SEQUENCE LISTING

<110> Kyowa Hakko Kirin Co., Ltd.
Research Organization of Information and Systems

<120> Protein production method

<130> W503694

<150> JP2010-279849

<151> 2010-12-15

<160> 60

<170> PatentIn version 3.3

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<212> DNA
<213> Artificial

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<223> Description of artificial sequence; nonautologus Tol2 transposon

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gaagaaaatg gaggaagtat gtgattcatc agcagctgcg agcagcacag tccaaaatca 480

gccacaggat caagagcacc cgtggccgta tcttcgcgaa ttcttttctt taagtggtgt 540

aaataaagat tcattcaaga tgaaatgtgt cctctgtctc ccgcttaata aagaaatatc 600

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aggcttgaca ctaacaattt tgagaatcag cttctactga agttaaatct gaggttttac 180

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caagtacaat tttaatggag tacttttta cttttactca agtaagattc tagccagata 420

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gct gcg agc agc aca gtc caa aat cag cca cag gat caa gag cac ccg 159
Ala Ala Ser Ser Thr Val Gln Asn Gln Pro Gln Asp Gln Glu His Pro
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tgg ccg tat ctt cgc gaa ttc ttt tct tta agt ggt gta aat aaa gat 207
Trp Pro Tyr Leu Arg Glu Phe Phe Ser Leu Ser Gly Val Asn Lys Asp
30 35 40

tca ttc aag atg aaa tgt gtc ctc tgt ctc ccg ctt aat aaa gaa ata 255
Ser Phe Lys Met Lys Cys Val Leu Cys Leu Pro Leu Asn Lys Glu Ile
45 50 55

tcg gcc ttc aaa agt tcg cca tca aac cta agg aag cat att gag aga 303
Ser Ala Phe Lys Ser Ser Pro Ser Asn Leu Arg Lys His Ile Glu Arg
60 65 70

atg cac cca aat tac ctc aaa aac tac tct aaa ttg aca gca cag aag 351
Met His Pro Asn Tyr Leu Lys Asn Tyr Ser Lys Leu Thr Ala Gln Lys
75 80 85

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aga aag atc ggg acc tcc acc cat gct tcc agc agt aag caa ctg aaa      399
Arg Lys Ile Gly Thr Ser Thr His Ala Ser Ser Ser Lys Gln Leu Lys
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Val Asp Ser Val Phe Pro Val Lys His Val Ser Pro Val Thr Val Asn
                110                 115                 120

aaa gct ata tta agg tac atc att caa gga ctt cat cct ttc agc act      495
Lys Ala Ile Leu Arg Tyr Ile Ile Gln Gly Leu His Pro Phe Ser Thr
            125                 130                 135

gtt gat ctg cca tca ttt aaa gag ctg att agt aca ctg cag cct ggc      543
Val Asp Leu Pro Ser Phe Lys Glu Leu Ile Ser Thr Leu Gln Pro Gly
        140                 145                 150

att tct gtc att aca agg cct act tta cgc tcc aag ata gct gaa gct      591
Ile Ser Val Ile Thr Arg Pro Thr Leu Arg Ser Lys Ile Ala Glu Ala
    155                 160                 165

gct ctg atc atg aaa cag aaa gtg act gct gcc atg agt gaa gtt gaa      639
Ala Leu Ile Met Lys Gln Lys Val Thr Ala Ala Met Ser Glu Val Glu
170                 175                 180                 185

tgg att gca acc aca acg gat tgt tgg act gca cgt aga aag tca ttc      687
Trp Ile Ala Thr Thr Thr Asp Cys Trp Thr Ala Arg Arg Lys Ser Phe
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att ggt gta act gct cac tgg atc aac cct gga agt ctt gaa aga cat      735
Ile Gly Val Thr Ala His Trp Ile Asn Pro Gly Ser Leu Glu Arg His
            205                 210                 215

