

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR2 (Table 5)

<400> 129

ggcacatcca acctggcttc t 21

<210> 130

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR3 (Table 5)

<400> 130

caacagtgga gtagttaccc gtacatgtac acg 33

<210> 131

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR1 (Table 5)

<400> 131

ggctacacca tgaac 15

<210> 132

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR2 (Table 5)

<400> 132

cttattactc cttacaatgg tgcttctagc tacaaccaga agttcagggg c 51

<210> 133

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR3 (Table 5)

<400> 133

gggggttacg acgggagggg ttttgactac 30

<210> 134

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR1 (Table 5)

<400> 134

agtgccagct caagtgaag ttacatgcac 30

<210> 135

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR2 (Table 5)

<400> 135

gacacatcca aactggcttc t

21

<210> 136

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR3 (Table 5)

<400> 136

cagcagtgga gtaagcaccc tctcacg

27

<210> 137

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR1 (Table 5)

<400> 137

agcgatgcaa taagc

15

<210> 138

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR2 (Table 5)

<400> 138

atcattaatg gtggtggtaa cacatactac gcgagctggg cgaaaggc 48

<210> 139

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR3 (Table 5)

<400> 139

ggcattcaac atggtggtgg taatagtgat tattattatt acggcatgga cctc 54

<210> 140

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR1 (Table 5)

<400> 140

caggccagtc agagcattag tagtgtcttg tcc 33

<210> 141

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR2 (Table 5)

<400> 141

ctggcatcca ctctggcatc t 21

<210> 142

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR3 (Table 5)

<400> 142

caaaccaatt atggtactag tagtagtaat tatggttttg ct 42

<210> 143

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR1 (Table 5)

<400> 143

tccgacgcga ttagc 15

<210> 144

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR2 (Table 5)

<400> 144

atcatcaacg gcggcggaaa cacctactac gcctcctggg ccaagggc 48

<210> 145

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR3 (Table 5)

<400> 145

ggcatccagc acggtggtgg aaacagcgac tactactact atgggatgga tctg 54

<210> 146

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR1 (Table 5)

<400> 146

caggcgtccc agtcaattag cagcgtgctc tcc 33

<210> 147

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR2 (Table 5)

<400> 147

ttggcctcca ctctggcctc g 21

<210> 148

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR3 (Table 5)

<400> 148

caaaccaact acggaacctc cagctccaac tacggctttg cc 42

<210> 149

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR1 (Table 5)

<400> 149

aactatgcaa tgagc 15

<210> 150

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR2 (Table 5)

<400> 150

tccattagta ctggtggtct cgcattctac gcgaactggg caaaaggc 48

<210> 151

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR3 (Table 5)

<400> 151

aatggtggtg gtagttatat tttctattat tttgacttg 39

<210> 152

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR1 (Table 5)

<400> 152

caggccagtc agagcattag tagttactta tcc 33

<210> 153

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR2 (Table 5)

<400> 153

tctgcatcca ctctggcatc t

21

<210> 154

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR3 (Table 5)

<400> 154

caaagctatt atgatattgg tactagtact

30

<210> 155

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR1 (Table 5)

<400> 155

aactacgccca tgtcc

15

<210> 156

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR2 (Table 5)

<400> 156

tccatcagca caggcggcct ggccttctac gccaatggg ccaagggc 48

<210> 157

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR3 (Table 5)

<400> 157

aacggcggag gctcctacat cttctactac ttcgacctg 39

<210> 158

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR1 (Table 5)

<400> 158

caggcctccc agtccatctc ctctacctg tcc 33

<210> 159

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR2 (Table 5)

<400> 159

tctgcctcca cactggcctc c 21

<210> 160

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR3 (Table 5)

<400> 160

cagtcctact acgacatcgg cacctccacc 30

<210> 161

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR1 (Table 5)

<400> 161

agctatgcaa tgggc 15

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR2 (Table 5)

<400> 162

accattaata ttggtggtcg cgtatattac gcgagctggg caaaaggc 48

<210> 163

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR3 (Table 5)

<400> 163

tattataatg gtggtagtta tgacatc 27

<210> 164

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR1 (Table 5)

<400> 164

caggccagtg agagcattta tcgcgtattg gcc 33

<210> 165

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR2 (Table 5)

<400> 165

gatacatcca ctctggcatc t 21

<210> 166

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR3 (Table 5)

<400> 166

caaggcggtt attatgctga tagttatggt attgct

36

<210> 167

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR1 (Table 5)

<400> 167

tcctacgcta tgggc

15

<210> 168

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR2 (Table 5)

<400> 168

accatcaaca tcggcggcag agtgtactac gcctcctggg ccaagggc

48

<210> 169

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR3 (Table 5)

<400> 169

tactacaacg gcggctccta cgatatc

27

<210> 170

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR1 (Table 5)

<400> 170

caggcctccg agtccatcta ccgggtgctg gcc

33

<210> 171

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR2 (Table 5)

<400> 171

gacaccagca cactggcctc c 21

<210> 172

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR3 (Table 5)

<400> 172

cagggcggct actacgccga ctctacgga atcgct 36

<210> 173

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR1 (Table 5)

<400> 173

agttatgcaa tgatc 15

<210> 174

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR2 (Table 5)

<400> 174

accattagta ctggtggtat cacatactac gcgagctggg cgaaaggc 48

<210> 175

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR3 (Table 5)

<400> 175

gggggatatg ctgctagtag tgcttattat ctccgtact acttgactt g 51

<210> 176

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR1 (Table 5)

<400> 176

cagtcctccc agtccgtgta taacaacaac aacctggcc 39

<210> 177

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR2 (Table 5)

<400> 177

ctggcatcca ctctggcatc t 21

<210> 178

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR3 (Table 5)

<400> 178

ctaggtggtt gtgatgatga tgctgatact tttgct 36

<210> 179

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR1 (Table 5)

<400> 179

tcctacgcta tgatc 15

<210> 180

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR2 (Table 5)

<400> 180

accatctcta ccggcggaat tacctactac gcctcctggg ccaagggc 48

<210> 181

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR3 (Table 5)

<400> 181

ggcggctacg ccgccagctc cgcttactac ctgccctact acttcgacct g 51

<210> 182

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR1 (Table 5)

<400> 182

cagtcctccc agtcggtgta taacaacaac aacctggcc 39

<210> 183

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR2 (Table 5)

<400> 183

ctggcctcca cactggcctc t 21

<210> 184

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR3 (Table 5)

<400> 184

ctgggcggct gcgacgacga cgccgatacc ttgct

36

<210> 185

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR1 (Table 6)

<400> 185

Gly Tyr Ser Phe Thr Gly Tyr Thr

1 5

<210> 186

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR2 (Table 6)

<400> 186

Ile Thr Pro Tyr Asn Gly Ala Ser

1 5

<210> 187

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR3 (Table 6)

<400> 187

Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr

1 5 10

<210> 188

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR1 (Table 6)

