SEQUENCE LISTING

<110> WYETH HOLDINGS CORPORATION.

<120> CALICHEAMICIN DERIVATIVE-CARRIER CONJUGATES

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Gly

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Arg Ser Ser Gln Ser Leu Ala Asn Ser Tyr Gly Asn Thr Phe Leu Ser
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Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Ala Asn Ser
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Tyr Gly Asn Thr Phe Leu Ser Trp Tyr Leu His Lys Pro Gly Gln Ser
35 40 45

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

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

Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr Cys Leu Gln Gly
85 90 95

Thr His Gln Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg

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Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Arg Phe Thr Asn Tyr
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Trp Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gly Ile Asn Pro Gly Asn Asn Tyr Thr Thr Tyr Lys Arg Asn Leu
50 55 60

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

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

Thr Arg Glu Gly Tyr Gly Asn Tyr Gly Ala Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
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Gly

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Gly Asn Asn Tyr Thr Thr Tyr Arg Arg Asn Leu Lys Gly
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Gly

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Gly

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Asp Arg Val Thr Ile Thr Cys Trp Tyr Gln Gln Lys Pro Gly Lys Ala
20 25 30

Pro Lys Leu Leu Ile Tyr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
35 40 45

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

Phe Ala Thr Tyr Tyr Cys
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Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Asp Val Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Tyr Gly Asn Thr Phe Leu Ser Trp Tyr Leu His Lys Pro Gly Lys Ala
35 40 45

Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

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

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

Thr His Gln Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg

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1 5 10 15

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

Tyr Gly Asn Thr Phe Leu Ser Trp Tyr Leu His Lys Pro Gly Lys Ala
35 40 45

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

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

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

Thr His Gln Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Trp Val
20 25 30

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

Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
50 55 60

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
65 70 75 80

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<400> 22
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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<400> 23
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Arg Phe Thr Asn Tyr
20 25 30

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

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

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

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

Thr Arg Glu Gly Tyr Gly Asn Tyr Gly Ala Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<223> gH4

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<400> 24
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

35 40 45

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

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

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

Thr Arg Glu Gly Tyr Gly Asn Tyr Gly Ala Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 25
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<212> PRT
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<223> gH5

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<400> 25
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

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

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

Thr Arg Glu Gly Tyr Gly Asn Tyr Gly Ala Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<400> 26
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Arg Phe Thr Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Gly Asn Asn Tyr Ala Thr Tyr Arg Arg Lys Phe
50 55 60

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

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

Thr Arg Glu Gly Tyr Gly Asn Tyr Gly Ala Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 27
<211> 121
<212> PRT
<213> Artificial Sequence

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<223> gH7

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<400> 27
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

Gly Gly Ile Asn Pro Gly Asn Asn Tyr Ala Thr Tyr Arg Arg Lys Phe

50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Thr Arg Glu Gly Tyr Gly Asn Tyr Gly Ala Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 28
<211> 239
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<223> Full sequence of grafted light chain

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<400> 28
Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Leu Phe Trp Ile Pro
1 5 10 15

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

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

Leu Ala Asn Ser Tyr Gly Asn Thr Phe Leu Ser Trp Tyr Leu His Lys
50 55 60

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

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

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

Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gln Gly Thr Lys
115 120 125

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145 150 155 160

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

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

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

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 29
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<213> Artificial Sequence

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Met Asp Phe Gly Phe Ser Leu Val Phe Leu Ala Leu Ile Leu Lys Gly

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

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

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

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

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

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

Tyr Tyr Cys Thr Arg Glu Gly Tyr Gly Asn Tyr Gly Ala Trp Phe Ala
115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Gly Lys
465

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<223> 544gH1 T1

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<210> 33
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<223> 544gH1 T2

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<400> 33
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<223> 544gH1 T3

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<400> 34
agagaaggct acggtaatta cggagcctgg ttcgcctact ggggccaggg taccctagtc 60
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<212> DNA
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<223> 544 gH1 B1

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<400> 35
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<223> 544gH1 B2

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<400> 36
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<210> 38
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<400> 38
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<210> 39
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<400> 39
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<210> 40
<211> 87
<212> DNA