tcc gct gca ctt gcc tgc aaa aga tta atg ggc tct cat act ttt gag      783
Ser Ala Ala Leu Ala Cys Lys Arg Leu Met Gly Ser His Thr Phe Glu
        220                 225                 230

gta ctg gcc agt gcc atg aat gat atc cac tca gag tat gaa ata cgt      831
Val Leu Ala Ser Ala Met Asn Asp Ile His Ser Glu Tyr Glu Ile Arg
    235                 240                 245

gac aag gtt gtt tgc aca acc aca gac agt ggt tcc aac ttt atg aag      879
Asp Lys Val Val Cys Thr Thr Thr Asp Ser Gly Ser Asn Phe Met Lys
250                 255                 260                 265

gct ttc aga gtt ttt ggt gtg gaa aac aat gat atc gag act gag gca      927
Ala Phe Arg Val Phe Gly Val Glu Asn Asn Asp Ile Glu Thr Glu Ala
                270                 275                 280

aga agg tgt gaa agt gat gac act gat tct gaa ggc tgt ggt gag gga      975
Arg Arg Cys Glu Ser Asp Asp Thr Asp Ser Glu Gly Cys Gly Glu Gly
            285                 290                 295

agt gat ggt gtg gaa ttc caa gat gcc tca cga gtc ctg gac caa gac     1023
Ser Asp Gly Val Glu Phe Gln Asp Ala Ser Arg Val Leu Asp Gln Asp
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gat ggc ttc gaa ttc cag cta cca aaa cat caa aag tgt gcc tgt cac     1071
Asp Gly Phe Glu Phe Gln Leu Pro Lys His Gln Lys Cys Ala Cys His
    315                 320                 325

tta ctt aac cta gtc tca agc gtt gat gcc caa aaa gct ctc tca aat     1119
Leu Leu Asn Leu Val Ser Ser Val Asp Ala Gln Lys Ala Leu Ser Asn
330                 335                 340                 345

gaa cac tac aag aaa ctc tac aga tct gtc ttt ggc aaa tgc caa gct     1167
Glu His Tyr Lys Lys Leu Tyr Arg Ser Val Phe Gly Lys Cys Gln Ala
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tta tgg aat aaa agc agc cga tcg gct cta gca gct gaa gct gtt gaa     1215
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            365                 370                 375

tca gaa agc cgg ctt cag ctt tta agg cca aac caa acg cgg tgg aat     1263
Ser Glu Ser Arg Leu Gln Leu Leu Arg Pro Asn Gln Thr Arg Trp Asn
        380                 385                 390

tca act ttt atg gct gtt gac aga att ctt caa att tgc aaa gaa gca     1311
Ser Thr Phe Met Ala Val Asp Arg Ile Leu Gln Ile Cys Lys Glu Ala
    395                 400                 405

gga gaa ggc gca ctt cgg aat ata tgc acc tct ctt gag gtt cca atg     1359
Gly Glu Gly Ala Leu Arg Asn Ile Cys Thr Ser Leu Glu Val Pro Met
410                 415                 420                 425

ttt aat cca gca gaa atg ctg ttc ttg aca gag tgg gcc aac aca atg     1407
Phe Asn Pro Ala Glu Met Leu Phe Leu Thr Glu Trp Ala Asn Thr Met
                430                 435                 440

cgt cca gtt gca aaa gta ctc gac atc ttg caa gcg gaa acg aat aca     1455
Arg Pro Val Ala Lys Val Leu Asp Ile Leu Gln Ala Glu Thr Asn Thr
            445                 450                 455

cag ctg ggg tgg ctg ctg cct agt gtc cat cag tta agc ttg aaa ctt     1503
Gln Leu Gly Trp Leu Leu Pro Ser Val His Gln Leu Ser Leu Lys Leu
        460                 465                 470

cag cga ctc cac cat tct ctc agg tac tgt gac cca ctt gtg gat gcc     1551
Gln Arg Leu His His Ser Leu Arg Tyr Cys Asp Pro Leu Val Asp Ala
    475                 480                 485