<400> 188

Ser Ser Val Ser Tyr

1 5

<210> 189

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR2 (Table 6)

<400> 189

Asp Thr Ser

1

<210> 190

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR3 (Table 6)

<400> 190

Gln Gln Trp Ser Lys His Pro Leu Thr

1 5

<210> 191

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab HC CDR1 (Table 6)

<400> 191

Gly Phe Asn Ile Lys Asp Thr Tyr

1 5

<210> 192

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab HC CDR2 (Table 6)

<400> 192

Ile Tyr Pro Thr Asn Gly Tyr Thr

1 5

<210> 193

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab HC CDR3 (Table 6)

<400> 193

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr

1 5 10

<210> 194

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab LC CDR1 (Table 6)

<400> 194

Gln Asp Val Asn Thr Ala

1 5

<210> 195

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab LC CDR2 (Table 6)

<400> 195

Ser Ala Ser

1

<210> 196

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab LC CDR3 (Table 6)

<400> 196

Gln Gln His Tyr Thr Thr Pro Pro Thr

1 5

<210> 197

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR1 (Table 6)

<400> 197

Gly Ile Ser Leu Ser Ser Asp Ala

1 5

<210> 198

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR2 (Table 6)

<400> 198

Ile Asn Gly Gly Gly Asn Thr

1 5

<210> 199

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR3 (Table 6)

<400> 199

Ala Arg Gly Ile Gln His Gly Gly Gly Asn Ser Asp Tyr Tyr Tyr Tyr

1 5 10 15

Gly Met Asp Leu

20

<210> 200

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR1 (Table 6)

<400> 200

Gln Ser Ile Ser Ser Val

1 5

<210> 201

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR2 (Table 6)

<400> 201

Leu Ala Ser

1

<210> 202

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR3 (Table 6)

<400> 202

Gln Thr Asn Tyr Gly Thr Ser Ser Ser Asn Tyr Gly Phe Ala

1 5 10

<210> 203

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR1 (Table 6)

<400> 203

Gly Ile Ser Leu Ser Ser Asp Ala

1 5

<210> 204

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR2 (Table 6)

<400> 204

Ile Asn Gly Gly Gly Asn Thr

1 5

<210> 205

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR3 (Table 6)

<400> 205

Ala Arg Gly Ile Gln His Gly Gly Gly Asn Ser Asp Tyr Tyr Tyr Tyr

1 5 10 15

Gly Met Asp Leu

20

<210> 206

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR1 (Table 6)

<400> 206

Gln Ser Ile Ser Ser Val

1 5

<210> 207

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR2 (Table 6)

<400> 207

Leu Ala Ser

1

<210> 208

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR3 (Table 6)

<400> 208

Gln Thr Asn Tyr Gly Thr Ser Ser Ser Asn Tyr Gly Phe Ala

1 5 10

<210> 209

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR1 (Table 6)

<400> 209

Gly Phe Ser Leu Asn Asn Tyr Ala

1 5

<210> 210

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR2 (Table 6)

<400> 210

Ile Ser Thr Gly Gly Leu Ala

1 5

<210> 211

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR3 (Table 6)

<400> 211

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

1 5 10 15

<210> 212

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR1 (Table 6)

<400> 212

Gln Ser Ile Ser Ser Tyr

1 5

<210> 213

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR2 (Table 6)

<400> 213

Ser Ala Ser

1

<210> 214

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR3 (Table 6)

<400> 214

Gln Ser Tyr Tyr Asp Ile Gly Thr Ser Thr

1

5

10

<210> 215

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR1 (Table 6)

<400> 215

Gly Phe Ser Leu Asn Asn Tyr Ala

1 5

<210> 216

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR2 (Table 6)

<400> 216

Ile Ser Thr Gly Gly Leu Ala

1 5

<210> 217

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR3 (Table 6)

<400> 217

Ala Arg Asn Gly Gly Gly Ser Tyr Ile Phe Tyr Tyr Phe Asp Leu

1 5 10 15

<210> 218

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR1 (Table 6)

<400> 218

Gln Ser Ile Ser Ser Tyr

1 5

<210> 219

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR2 (Table 6)

<400> 219

Ser Ala Ser

1

<210> 220

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR3 (Table 6)

<400> 220

Gln Ser Tyr Tyr Asp Ile Gly Thr Ser Thr

1 5 10

<210> 221

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR1 (Table 6)

<400> 221

Gly Ile Asp Leu Ser Ser Tyr Ala

1 5

<210> 222

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR2 (Table 6)

<400> 222

Ile Asn Ile Gly Gly Arg Val

1 5

<210> 223

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR3 (Table 6)

<400> 223

Ala Arg Tyr Tyr Asn Gly Gly Ser Tyr Asp Ile

1 5 10

<210> 224

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR1 (Table 6)

<400> 224

Glu Ser Ile Tyr Arg Val

1 5

<210> 225

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR2 (Table 6)

<400> 225

Asp Thr Ser

1

<210> 226

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR3 (Table 6)

<400> 226

Gln Gly Gly Tyr Tyr Ala Asp Ser Tyr Gly Ile Ala

1 5 10

<210> 227

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR1 (Table 6)

<400> 227

Gly Ile Asp Leu Ser Ser Tyr Ala

1 5

<210> 228

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR2 (Table 6)

<400> 228

Ile Asn Ile Gly Gly Arg Val

1 5

<210> 229

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR3 (Table 6)

<400> 229

Ala Arg Tyr Tyr Asn Gly Gly Ser Tyr Asp Ile

1 5 10

<210> 230

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR1 (Table 6)

<400> 230

Glu Ser Ile Tyr Arg Val

1 5

<210> 231

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR2 (Table 6)

<400> 231

Asp Thr Ser

1

<210> 232

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR3 (Table 6)

<400> 232

Gln Gly Gly Tyr Tyr Ala Asp Ser Tyr Gly Ile Ala

1 5 10

<210> 233

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR1 (Table 6)

<400> 233

Gly Phe Ser Leu Ser Ser Tyr Ala

1 5

<210> 234

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR2 (Table 6)

<400> 234

Ile Ser Thr Gly Gly Ile Thr

1 5

<210> 235

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR3 (Table 6)

<400> 235

Ala Arg Gly Gly Tyr Ala Ala Ser Ser Ala Tyr Tyr Leu Pro Tyr Tyr

1 5 10 15

Phe Asp Leu

<210> 236

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR1 (Table 6)

<400> 236

Gln Ser Val Tyr Asn Asn Asn Asn

1 5

<210> 237

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR2 (Table 6)

<400> 237

Leu Ala Ser

1

<210> 238

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR3 (Table 6)

<400> 238

Leu Gly Gly Cys Asp Asp Asp Ala Asp Thr Phe Ala

1

5

10

<210> 239

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR1 (Table 6)

<400> 239

Gly Phe Ser Leu Ser Ser Tyr Ala

1 5

<210> 240

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR2 (Table 6)