<213> Artificial Sequence

<220>
<223> 544gL1 T1

<220>
<221>

<400> 40
gcttcccggg gtgacgttca agtgacccag agcccatcca gcctgagcgc atctgtagga 60
gaccgggtca ccatcacttg tagatcc 87

<210> 41
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> 544gL1 T2

<220>
<221>

<400> 41
tatctgcaca aaccaggtaa agccccacaa ttgctcatct acggaatctc taacagattt 60
agtggtgtac cagacaggtt cagcggttcc 90

<210> 42
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> 544gL1 T3

<220>
<221>

<400> 42
agatttcgcc acttattact gtttacaagg tacacatcag ccgtacacat tcggtcaggg 60
tactaaagta gaaatcaaac gtacggcgtg c 91

<210> 43
<211> 88
<212> DNA
<213> Artificial Sequence

<220>
<223> 544gL1 B1

<220>
<221>

<400> 43
gaacgtcacc ccgggaagca ggaatccaga acaacagaag caccaacagc ctaacaggca 60
acttcatggt ggcggcttcg aatcatcc 88

<210> 44
<211> 88
<212> DNA
<213> Artificial Sequence

<220>
<223> 544gL1 B2

<220>
<221>

<400> 44
ctttacctgg tttgtgcaga taccaagaca aaaaggtgtt cccataactg tttgcaagac 60
tctgactgga tctacaagtg atggtgac 88

<210> 45
<211> 90

<212> DNA
<213> Artificial Sequence

<220>
<223> 544gL1B3

<220>
<221>

<400> 45
aacagtaata agtggcgaaa tcttctggct ggagagacga gatcgtgagg gtgaaatcag 60
taccacttcc ggaaccgctg aacctgtctg 90

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> 544gL1 F1

<220>
<221>

<400> 46
ggatgattcg aagccgccac 20

<210> 47
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> 544gL1 R1

<220>
<221>

<400> 47
gcacgccgta cgtttgattt c 21

<210> 48
<211> 339
<212> DNA
<213> mouse

<220>
<223> DNA sequence of mouse monoclonal 5/44 VL

<220>
<221>

<400> 48
gatgttgtgg tgactcaaac tccactctcc ctgcctgtca gctttggaga tcaagtttct 60
atctcttgca ggtctagtca gagtcttgca aacagttatg ggaacacctt tttgtcttgg 120
tacctgcaca agcctggcca gtctccacag ctcctcatct atgggatttc caacagattt 180
tctggggtgc cagacaggtt cactggcagt ggttcaggga cagatttcac actcaagatc 240
agcacaataa agcctgagga cttgggaatg tattactgct tacaaggtac acatcagccg 300
tacacgttcg gaggggggac caagctggaa ataaaacgt 339

<210> 49
<211> 363
<212> DNA
<213> mouse

<220>
<223> DNA sequence of mouse monoclonal 5/44 VH

<220>
<221>

<400> 49
gaggtccaac tgcagcagtc tgggactgta ctggcaaggc ctggggcttc cgtgaagatg 60
tcctgcaagg cttctggcta caggtttacc aactactgga ttcactgggt aaaacagagg 120

cctgggcagg gtctagaatg gattggtggt attaatcctg gaaataatta tactacgtat 180

aagaggaact tgaagggcaa ggccacactg actgcagtca catccgccag cactgcctac 240

atggacctca gcagcctgac aagtgaggac tctgcggtct attactgtac aagagagggc 300

tatggtaact acggggcctg gtttgcttac tggggccagg ggactctggt caccgtctcc 360

tca 363

<210> 50
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence within oligonucleotide primer

<400> 50
gccgccacc 9

<210> 51
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligonucleotide primer