cta caa caa gga atc caa aca cga ttc aag cat atg ttt gaa gat cct     1599
Leu Gln Gln Gly Ile Gln Thr Arg Phe Lys His Met Phe Glu Asp Pro
490                 495                 500                 505

gag atc ata gca gct gcc atc ctt ctc cct aaa ttt cgg acc tct tgg     1647
Glu Ile Ile Ala Ala Ala Ile Leu Leu Pro Lys Phe Arg Thr Ser Trp
                510                 515                 520

aca aat gat gaa acc atc ata aaa cga ggc atg gac tac atc aga gtg     1695
Thr Asn Asp Glu Thr Ile Ile Lys Arg Gly Met Asp Tyr Ile Arg Val
            525                 530                 535

cat ctg gag cct ttg gac cac aag aag gaa ttg gcc aac agt tca tct     1743
His Leu Glu Pro Leu Asp His Lys Lys Glu Leu Ala Asn Ser Ser Ser
        540                 545                 550

gat gat gaa gat ttt ttc gct tct ttg aaa ccg aca aca cat gaa gcc     1791
Asp Asp Glu Asp Phe Phe Ala Ser Leu Lys Pro Thr Thr His Glu Ala
    555                 560                 565

agc aaa gag ttg gat gga tat ctg gcc tgt gtt tca gac acc agg gag     1839
Ser Lys Glu Leu Asp Gly Tyr Leu Ala Cys Val Ser Asp Thr Arg Glu
570                 575                 580                 585

tct ctg ctc acg ttt cct gct att tgc agc ctc tct atc aag act aat     1887
Ser Leu Leu Thr Phe Pro Ala Ile Cys Ser Leu Ser Ile Lys Thr Asn
                590                 595                 600

aca cct ctt ccc gca tcg gct gcc tgt gag agg ctt ttc agc act gca     1935
Thr Pro Leu Pro Ala Ser Ala Ala Cys Glu Arg Leu Phe Ser Thr Ala
            605                 610                 615

gga ttg ctt ttc agc ccc aaa aga gct agg ctt gac act aac aat ttt     1983
Gly Leu Leu Phe Ser Pro Lys Arg Ala Arg Leu Asp Thr Asn Asn Phe
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Glu Asn Gln Leu Leu Leu Lys Leu Asn Leu Arg Phe Tyr Asn Phe Glu
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Phe Ser Leu Ser Gly Val Asn Lys Asp Ser Phe Lys Met Lys Cys Val
        35                  40                  45

Leu Cys Leu Pro Leu Asn Lys Glu Ile Ser Ala Phe Lys Ser Ser Pro
    50                  55                  60

Ser Asn Leu Arg Lys His Ile Glu Arg Met His Pro Asn Tyr Leu Lys
65                  70                  75                  80

Asn Tyr Ser Lys Leu Thr Ala Gln Lys Arg Lys Ile Gly Thr Ser Thr
                85                  90                  95

His Ala Ser Ser Ser Lys Gln Leu Lys Val Asp Ser Val Phe Pro Val
            100                 105                 110

Lys His Val Ser Pro Val Thr Val Asn Lys Ala Ile Leu Arg Tyr Ile
        115                 120                 125

Ile Gln Gly Leu His Pro Phe Ser Thr Val Asp Leu Pro Ser Phe Lys
    130                 135                 140

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

Thr Leu Arg Ser Lys Ile Ala Glu Ala Ala Leu Ile Met Lys Gln Lys
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Val Thr Ala Ala Met Ser Glu Val Glu Trp Ile Ala Thr Thr Thr Asp
            180                 185                 190

Cys Trp Thr Ala Arg Arg Lys Ser Phe Ile Gly Val Thr Ala His Trp
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Ile Asn Pro Gly Ser Leu Glu Arg His Ser Ala Ala Leu Ala Cys Lys
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Arg Leu Met Gly Ser His Thr Phe Glu Val Leu Ala Ser Ala Met Asn
225                 230                 235                 240