<400> 240

Ile Ser Thr Gly Gly Ile Thr

1 5

<210> 241

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR3 (Table 6)

<400> 241

Ala Arg Gly Gly Tyr Ala Ala Ser Ser Ala Tyr Tyr Leu Pro Tyr Tyr

1 5 10 15

Phe Asp Leu

<210> 242

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR1 (Table 6)

<400> 242

Gln Ser Val Tyr Asn Asn Asn Asn

1 5

<210> 243

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR2 (Table 6)

<400> 243

Leu Ala Ser

1

<210> 244

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR3 (Table 6)

<400> 244

Leu Gly Gly Cys Asp Asp Asp Ala Asp Thr Phe Ala

1

5

10

<210> 245

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR1 (Table 7)

<400> 245

ggcttcacct tcagcggcta tggg

24

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR2 (Table 7)

<400> 246

attagtagtg gtgtagtta tacc

24

<210> 247

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 HC CDR3 (Table 7)

<400> 247

gcaagacatg gggacgatcc cgcctgggtc gcttat

36

<210> 248

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR1 (Table 7)

<400> 248

tcaagtataa gttccaacaa c 21

<210> 249

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR2 (Table 7)

<400> 249

ggcacatcc 9

<210> 250

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 LC CDR3 (Table 7)

<400> 250

caacagtgga gtagttaccc gtacatgtac acg 33

<210> 251

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR1 (Table 7)

<400> 251

ggttactcat tcactggcta cacc 24

<210> 252

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR2 (Table 7)

<400> 252

attactcctt acaatgggtgc ttct 24

<210> 253

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 HC CDR3 (Table 7)

<400> 253

gcaagggggg gttacgacgg gaggggtttt gactac

36

<210> 254

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR1 (Table 7)

<400> 254

tcaagtgtaa gttac

15

<210> 255

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR2 (Table 7)

<400> 255

gacacatcc

9

<210> 256

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 LC CDR3 (Table 7)

<400> 256

cagcagtgga gtaagcaccc ttcacg 27

<210> 257

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR1 (Table 7)

<400> 257

ggaatctccc tcagtagcga tgca 24

<210> 258

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR2 (Table 7)

<400> 258

attaatgggtg gtggtaacac a 21

<210> 259

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi HC CDR3 (Table 7)

<400> 259

gccagaggca ttcaacatgg tgggtgtaat agtgattatt attattacgg catggacctc 60

<210> 260

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR1 (Table 7)

<400> 260

cagagcatta gtagtgtc 18

<210> 261

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR2 (Table 7)

<400> 261

ctggcatct

9

<210> 262

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi LC CDR3 (Table 7)

<400> 262

caaaccaatt atggtactag tagtagtaat tatggttttg ct

42

<210> 263

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR1 (Table 7)

<400> 263

ggaatttccc tctctccga cgcg

24

<210> 264

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR2 (Table 7)

<400> 264

atcaacggcg gcggaaacac c

21

<210> 265

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu HC CDR3 (Table 7)

<400> 265

gcgcgcggca tccagcacgg tggaggaaac agcgactact actactatgg gatggatctg 60

<210> 266

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR1 (Table 7)

<400> 266

cagtcaatta gcagcgtg 18

<210> 267

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR2 (Table 7)

<400> 267

ttggcctcc 9

<210> 268

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu LC CDR3 (Table 7)

<400> 268

caaaccaact acggaacctc cagctccaac tacggctttg cc 42

<210> 269

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR1 (Table 7)

<400> 269

ggattctccc tcaataacta tgca 24

<210> 270

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR2 (Table 7)

<400> 270

attagtactg gtggtctcgc a 21

<210> 271

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi HC CDR3 (Table 7)

<400> 271

ggcagaaatg gtggtgtag ttatatttc tattatttg acttg 45

<210> 272

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR1 (Table 7)

<400> 272

cagagcatta gtagttac 18

<210> 273

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR2 (Table 7)

<400> 273

tctgcatcc 9

<210> 274

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi LC CDR3 (Table 7)

<400> 274

caaagctatt atgatattgg tactagtact 30

<210> 275

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR1 (Table 7)

<400> 275

ggcttctccc tgaacaacta cgcc 24

<210> 276

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR2 (Table 7)

<400> 276

atcagcacag gcggcctggc c

21

<210> 277

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu HC CDR3 (Table 7)

<400> 277

gccagaaacg gcggaggctc ctacatcttc tactacttcg acctg

45

<210> 278

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR1 (Table 7)

<400> 278

cagtccatct cctcctac

18

<210> 279

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR2 (Table 7)

<400> 279

tctgcctcc 9

<210> 280

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu LC CDR3 (Table 7)

<400> 280

cagtcctact acgacatcgg cacctccacc 30

<210> 281

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR1 (Table 7)

<400> 281

ggaatcgacc tcagtagcta tgca 24

<210> 282

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR2 (Table 7)

<400> 282

attaatattg gtggtcgcgt a 21

<210> 283

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi HC CDR3 (Table 7)

<400> 283

gccagatatt ataatggtgg tagttatgac atc 33

<210> 284

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR1 (Table 7)

<400> 284

gagagcattt atcgcgta 18

<210> 285

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR2 (Table 7)

<400> 285

gatacatcc 9

<210> 286

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi LC CDR3 (Table 7)

<400> 286

caaggcgggtt attatgctga tagttatggt attgct 36

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR1 (Table 7)

<400> 287

ggaatcgacc tgcctccta cgct 24

<210> 288

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR2 (Table 7)

<400> 288

atcaacatcg gcggcagagt g 21

<210> 289

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu HC CDR3 (Table 7)

<400> 289

gcccgggtact acaacggcgg ctctacgat atc

33

<210> 290

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR1 (Table 7)

<400> 290

gagtccatct accgggtg

18

<210> 291

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR2 (Table 7)

<400> 291

gacaccagc

9

<210> 292

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu LC CDR3 (Table 7)

<400> 292

cagggcggct actacgccga ctctacgga atcgct 36

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR1 (Table 7)

<400> 293

ggattctccc tcagtagtta tgca 24

<210> 294

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR2 (Table 7)

<400> 294

attagtactg gtggtatcac a 21

<210> 295

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi HC CDR3 (Table 7)

<400> 295

gccagagggg gatatgctgc tagtagtgct tattatctcc cgtactactt tgacttg 57

<210> 296

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR1 (Table 7)

<400> 296

cagagtgttt ataataataa caac 24

<210> 297

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR2 (Table 7)

<400> 297

ctggcatcc 9

<210> 298

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi LC CDR3 (Table 7)

<400> 298

ctaggtgggtt gtgatgatga tgctgatact tttgct 36

<210> 299

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR1 (Table 7)

<400> 299

ggcttctccc tgcctccta cgct 24

<210> 300

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR2 (Table 7)

<400> 300

atctctaccg gcggaattac c 21

<210> 301

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu HC CDR3 (Table 7)