<400> 51
gcgcgcaagc ttgccgccac catggacttc ggattctctc tcgtgttcct ggcactcatt 60

ctcaagggag tgcagtgtga ggtgcagctc gtcgagtctg g 101

<210> 52
<211> 339
<212> DNA
<213> Mus musculus

<220>
<223> DNA noncoding strand for mouse monoclonal 5/44 VL domain

<400> 52
ctacaacacc actgagtttg aggtgagagg gacggacagt cgaaacctct agttcaaaga 60

tagagaacgt ccagatcagt ctcagaacgt ttgtcaatac ccttgtggaa aaacagaacc 120

atggacgtgt tcggaccggt cagaggtgtc gaggagtaga taccctaaag gttgtctaaa 180

agaccccacg gtctgtccaa gtgaccgtca ccaagtccct gtctaaagtg tgagttctag 240

tcgtgttatt tcggactcct gaacccttac ataatgacga atgttccatg tgtagtcggc 300

atgtgcaagc ctccccccctg gttcgacctt tattttgca 339

<210> 53
<211> 363
<212> DNA
<213> Mus musculus

<220>
<223> DNA noncoding strand for mouse monoclonal 5/44 VH domain

<400> 53
ctccaggttg acgtcgtcag accctgacat gaccgttccg gaccccgaag gcacttctac 60

aggacgttcc gaagaccgat gtccaaatgg ttgatgacct aagtgaccca ttttgtctcc 120

ggacccgtcc cagatcttac ctaaccacca taattaggac ctttattaat atgatgcata 180

ttctccttga acttcccgtt ccggtgtgac tgacgtcagt gtaggcggtc gtgacggatg 240

tacctggagt cgtcggactg ttcactcctg agacgccaga taatgacatg ttctctcccg 300

ataccattga tgccccggac caaacgaatg accccggtcc cctgagacca gtggcagagg 360

agt 363

<210> 54
<211> 110
<212> DNA
<213> Artificial Sequence

<220>
<223> gH4 oligonucleotide

<400> 54
ccgggaataa ctacgctaca tataggagaa atctaaaggg cagagcaacg ctgaccgcct 60

tattgatgcg atgtatatcc tctttagatt tcccgtctcg ttgcgactgg 110

<210> 55
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> gH4 graft

<400> 55

Pro Gly Asn Asn Tyr Ala Thr Tyr Arg Arg Asn Leu Lys Gly Arg Ala
1 5 10 15

Thr Leu Thr Ala
20

<210> 56
<211> 109
<212> DNA
<213> Artificial Sequence

<220>
<223> gH5 oligonucleotide

<400> 56
ccgggaataa ctacgctaca tataggagaa atctaaaggg cagagttacg atgaccgcct 60

tattgatgcg atgtatatcc tctttagatt tcccgtctca atgctactgg 110

<210> 57
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> gH5 graft

<400> 57

Pro Gly Asn Asn Tyr Ala Thr Tyr Arg Arg Lys Phe Gln Gly Arg Val
1 5 10 15

Thr Met Thr Ala
20

<210> 58
<211> 110
<212> DNA
<213> Artificial Sequence

<220>
<223> gH6 oligonucleotide

<400> 58
ccgggaataa ctacgctaca tataggagaa aattccaggg cagagcaacg ctgaccgcct 60

tattgatgcg atgtatatcc tcttttaagg tcccgtctcg ttgcgactgg 110

<210> 59
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> gH6 graft

<400> 59

Pro Gly Asn Asn Tyr Ala Thr Tyr Arg Arg Lys Phe Gln Gly Arg Ala
1 5 10 15

Thr Leu Thr Ala
20

<210> 60
<211> 110
<212> DNA
<213> Artificial Sequence

<220>
<223> gH7 oligonucleotide

<400> 60
ccgggaataa ctacgctaca tataggagaa aattccaggg cagagttacg atgaccgcct 60

tattgatgcg atgtatatcc tcttttaagg tcccgtctca atgctactgg 110

<210> 61
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> gH7 graft

<400> 61

Pro Gly Asn Asn Tyr Ala Thr Tyr Arg Arg Lys Phe Gln Gly Arg Val
1 5 10 15

Thr Met Thr Ala
20

<210> 62
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> gL2 oligonucleotide

<400> 62
ccggggtgac gttgtcgtga cccagagccc atccagcctg agcgcatctg taggagaccg 60

gccactgcaa cagcactggg tctcgggtag gtcggactcg cgtagacatc ctctggccca 120

gtg 123

<210> 63
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> gL2 graft

<400> 63

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

Ser Val Gly Asp Arg Val Thr
20

<210> 64
<211> 781
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA noncoding strand for g5/44 light chain