Asp Ile His Ser Glu Tyr Glu Ile Arg Asp Lys Val Val Cys Thr Thr
                245                 250                 255

Thr Asp Ser Gly Ser Asn Phe Met Lys Ala Phe Arg Val Phe Gly Val
            260                 265                 270

Glu Asn Asn Asp Ile Glu Thr Glu Ala Arg Arg Cys Glu Ser Asp Asp
        275                 280                 285

Thr Asp Ser Glu Gly Cys Gly Glu Gly Ser Asp Gly Val Glu Phe Gln
    290                 295                 300

Asp Ala Ser Arg Val Leu Asp Gln Asp Asp Gly Phe Glu Phe Gln Leu
305                 310                 315                 320

Pro Lys His Gln Lys Cys Ala Cys His Leu Leu Asn Leu Val Ser Ser
                325                 330                 335

Val Asp Ala Gln Lys Ala Leu Ser Asn Glu His Tyr Lys Lys Leu Tyr
            340                 345                 350

Arg Ser Val Phe Gly Lys Cys Gln Ala Leu Trp Asn Lys Ser Ser Arg
        355                 360                 365

Ser Ala Leu Ala Ala Glu Ala Val Glu Ser Glu Ser Arg Leu Gln Leu
    370                 375                 380

Leu Arg Pro Asn Gln Thr Arg Trp Asn Ser Thr Phe Met Ala Val Asp
385                 390                 395                 400

Arg Ile Leu Gln Ile Cys Lys Glu Ala Gly Glu Gly Ala Leu Arg Asn
                405                 410                 415

Ile Cys Thr Ser Leu Glu Val Pro Met Phe Asn Pro Ala Glu Met Leu
            420                 425                 430

Phe Leu Thr Glu Trp Ala Asn Thr Met Arg Pro Val Ala Lys Val Leu
        435                 440                 445

Asp Ile Leu Gln Ala Glu Thr Asn Thr Gln Leu Gly Trp Leu Leu Pro
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Ser Val His Gln Leu Ser Leu Lys Leu Gln Arg Leu His His Ser Leu
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465                 470                 475                 480

Arg Tyr Cys Asp Pro Leu Val Asp Ala Leu Gln Gln Gly Ile Gln Thr
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Arg Phe Lys His Met Phe Glu Asp Pro Glu Ile Ile Ala Ala Ala Ile
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Leu Leu Pro Lys Phe Arg Thr Ser Trp Thr Asn Asp Glu Thr Ile Ile
        515                 520                 525

Lys Arg Gly Met Asp Tyr Ile Arg Val His Leu Glu Pro Leu Asp His
    530                 535                 540

Lys Lys Glu Leu Ala Asn Ser Ser Ser Asp Asp Glu Asp Phe Phe Ala
545                 550                 555                 560

Ser Leu Lys Pro Thr Thr His Glu Ala Ser Lys Glu Leu Asp Gly Tyr
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Leu Ala Cys Val Ser Asp Thr Arg Glu Ser Leu Leu Thr Phe Pro Ala
            580                 585                 590

Ile Cys Ser Leu Ser Ile Lys Thr Asn Thr Pro Leu Pro Ala Ser Ala
        595                 600                 605

Ala Cys Glu Arg Leu Phe Ser Thr Ala Gly Leu Leu Phe Ser Pro Lys
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<213> Oryzias latipes