<400> 301

gctagaggcg gctacgccgc cagctccgct tactacctgc cctactactt cgacctg 57

<210> 302

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR1 (Table 7)

<400> 302

cagtccgtgt ataacaacaa caac

24

<210> 303

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR2 (Table 7)

<400> 303

ctggcctcc

9

<210> 304

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu LC CDR3 (Table 7)

<400> 304

ctgggcggct gcgacgacga cgccgatacc ttgct

36

<210> 305

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 Heavy chain (Table 8)

<400> 305

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala

1 5 10 15

Ser Val 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 Ser Leu Glu Trp Ile

35 40 45

Gly Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe

50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Asp Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr Trp Gly Ser Gly

100 105 110

Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe

115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu

130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp

145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu

165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser

180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro

195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys

210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro

225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser

245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp

260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn

275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val

290 295 300

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

305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys

325 330 335

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

340

345

350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr

355

360

365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu

370

375

380

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

385

390

395

400

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

405

410

415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu

420

425

430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

435

440

445

Lys

<210> 306

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> MORAb-009 Light chain (Table 8)

<400> 306

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

1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met

20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr

35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Gly Arg Phe Ser Gly Ser

50 55 60

Gly Ser Gly Asn Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Glu

65 70 75 80

Asp Asp Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Lys His Pro Leu Thr

85 90 95

Phe Gly Ser Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro

100 105 110

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

115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys

130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu

145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser

165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala

180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe

195 200 205

Asn Arg Gly Glu Cys

210

<210> 307

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab Heavy chain (Table 8)

<400> 307

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr

20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val

115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala

130 135 140

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

145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val

165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro

180 185 190

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

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

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

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

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

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

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

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

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

370 375 380

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

385 390 395 400

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

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly Lys

450

<210> 308

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> trastuzumab Light chain (Table 8)

<400> 308

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 Asp Val Asn Thr Ala

20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Arg 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 His Tyr Thr Thr Pro Pro

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

100 105 110

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

115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala

130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln

145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser

165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr

180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser

195 200 205

Phe Asn Arg Gly Glu Cys

210

<210> 309

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi Heavy chain (Table 8)

<400> 309

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

1 5 10 15

Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Ser Leu Ser Ser Asp Ala

20 25 30

Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile Gly

35 40 45

Ile Ile Asn Gly Gly Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly

50 55 60

Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu Lys Ile Thr

65 70 75 80

Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Gly Ile

85 90 95

Gln His Gly Gly Gly Asn Ser Asp Tyr Tyr Tyr Tyr Gly Met Asp Leu

100 105 110

Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly

115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130 135 140

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

145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165 170 175

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

180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val

195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys

210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu

225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260 265 270

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

275 280 285

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

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

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

355

360

365

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

370

375

380

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

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

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

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

Leu Ser Pro Gly Lys
450

<210> 310

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-xi Light chain (Table 8)

<400> 310

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

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

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile

35 40 45

Tyr Leu Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Arg Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Asp Leu Glu Cys

65 70 75 80

Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Thr Asn Tyr Gly Thr Ser Ser

85 90 95

Ser Asn Tyr Gly Phe Ala Phe Gly Gly Gly Thr Glu Val Val Val Lys

100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

130 135 140

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

145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser

165

170

175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu

180

185

190

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

195

200

205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210

215

<210> 311

<211> 456

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu Heavy chain (Table 8)

<400> 311

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Ser Leu Ser Ser Asp

20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile

35 40 45

Gly Ile Ile Asn Gly Gly Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys

50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Ile Gln His Gly Gly Gly Asn Ser Asp Tyr Tyr Tyr Tyr Gly

100 105 110

Met Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser

115 120 125

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr

130 135 140

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

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

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
 180 185 190

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

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

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

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 245 250 255

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

275 280 285

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln

290 295 300

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln

305 310 315 320

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

325 330 335

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

340 345 350

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr

355 360 365

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

370 375 380

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

385 390 395 400

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

405 410 415

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

420 425 430

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

435 440 445

Ser Leu Ser Leu Ser Pro Gly Lys

450 455

<210> 312

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> 33011-zu Light chain (Table 8)

<400> 312

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 Gln Ser Ile Ser Ser Val

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Leu Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Cys

65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Thr Asn Tyr Gly Thr Ser Ser

85 90 95

Ser Asn Tyr Gly Phe Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

130 135 140

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

145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser

165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu

180 185 190

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

195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 313

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi Heavy chain (Table 8)

<400> 313

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

1 5 10 15

Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Asn Asn Tyr Ala

20 25 30

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly

35 40 45

Ser Ile Ser Thr Gly Gly Leu Ala Phe Tyr Ala Asn Trp Ala Lys Gly

50 55 60

Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu Lys Met Thr

65 70 75 80

Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Gly Arg Asn Gly

85 90 95

Gly Gly Ser Tyr Ile Phe Tyr Tyr Phe Asp Leu Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro

115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln

165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser

195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr

210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser

225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg

245

250

255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro

260

265

270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala

275

280

285

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

290

295

300

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

305

310

315

320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr

325

330

335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu

340

345

350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys

355

360

365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser

370

375

380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp

385

390

395

400

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

405

410

415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala

420

425

430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

435

440

445

<210> 314

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-xi Light chain (Table 8)

<400> 314

Ala Phe Glu Leu Thr Gln Thr Pro Ser Ser Val Glu Ala Ala Val Gly

1 5 10 15

Gly Thr Ile Thr Ile Lys Cys Gln Ala Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile

35 40 45

Tyr Ser Ala Ser Thr Leu Ala Ser Gly Val Ser Ser Arg Phe Lys Gly

50 55 60

Ser Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Asp Leu Glu Cys

65 70 75 80

Ala Asp Ala Ala Thr Tyr Phe Cys Gln Ser Tyr Tyr Asp Ile Gly Thr

85 90 95

Ser Thr Phe Gly Gly Gly Thr Glu Val Val Val Lys Arg Thr Val Ala

100 105 110

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

115 120 125

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

130

135

140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser

145

150

155

160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu

165

170

175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val

180

185

190

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

195

200

205

Ser Phe Asn Arg Gly Glu Cys

210

215

<210> 315

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu Heavy chain (Table 8)

<400> 315

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Asn Asn Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Ser Ile Ser Thr Gly Gly Leu Ala Phe Tyr Ala Asn Trp Ala Lys

50 55 60

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

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asn Gly Gly Gly Ser Tyr Ile Phe Tyr Tyr Phe Asp Leu Trp Gly

100 105 110

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

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

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

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

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

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

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

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

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

305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

370 375 380

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

385 390 395 400

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

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly Lys

450

<210> 316

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> 111B10-zu Light chain (Table 8)

<400> 316

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 Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ser Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Cys

65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Ser Tyr Tyr Asp Ile Gly Thr