<400> 64
aagcttcggc ggtggtactt caacggacaa tccgacaacc acgaagacaa caagacctaa 60

ggacgaaggg ccccactgca agttcactgg gtctcgggta ggtcggactc gcgtagacat 120

cctctggccc agtggtagtg aacatctagg tcagtctcag aacgtttgtc aataccttg 180

tggaaaaaca gaaccataga cgtgtttggt ccatttcggg gtgttaacga gtagatgcct 240

tagagattgt ctaaatcacc acatggtctg tccaagtcgc caaggccttc accatgacta 300

aagtgggagt gctagagcag agaggtcggt cttctaaagc ggtgaataat gacaaatgtt 360

ccatgtgtag tcggcatgtg taagccagtc ccatgatttc atctttagtt tgcatgccat 420

cgccggggta gacagaagta gaagggcggt agactactcg tcaactttag accttgacgg 480

agacaacaca cggacgactt attgaagata gggtctctcc ggtttcatgt caccttccac 540

ctattgcggg aggttagccc attgagggtc ctctcacagt gtctcgtcct gtcgttcctg 600

tcgtggatgt cggagtcgtc gtgggactgc gactcgtttc gtctgatgct ctttgtgttt 660

cagatgcgga cgcttcagtg ggtagtcccg gactcgagcg ggcagtgttt ctcgaagttg 720

tcccctctca caatctccct cttcacgggg gtggacgagg agtcaaggtc ggacccttaa 780

g 781

<210> 65
<211> 2160
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA noncoding strand for g5/44 heavy chain

<400> 65
ttcgaacggc ggtggtacct gaagcctaag agagagcaca aggaccgtga gtaagagttc 60

cctcacgtca cactccacgt taaccaggtc agtcctcgtc tccaattctt cggaccacga 120

aggcagtttc aaagcacatt ccgatcgccg atgtccaagt gtttaataac ctaagtaacc 180

cagtccgtcc gaggccctgt tccggacctt acctagccac cgtaattagg gcccttattg 240

atgcgatgta tatcctcttt taaggtcccg tctcaatgct actggcgcct gtggaggtgt 300

tcgtgacaga tgtacctcga cagtagagac tctaggctcc tgtggcgtca catgataaca 360

tgatctcttc cgatgccatt aatgcctcgg accaagcgga tgaccccggt cccatgggat 420

cagtgtcaga ggagtcgaag atgtttcccg ggtaggcaga agggggaccg cgggacgagg 480

tcctcgtgga ggctctcgtg tcggcgggac ccgacggacc agttcctgat gaaggggctt 540

ggccactgcc acagcacctt gagtccgcgg gactggtcgc cgcacgtgtg gaagggccga 600

caggatgtca ggagtcctga gatgagggag tcgtcgcacc actggcacgg gaggtcgtcg 660

aacccgtgct tctggatgtg gacgttgcat ctagtgttcg ggtcgttgtg gttccacctg 720

ttctctcaac cactctccgg tcgtgtccct ccctcccaca gacgaccttc ggtccgagtc 780

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agaggagggt ctagactcat tgagggttag aagagagacg tctcaggttt ataccagggg 1140

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ccacgggatc tcatcggacg taggtccctg tccggggtcg gcccacgact gcgtaggtgg 1260

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cactcggtcc ttctggggct ccaggtcaag ttgaccatgc acctaccgca cctccacgta 1440

ttacggttct gtttcggcgc cctcctcgtc aagttgtcgt gcatggcaca ccagtcgcag 1500

gagtggcagg acgtggtcct gaccgacttg ccgttcctca tgttcacgtt ccagaggttg 1560

tttccggagg gcaggaggta gctcttttgg tagaggtttc ggtttccacc ctgggtgccc 1620

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gtgcggaggg cacgacctga ggctgccgag gaagaaggag atgtcgtccg attggcacct 1920

gttctcgtcc accgtcctcc ccttacagaa gagtacgagg cactacgtac tccgagacgt 1980

gttggtgatg tgtgtcttct cggagaggga cagagaccca tttactcacg gtcccggccg 2040

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