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ccaagacgat ggcttcgaat tccagctacc aaaacatcaa aagtgtgcct gtcacttact 2940

taacctagtc tcaagcgttg atgcccaaaa agctctctca aatgaacact acaagaaact 3000

ctacagatct gtctttggca aatgccaagc tttatggaat aaaagcagcc gatcggctct 3060

agcagctgaa gctgttgaat cagaaagccg gcttcagctt ttaaggccaa accaaacgcg 3120

gtggaattca acttttatgg ctgttgacag aattcttcaa atttgcaaag aagcaggaga 3180

aggcgcactt cggaatatat gcacctctct tgaggttcca atgtaagtgt ttttcccctc 3240

tatcgatgta aacaaatgtg ggttgttttt gtttaatact ctttgattat gctgatttct 3300

cctgtaggtt taatccagca gaaatgctgt tcttgacaga gtgggccaac acaatgcgtc 3360

cagttgcaaa agtactcgac atcttgcaag cggaaacgaa tacacagctg gggtggctgc 3420

tgcctagtgt ccatcagtta agcttgaaac ttcagcgact ccaccattct ctcaggtact 3480

gtgacccact tgtggatgcc ctacaacaag gaatccaaac acgattcaag catatgtttg 3540

aagatcctga gatcatagca gctgccatcc ttctccctaa atttcggacc tcttggacaa 3600

atgatgaaac catcataaaa cgaggtaaat gaatgcaagc aacatacact tgacgaattc 3660

taatctgggc aacctttgag ccataccaaa attattcttt tatttattta tttttgcact 3720

ttttaggaat gttatatccc atctttggct gtgatctcaa tatgaatatt gatgtaaagt 3780

attcttgcag caggttgtag ttatccctca gtgtttcttg aaaccaaact catatgtatc 3840

atatgtggtt tggaaatgca gttagatttt atgctaaaat aagggatttg catgatttta 3900

gatgtagatg actgcacgta aatgtagtta atgacaaaat ccataaaatt tgttcccagt 3960

cagaagcccc tcaaccaaac ttttctttgt gtctgctcac tgtgcttgta ggcatggact 4020

acatcagagt gcatctggag cctttggacc acaagaagga attggccaac agttcatctg 4080

atgatgaaga ttttttcgct tctttgaaac cgacaacaca tgaagccagc aaagagttgg 4140

atggatatct ggcctgtgtt tcagacacca gggagtctct gctcacgttt cctgctattt 4200

gcagcctctc tatcaagact aatacacctc ttcccgcatc ggctgcctgt gagaggcttt 4260

tcagcactgc aggattgctt ttcagcccca aaagagctag gcttgacact aacaattttg 4320

agaatcagct tctactgaag ttaaatctga ggttttacaa ctttgagtag cgtgtactgg 4380

cattagattg tctgtcttat agtttgataa ttaaatacaa acagttctaa agcaggataa 4440

aaccttgtat gcatttcatt taatgttttt tgagattaaa agcttaaaca agaatctcta 4500

gttttctttc ttgcttttac ttttacttcc ttaatactca agtacaattt taatggagta 4560

ctttttact tttactcaag taagattcta gccagatact tttactttta attgagtaaa 4620

attttcccta agtacttgta ctttcacttg agtaaaattt ttgagtactt tttacacctc 4680

tg 4682

<210> 7
<211> 321
<212> DNA
<213> Artificial

<220>
<223> Description of artificial sequence; Cycloheximide resistant gene

<220>
<221> CDS
<222> (1)..(321)

<400> 7
atg gtc aac gta cct aaa acc cga aga acc ttc tgt aag aag tgt ggc 48
Met Val Asn Val Pro Lys Thr Arg Arg Thr Phe Cys Lys Lys Cys Gly
1 5 10 15

aag cat cag cct cac aaa gtg aca cag tat aag aag ggc aag gat tct 96
Lys His Gln Pro His Lys Val Thr Gln Tyr Lys Lys Gly Lys Asp Ser
20 25 30

ttg tat gcc cag gga agg agg cgc tat gat cgg aag cag agt ggc tat 144
Leu Tyr Ala Gln Gly Arg Arg Arg Tyr Asp Arg Lys Gln Ser Gly Tyr
35 40 45