85 90 95

Ser Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala

100 105 110

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

115 120 125

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

130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser

145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu

165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val

180 185 190

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

195 200 205

Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 317

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi Heavy chain (Table 8)

<400> 317

Gln Ser Val Lys Glu Ser Gly Gly Arg Leu Val Thr Pro Gly Thr Pro

1 5 10 15

Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Ser Tyr Ala

20 25 30

Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile Gly

35 40 45

Thr Ile Asn Ile Gly Gly Arg Val Tyr Tyr Ala Ser Trp Ala Lys Gly

50 55 60

Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu Lys Ala Pro

65 70 75 80

Ser Leu Thr Ala Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Tyr Tyr

85 90 95

Asn Gly Gly Ser Tyr Asp Ile Trp Gly Pro Gly Thr Leu Val Thr Val

100 105 110

Ser Leu Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser

115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys

130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu

145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu

165 170 175

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr

180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val

195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro

210 215 220

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

275 280 285

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr

290 295 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

305 310 315 320

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

325 330 335

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

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

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

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 318

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-xi Light chain (Table 8)

<400> 318

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

1 5 10 15

Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Ser Ile Tyr Arg Val

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile

35 40 45

Tyr Asp Thr Ser Thr Leu Ala Ser Gly Ala Pro Ser Arg Phe Lys Gly

50 55 60

Ser Gly Tyr Gly Thr Glu Phe Thr Leu Thr Ile Ser Gly Val Gln Cys

65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gly Gly Tyr Tyr Ala Asp Ser

85 90 95

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

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 319

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu Heavy chain (Table 8)

<400> 319

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Ile Asp Leu Ser Ser Tyr

20 25 30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile

35 40 45

Gly Thr Ile Asn Ile Gly Gly Arg Val Tyr Tyr Ala Ser Trp Ala Lys

50 55 60

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

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Tyr Tyr Asn Gly Gly Ser Tyr Asp Ile Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu

115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys

130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser

145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser

165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser

180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn

195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His

210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val

225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr

245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu

260 265 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys

275 280 285

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

290 295 300

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

305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile

325 330 335

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

340 345 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu

355 360 365

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

370 375 380

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

385 390 395 400

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

405 410 415

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

420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

435 440 445

<210> 320

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> 201C15-zu Light chain (Table 8)

<400> 320

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

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Glu Ser Ile Tyr Arg Val

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Asp Thr Ser Thr Leu Ala 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 Cys

65 70 75 80

Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gly Gly Tyr Tyr Ala Asp Ser

85 90 95

Tyr Gly Ile Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr

100 105 110

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu

115 120 125

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro

130 135 140

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

145 150 155 160

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr

165 170 175

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His

180 185 190

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

195 200 205

Thr Lys Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 321

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi Heavy chain (Table 8)

<400> 321

Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Lys Pro Asp Glu Ser

1 5 10 15

Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser Ser Tyr Ala

20 25 30

Met Ile Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Ile Gly

35 40 45

Thr Ile Ser Thr Gly Gly Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly

50 55 60

Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu Lys Ile Thr

65 70 75 80

Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Gly Gly

85 90 95

Tyr Ala Ala Ser Ser Ala Tyr Tyr Leu Pro Tyr Tyr Phe Asp Leu Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro

115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr

130 135 140

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

145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro

165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr

180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn

195

200

205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser

210

215

220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu

225

230

235

240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu

245

250

255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

260

265

270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

275

280

285

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

290

295

300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

305

310

315

320

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

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

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

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

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

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

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

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

Ser Pro Gly Lys

450

<210> 322

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-xi Light chain (Table 8)

<400> 322

Ala Ala Val Leu Thr Gln Thr Pro Ser Pro Val Ser Ala Ala Val Gly

1 5 10 15

Gly Thr Val Thr Ile Ser Cys Gln Ser Ser Gln Ser Val Tyr Asn Asn

20 25 30

Asn Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu

35 40 45

Leu Ile Tyr Leu Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe

50 55 60

Ser Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Gly Val

65 70 75 80

Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Gly Cys Asp Asp

85 90 95

Asp Ala Asp Thr Phe Ala Phe Gly Gly Gly Thr Glu Val Val Val Lys

100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

130 135 140

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

145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser

165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu

180 185 190

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

195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 323

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu Heavy chain (Table 8)

<400> 323

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Ser Tyr

20 25 30

Ala Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Thr Ile Ser Thr Gly Gly Ile Thr Tyr Tyr Ala Ser Trp Ala Lys

50

55

60

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

65

70

75

80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85

90

95

Arg Gly Gly Tyr Ala Ala Ser Ser Ala Tyr Tyr Leu Pro Tyr Tyr Phe

100

105

110

Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr

115

120

125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser

130

135

140

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

145

150

155

160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His

165

170

175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser

180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys

195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu

210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr

290 295 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp

305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys

355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

370 375 380

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

385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

405 410 415

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

420

425

430

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

435

440

445

Leu Ser Leu Ser Pro Gly Lys

450

455

<210> 324

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> 346C6-zu Light chain (Table 8)

<400> 324

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 Ser Ser Gln Ser Val Tyr Asn Asn

20

25

30

Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu

35 40 45

Leu Ile Tyr Leu Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe

50 55 60

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu

65 70 75 80

Gln Cys Glu Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Gly Cys Asp Asp

85 90 95

Asp Ala Asp Thr Phe Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

130 135 140

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

145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser

165

170

175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu

180

185

190

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

195

200

205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210

215

<210> 325

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 Heavy chain (Table 9)

<400> 325

gaggtccaac tgggtggagag cgggtggaggt gttgtgcaac ctggccggtc cctgcgcctg 60

tcctgctccg catctggctt caccttcagc ggctatgggt tgtcttgggt gagacaggca 120

cctggaaaag gtcttgagtg ggttgcaatg attagtagtg gtggtagtta tacctactat 180

gcagacagtg tgaaggtag atttgaata tcgcgagaca acgccaagaa cacattgttc 240

ctgcaaatgg acagcctgag acccgaagac accggggtct atttttgtgc aagacatggg 300

gacgatcccg cctggttcgc ttattggggc caagggaccc cggtcaccgt ctctcagcc 360

tccaccaagg gcccatcggt cttccccctg gcaccctct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcaca gccccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtagaca aaactcacac atgccaccg tgccagcac ctgaactcct ggggggaccg 720

tcagtcttcc tcttcccccc aaaaccaag gacaccctca tgatctccg gaccctgag 780

gtcacatcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctcaa caaagccctc ccagcccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc cccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cttatattca aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc cgggaaatga 1350

<210> 326

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-003 Light chain (Table 9)