ggt ggg cag aca aag caa att ttc cgg aag aag gct aag acc aca aag 192
Gly Gly Gln Thr Lys Gln Ile Phe Arg Lys Lys Ala Lys Thr Thr Lys
50 55 60

aag att gtg cta agg ctg gaa tgt gtt gag cct aac tgc aga tcc aag 240
Lys Ile Val Leu Arg Leu Glu Cys Val Glu Pro Asn Cys Arg Ser Lys
65 70 75 80

agg atg ctg gcc att aag aga tgc aag cat ttt gaa ctg gga gga gat 288
Arg Met Leu Ala Ile Lys Arg Cys Lys His Phe Glu Leu Gly Gly Asp
85 90 95

aag aag aga aag ggc caa gtg atc cag ttc taa 321
Lys Lys Arg Lys Gly Gln Val Ile Gln Phe
100 105

<210> 8
<211> 106
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 8

Met Val Asn Val Pro Lys Thr Arg Arg Thr Phe Cys Lys Lys Cys Gly
1 5 10 15

Lys His Gln Pro His Lys Val Thr Gln Tyr Lys Lys Gly Lys Asp Ser
20 25 30

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Leu Tyr Ala Gln Gly Arg Arg Arg Tyr Asp Arg Lys Gln Ser Gly Tyr
        35                  40                  45

Gly Gly Gln Thr Lys Gln Ile Phe Arg Lys Lys Ala Lys Thr Thr Lys
    50                  55                  60

Lys Ile Val Leu Arg Leu Glu Cys Val Glu Pro Asn Cys Arg Ser Lys
65                  70                  75                  80

Arg Met Leu Ala Ile Lys Arg Cys Lys His Phe Glu Leu Gly Gly Asp
                85                  90                  95

Lys Lys Arg Lys Gly Gln Val Ile Gln Phe
            100                 105
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<210> 9
<211> 1404
<212> DNA
<213> Artificial

<220>
<223> M2Z3 Heavy chain

<220>
<221> CDS
<222> (1)..(1404)

<400> 9

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atg gac tgg acc tgg agc atc ctt ttc ttg gtg gca gca gca aca ggt       48
Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1               5                   10                  15

gcc cac tcc cag gtt cag ctg gtg cag tct gga gct gag gtg aag aag       96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gcc tca gtg aag gtc tcc tgc aag gct tct ggt tac acc ttt      144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc agc tat ggt atc agc tgg gtg cga cag gcc cct gga caa ggg ctt      192
Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

gag tgg atg gga tgg atc agc gct tac aat ggt aac aca aac tat gca      240
Glu Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala
65                  70                  75                  80

cag aag ctc cag ggc aga gtc acc atg acc aca gac aca tcc acg agc      288
Gln Lys Leu Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
                85                  90                  95

aca gcc tac atg gag ctg agg agc ctg aga tct gac gac acg gcc gtg      336
Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
            100                 105                 110

tat tac tgt gcg agg gca gca gct ggc gga tac ttc cag cac tgg ggc      384
Tyr Tyr Cys Ala Arg Ala Ala Ala Gly Gly Tyr Phe Gln His Trp Gly
        115                 120                 125

cag ggc acc ctg gtc acc gtc tcc tca gct agc acc aag ggc cca tcg      432
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```
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg      480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc     1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc     1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg     1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc     1152
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag     1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc     1248
```

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

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg     1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg     1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct     1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccg ggt aaa tga                                                     1404
Pro Gly Lys
465
```

<210> 10
<211> 467
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 10

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Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1               5                   10                  15