<400> 326

gacatccagc tgaccagag cccaagcagc ctgagcgcca gcgtgggtga cagagtgacc 60

atcacctgta gtgtcagctc aagtataagt tccaacaact tgactggta ccagcagaag 120

ccaggtaagg ctccaaagcc atggatctac ggcacatcca acctggcttc tgggtgcca 180

agcagattca gcggtagcgg tagcgggtacc gactacacct tcaccatcag cagcctccag 240

ccagaggaca tcgccaccta ctactgcca cagtggagta gttaccgta catgtacacg 300

ttcggccaag ggaccaaggt ggaaatcaaa cgaactgtgg ctgcaccatc tgtcttcac 360

ttcccccat ctgatgagca gttgaaatct ggaactgcct ctgttggtg cctgctgaat 420

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600

catcagggcc tgagctgcc cgtcacaaag agcttcaaca ggggagagtg ttaa 654

<210> 327

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 Heavy chain (Table 9)

<400> 327

caggtacaac tgcagcagtc tgggcctgag ctggagaagc ctggcgcttc agtgaagata 60

tcctgcaagg cttctggtta ctattcact ggctacacca tgaactgggt gaagcagagc 120

catggaaaga gccttgagtg gattggactt attactcctt acaatggtgc ttctagctac 180

aaccagaagt tcaggggcaa ggccacatta actgtagaca agtcatccag cacagcctac 240

atggacctcc tcagtctgac atctgaagac tctgcagtct atttctgtgc aagggggggt 300

tacgacggga ggggttttga ctactgggga tccgggaccc cggtcaccgt ctctcagcc 360

tccaccaagg gcccatcggg cttccccctg gcacctctct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacia gccagcaac accaagggtg acaagaaagt tgagcccaaa 660

tcttgtagca aaactcacac atgcccaccg tgcccagcac ctgaactcct ggggggaccg 720

tcagtcttcc tcttcccccc aaaaccaag gacacctca tgatctccc gacctctgag 780

gtcacatgcg tgggtggtgga cgtgagccac gaagacctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctcaa caaagccctc ccagcccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacacctgc ccccatccc ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccagcc tccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc cgggaaatga 1350

<210> 328

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> MORAb-009 Light chain (Table 9)

<400> 328

gacatcgagc tcactcagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60

atgacctgca gtgccagctc aagtgttaagt tacatgcact ggtaccagca gaagtcaggc 120

acctcccca aaagatggat ttatgacaca tccaaactgg cttctggagt cccaggtcgc 180

ttcagtggca gtgggtctgg aaactcttac tcttcacaa tcagcagcgt ggaggctgaa 240

gatgatgcaa cttattactg ccagcagtgg agtaagcacc ctctcacgtt cggatccggg 300

accaaggtgg aaatcaaacg aactgtggct gcaccatctg tcttcatctt cccgccatct 360

gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420

agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 480

agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540

agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcaggcctg 600

agctcgcccg tcacaaagag cttcaacagg ggagagtgtt aa 642

<210> 329

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi Heavy chain (Table 9)

<400> 329

cagtcggtgg aggagtccgg gggtcgctg gtcacgcctg ggacaccct gacactcacc 60

tgaccgtct ctggaatctc ctcagtagc gatgcaataa gctgggtccg ccaggctcca 120

gggaaggggc tcgaatacat cggaatcatt aatggtggg gtaacacata ctacgcgagc 180

tgggcgaaag gccgattcac catctcaaa acctcgacca cgggtgatct gaaaatcacc 240

agtccgacaa ccgaggacac ggccacctat ttctgtgcca gaggcattca acatggtggt 300

ggtaatagt attattatta ttacggcatg gacctctggg gcccaggcac cctggtcact 360

gtctcttcag catccaccaa gggcccatcg gtcttcccc tggcacccct ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc caaaaacca aggacaccct catgatctcc 780

cggaccctg aggtcacatg cgtgggtgtg gacgtgagcc acgaagacc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccag 1200

cctcccgtgc tggactccga cggctccttc ttcttatatt caaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac 1320

cactacacgc agaagagcct ctccctgtct cccgggaaat ga 1362

<210> 330

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-xi Light chain (Table 9)

<400> 330

gaagtgttga tgaccagac tccatcctcc gtgtctgcag ctgtgggaga cacagtcacc 60

atcaagtgcc aggccagtca gagcattagt agtgtcttgt cctggtatca gcagaaacca 120

gggcagcctc ccaagctcct gatctatctg gcatccactc tggcatctgg ggtcccatcg 180

cggttcagcg gcagtagatc tgggacagag ttactctca ccatcagcga cctggagtgt 240

gacgatgctg ccacttacta ctgtcaaacc aattatggta ctagtagtag taattatggt 300

tttgctttcg gcggaggagc cgaggtggtc gtcaaacgaa ctgtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctcaa 480

tcgggtaact ccaggagag tgtcacagag caggacagca aggacagcac ctacgcctc 540

agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgctgcgaa 600

gtcacccatc agggcctgag ctgcccgtc acaaagagct tcaacagggg agagtgttga 660

<210> 331

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu Heavy chain (Table 9)

<400> 331

gaagtccaac tggaggaaag cgggggagga ctggtgcagc cgggcggatc cctccggctg 60

tcatgtgctg catcgggaat ttccctctcc tccgacgcga ttagctgggt cagacaggcc 120

cccggaaagg ggctggagta catcggatc atcaacggcg gcggaaacac ctactacgcc 180

tcctgggccca agggccgctt caccatctcg cggcataatt ccaagaacac tctgtacttg 240

caaatgaact ccctgagggc cgaggacacc gccgtgtact actgcgcgcg cggcatccag 300

cacggtggtg gaaacagcga ctactactac tatgggatgg atctgtgggg ccagggaact 360

cttgtgaccg tgcgtcagc atccaccaag ggcccatcgg tcttcccctt ggcaccctcc 420

tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc 480

gaaccggtga cgggtgcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 540

gctgtcctac agtcctcagg actctactcc ctacgacgcg tggtagaccgt gccctccagc 600

agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 660

gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 720

cctgaactcc tggggggacc gtcagtcttc ctcttcccc caaaaccaa ggacaccctc 780

atgatctccc ggaccctga ggtcacatgc gtgggtgtgg acgtgagcca cgaagaccct 840

gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg 900

cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 960

gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagcccc 1020

atcgagaaaa ccatctcaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1080

ccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1140

ttctatcca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1200

aagaccagc ctcccgtgct ggactccgac ggctccttct tcttatattc aaagctcacc 1260

gtggacaaga gcaggtggca gcagggaac gtcttctcat gtcctgat gcatgaggct 1320

ctgcacaacc actacagca gaagagcctc tccctgtctc ccgggaaatg a 1371

<210> 332

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> 33011-zu Light chain (Table 9)

<400> 332

gacattcaga tgaccagtc cccaagctcg ctgtccgcct ccgtgggcga ccgcgtgacc 60

atcacgtgcc aggcgtccca gtcaattagc agcgtgctct cctggtacca acagaagccg 120

gggaaagcac ccaagctgct gatctacttg gcctccactc tggcctcggg agtgccttca 180

cggttctccg gatcgggac tggtactgat ttcaccctca ccatctcgag ccttcagtgc 240

gaggacatcg ctacttacta ttgtcaaacc aactacggaa cctccagctc caactacggc 300

tttccttcg gtggcgggac caagtcgaa atcaaacgaa ctgtggctgc accatctgtc 360

ttcatcttc cgccatctga tgagcagtg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctcaa 480

tcgggtaact ccaggagag tgtcacagag caggacagca aggacagcac ctacagctc 540

agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgctgcgaa 600

gtcaccatc agggcctgag ctgcccgtc acaaagagct tcaacagggg agagtgttga 660

<210> 333

<211> 1347

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi Heavy chain (Table 9)

<400> 333

cagtcggtgg aggagtccgg gggtcgcctg gtcacgcctg ggacaccctt gacactcacc 60

tgcacagtct ctggattctc cctcaataac tatgcaatga gctgggtccg ccagggtcca 120

gggaaggggc tggaatggat cggatccatt agtactggtg gtctgcatt ctacgcgaac 180

tgggcaaaag gccgattcac catctccaga acctcgacca cgggtgatct gaaaatgacc 240

agtctgacaa ccgaggacac ggccacctat ttctgtggca gaaatggtgg tggtagttat 300

atthtttatt atthttgactt gtggggccaa ggcaccctcg tcaactgtctc ttcagcatcc 360

accaagggcc catcgtctt cccctggca cctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttcccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgcc tccagcagct tgggcacca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720

gtcttctct tcccccaaa acccaaggac acctcatga tctccggac ccctgaggtc 780

acatgcgtgg tgggtgacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gagggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgaagg tctccaacaa agccctcca gcccctatcg agaaaacat ctcaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttctt atattcaaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctcccg gaaatga 1347

<210> 334

<211> 648

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-xi Light chain (Table 9)

<400> 334

gcattcgaat tgaccagac tccatcctcc gtggaggcag ctgtgggagg cacaatcacc 60

atcaagtgcc aggccagtca gagcattagt agttacttat cctggtatca gcagaaacca 120

gggcagcctc ccaagctcct gatctattct gcatccactc tggcatctgg ggtctcatcg 180

cggttcaaag gcagtggatc tgggacagag tacactctca ccatcagcga cctggagtgt 240

gccgatgctg ccacttactt ctgtcaaagc tattatgata ttggtactag tactttcggc 300

ggagggaccg aggtggctgt caaacgaact gtggctgcac catctgtctt catcttccc 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg 540

acgtgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgctac aaagagcttc aacaggggag agtgttga 648

<210> 335

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu Heavy chain (Table 9)

<400> 335

gaagtgcagc tgggtggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg 60

tcttgtgccg cctccggctt ctccctgaac aactacgcca tgtctgggt gcgacaggcc 120

cctggcaaag gcctggaatg gatcggctcc atcagcacag gcggcctggc cttctacgcc 180

aattgggccca agggccgggt caccatcagc cgggacaact ccaagaacac cctgtacctc 240

cagatgaact ccctcgggc cgaggacacc gccgtgtact actgtgccag aaacggcgga 300

ggctcctaca tcttctacta cttcgacctg tggggccagg gcaccctgt gacagtgtca 360

tctgcatcca ccaagggcc atcggcttc cccctggcac cctcctcaa gagcacctct 420

gggggcacag cggccctggg ctgcctgtc aaggactact tcccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720

ggaccgtcag tcttctctt cccccaaaa ccaaggaca ccctcatgat ctccggacc 780

cctgaggta catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggta aaggcttcta tcccagcgac 1140

atgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200

gtgctggact ccgacggctc cttcttcta tattcaaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcctgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccggg aaatga 1356

<210> 336

<211> 648

<212> DNA

<213> Artificial Sequence

<220>

<223> 111B10-zu Light chain (Table 9)

<400> 336

gatattcaga tgaccagtc cccctccagc ctgtccgctt ctgtggcgca cagagtgacc 60

atcacctgtc aggcctcca gtccatctcc tctacctgt cctggatatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactct gcctccacac tggcctccgg cgtgccctct 180

agattctccg gctctggctc tggcaccgac ttaccctga ccatcagctc cctccagtgc 240

gaggatgccg ccacctacta ctgccagtcc tactacgaca tcggcacctc caccttcggc 300

ggaggcacca aggtggaaat caaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttga 648

<210> 337

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi Heavy chain (Table 9)

<400> 337

cagtcagtga aggagtccgg gggctgcctg gtcacgcctg ggacaccctc gacactcacc 60

tgcacagtct ctggaatcga cctcagtagc tatgcaatgg gctggttccg ccaggctcca 120

gggaaggggc tggaatacat cggaaccatt aatattggtg gtcgcgtata ttacgcgagc 180

tgggcaaaag gccgattcac catctccaga acctcgacca cgggtgatct gaaagcgccc 240
 agtctgacag ccgaggacac ggccacctat ttctgtgcca gatattataa tgggtgtagt 300
 tatgacatct ggggcccagg caccctggtc accgtctctt tagcatccac caagggccca 360
 tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420
 tgcttggtca aggactactt cccgaaccg gtgacggtgt cgtggaactc aggcgccttg 480
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcagc 540
 agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg tgacaaaact 660
 cacacatgcc caccgtgcc agcacctgaa ctctggggg gaccgtcagt cttctcttc 720
 ccccaaaac ccaaggacac cctcatgatc tcccggaacc ctgaggtcac atgcgtggtg 780
 gtggacgtga gccacgaaga ccctgaggtc aagttaact ggtacgtgga cggcgtggag 840
 gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 900
 agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 960
 tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1020
 cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcttat attcaaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgagaagag cctctccctg 1320

tctcccgga aatga 1335

<210> 338

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-xi Light chain (Table 9)

<400> 338

gatgttgatga tgaccagac tccagcctcc gcgtctgaac ctgtgggagg cacagtcacc 60

atcaagtgcc aggccagtga gagcatttat cgctatttgg cctggatatca gcagaaacca 120

gggcagcctc ccaagctcct gatctatgat acatccactc tggcatctgg ggccccatcg 180

cggttcaaag gcagtggata tgggacagag ttcactctca ccatcagcgg cgtgcagtgt 240

gaagatgctg ccacttacta ctgtcaaggc ggttattatg ctgatagtta tggatttgct 300

ttcggcggag ggaccgaggt ggtggtcaaa cgaactgtgg ctgcaccatc tgtcttcac 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttggtg cctgctgaat 420

aacttctatc ccagagagggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg ttga 654

<210> 339

<211> 1344

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu Heavy chain (Table 9)

<400> 339

caggtgcagc tgggtggaatc tggcggagga ctggtgcagc ctggcggctc tctgagactg 60

tcctgttccg cctccggaat cgacctgtcc tctacgcta tgggctgggt gcgacaggct 120

cctggcaagg gcctggagta catcggcacc atcaacatcg gcggcagagt gtactacgcc 180

tcctgggccca agggccgggt caccatctcc agagacaact ccaagaacac cctgtacctc 240

cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgcgcccg gtactacaac 300

ggcggctcct acgatatctg gggccagggc acactcgtga ccgtgtcctc tgcattccacc 360

aaggggccat cggcttctcc cctggcacc cctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcggccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcttc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgcca gcacctgaac tcctgggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgctgtgtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cggtgtgtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggctc ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc 1200

gacggctcct tcttctata ttcaaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320

ctctccctgt ctcccgggaa atga 1344

<210> 340

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> 201C15-zu Light chain (Table 9)

<400> 340

gatatccaga tgaccagtc cccctccacc ctgtctgcct ctgtgggcga cagagtgacc 60

atcacctgtc aggcctccga gtccatctac cgggtgctgg cctggatatca gcagaagcct 120

ggcaaggccc ccaagctgct gatctacgac accagcacac tggcctccgg cgtgccctct 180

agattctccg gctctggctc tggcaccgag ttaccctga ccatctccag cctccagtgc 240

gacgacgccg ccacctacta ttgtcagggc ggctactacg ccgactccta cggaatcgct 300

ttcggcggag gcaccaaggt ggaaatcaaa cgaactgtgg ctgcaccatc tgtcttcac 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttggtg cctgctgaat 420

aacttctatc ccagagaggc caaagtacag tggaagggtg ataacgcct ccaatcgggt 480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg ttga 654

<210> 341

<211> 1359

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi Heavy chain (Table 9)

<400> 341

cagtcggtgg aggagtccgg cggtcgcctg gtaaagcctg acgaatccct gacactcacc 60

tgcacagcct ctggattctc cctcagtagt tatgcaatga tctgggtccg ccagggtcca 120

ggggaggggc tggaatggat cggaaccatt agtactggtg gtatcacata ctacgcgagc 180

tgggcgaaag gccgattcac catctcaaa acctcgacca cgggtgatct gaaaatcacc 240

agtccgacaa ccgaggacac ggccacctat ttctgtgcca gagggggata tgctgctagt 300

agtgcttatt atctcccgtg ctactttgac ttgtggggcc aaggggaccct ggtcaccgtc 360

tcctcagcat ccaccaaggc cccatcggtc tccccctgg caccctctc caagagcacc 420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgcctacag 540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600

cagacctaca tctgcaacgt gaatcacaa cccagcaaca ccaagggtga caagaaagtt 660

gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 720

gggggaccgt cagtcttctt cttccccca aaaccaagg acaccctcat gatctccgg 780

accctgagg tcacatgcgt ggtgggtggac gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1020

atctcaaag ccaaaggga gccccagaga ccacaggtgt acaccctgcc ccatccgg 1080

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

cccgtgctgg actccgacgg ctcttcttc ttatattcaa agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtctccc gggaaatga 1359

<210> 342

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-xi Light chain (Table 9)

<400> 342

gcagccgtgc tgaccagac accatcacc gtgtctgcag ctgtgggagg cacagtcacc 60

atcagttgcc agtcagtcag gagtggttat aataataaca acttagcctg gtttcagcag 120

aaacccgggc agcctccaa gcttctgac tatctggcat ccactctggc atctggggtc 180

ccatcacggt tcagcggcag tggatctggg acacagttca ctctacccat cagcggcgtg 240

cagtgtagc atgctgccac ttattactgt ctagggtggt gtgatgatga tgctgatact 300

tttgctttcg gcggaggagc tgaggtgggt gtcaaagaa ctgtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgcacagag caggacagca aggacagcac ctacagcctc 540

agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcaccatc agggcctgag ctgcccgtc acaaagagct tcaacagggg agagtgtga 660

<210> 343

<211> 1368

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu Heavy chain (Table 9)

<400> 343

gaagtgcagc tgggtggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg 60

tcttgtgccg cctccggctt ctccctgtcc tcctacgcta tgatctgggt gcgacaggcc 120

cctggcaagg gcctggaatg gatcggcacc atctctaccg gcggaattac ctactacgcc 180

tcctgggccca agggccggtt caccatctcc agagacaact ccaagaacac cctgtacctc 240

cagatgaact ccctgcgggc cgaggacacc gccgtgtact attgtgctag aggcgggtac 300

gccgccagct ccgcttacta cctgccctac tacttcgacc tgtggggcca gggcacctc 360

gtgacagtgt catctgcatc caccaagggc ccatcgttct tccccctggc accctctcc 420

aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480

ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggt 540

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660
 aagaaagtg agcccaaatt ttgtgacaaa actcacacat gccaccgtg cccagcacct 720
 gaactctgg ggggaccgtc agtcttctc ttcccccaa aaccaagga caccctcatg 780
 atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 840
 gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900
 gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 960
 tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agcccccatc 1020
 gagaaaacca tctcaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080
 ccatcccgga atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140
 tatcccgagc acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200
 accacgcctc ccgtgctgga ctccgacggc tccttcttct tatattcaaa gctcaccgtg 1260
 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320
 cacaaccact acacgcagaa gagcctctcc ctgtctcccg ggaaatga 1368

<210> 344

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> 346C6-zu Light chain (Table 9)

<400> 344

gatattcaga tgaccagtc cccctccagc ctgtccgctt ctgtgggcca cagagtgacc 60

atcacctgtc agtcctccca gtccgtgtat aacaacaaca acctggcctg gtatcagcag 120

aaacccggca aggtgccaa gctgctgac tacctggcct ccactggc ctctggcgtg 180

ccctctagat tctccggctc tggctctggc accgacttta ccctgacat cagctccctc 240

cagtgcgagg atgccgccac ctactattgc ctggcggt gcgacgacga cgccgatacc 300

tttgcttttg gcggaggcac caagtgga atcaaacgaa ctgtggctgc accatctgtc 360

ttcatcttc cgccatctga tgagcagtg aaatctgga ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtga aggtggataa cgccctcaa 480

tcgggtaact ccaggagag tgtcacagag caggacagca aggacagcac ctacgcctc 540

agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgctgcgaa 600

gtcacccatc agggcctgag ctgcccgtc acaaagagct tcaacagggg agagtgtga 660

<210> 345

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Epitope example 1

<400> 345

Ala His Lys Asp

1

<210> 346

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Epitole example 2

<400> 346

Asn Thr Ser Gln Glu Ala His Lys Asp Val Ser Tyr Leu

1 5 10

<210> 347

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Trastuzumab Heavy Chain

<400> 347

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr

20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val

115

120

125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala

130

135

140

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

145

150

155

160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val

165

170

175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro

180

185

190

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

195

200

205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp

210

215

220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly

225

230

235

240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile

245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu

260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg

290 295 300

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

305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu

325 330 335

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

340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu

355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp

370 375 380

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

385 390 395 400

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

405 410 415

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

420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro

435 440 445

Gly