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

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

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

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

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

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

Tyr Tyr Cys Ala Arg Ala Ala Ala Gly Gly Tyr Phe Gln His Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160
```

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

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

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

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His
        275                 280                 285

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val
            420                 425                 430
```

```
Asp Lys Ser Arg Trp Gln Gln 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


Pro Gly Lys
465


<210>  11
<211>  708
<212>  DNA
<213>  Artificial

<220>
<223>  M2Z3 Light chian


<220>
<221>  CDS
<222>  (1)..(708)

<400>  11
atg gcc agc ttc cct ctc ctc ctc acc ctc ctc act cac tgt gca ggg       48
Met Ala Ser Phe Pro Leu Leu Leu Thr Leu Leu Thr His Cys Ala Gly
1               5                   10                  15

tcc tgg gcc cag tct gtg ctg act cag cca ccc tca gcg tct ggg acc       96
Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr
            20                  25                  30

ccc ggg cag agg gtc acc atc tct tgt tct gga agc aac tcc aac atc      144
Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Asn Ser Asn Ile
        35                  40                  45

gga agt aaa act gta aac tgg tac cag cag ctc cca gga acg gcc ccc      192
Gly Ser Lys Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro
    50                  55                  60

aaa ctc ctc atc tct agt aat aat cag cgg ccc tca ggg gtc cct gac      240
Lys Leu Leu Ile Ser Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp
65                  70                  75                  80

cga ttc tct ggc tcc aag tct ggc acc tca gcc tcc ctg gcc atc agt      288
Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser
                85                  90                  95

ggg ctc cag tct gag gat gag gct gat tat tac tgt gca gca tgg gat      336
Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp
            100                 105                 110

gac agc ctg aat ggt gtg gta ttc ggc gga ggg acc aag ctg acc gtc      384
Asp Ser Leu Asn Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val
        115                 120                 125

cta ggt cag ccc aag gct gcc ccc tcg gtc act ctg ttc cca ccc tcc      432
Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser
    130                 135                 140

tct gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt      480
Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
145                 150                 155                 160
```

```
gac ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc      528
Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser
                165                 170                 175

ccc gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac      576
Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn
            180                 185                 190

aac aag tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg      624
Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
        195                 200                 205

aag tcc cac aaa agc tac agc tgc cag gtc acg cat gaa ggg agc acc      672
Lys Ser His Lys Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr
    210                 215                 220

gtg gag aag aca gtg gcc cct aca gaa tgt tca tag                      708
Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225                 230                 235


<210>  12
<211>  235
<212>  PRT
<213>  Artificial

<220>
<223>  Synthetic Construct

<400>  12

Met Ala Ser Phe Pro Leu Leu Leu Thr Leu Leu Thr His Cys Ala Gly
1               5                   10                  15


Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr
            20                  25                  30


Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Asn Ser Asn Ile
        35                  40                  45


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


Lys Leu Leu Ile Ser Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp
65                  70                  75                  80


Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser
                85                  90                  95


Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp
            100                 105                 110


Asp Ser Leu Asn Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val
        115                 120                 125


Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser
    130                 135                 140


Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
```

```
145                 150                 155                 160

Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser
                165                 170                 175

Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn
            180                 185                 190

Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
        195                 200                 205

Lys Ser His Lys Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr
    210                 215                 220

Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225                 230                 235
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<210> 13
<211> 1855
<212> DNA
<213> artificial

<220>
<223> nonautologus Tol1 transposon

<400> 13

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cagtagcggt tctaggcacg ggccgtccgg gcggtggcct ggggcggaaa actgaagggg     60

ggcggcaccg gcggctcagc cctttgtaat atattaatat gcaccactat tggtttactt    120

atgtcacagt ttgtaagttt gtaacagcct gaacctggcc gcgccgccgc cctcgccccg    180

cagctgcgct ctcctgtctt tgagaagtag acacaaatgt gtgtgaagaa ggagaaggga    240

gggggcgcgg ggtgagcacg gagcgtcgcc gcgtttgcgc atgcgcaaaa cctggctggc    300

tcatctttca ggggaggcga cggtcgcggg cttgatgaaa aaaataaaag taaaaactgc    360

gactgcgccg tcatgtagcg aatcagcgcc cctggctgta gctgcacgcg ctcctgctgg    420

aaatgtgtga agaggggggg gggggggggg gctgcgggga atcagttcaa ttgtgggacg    480

cttccaaatt aagtggctag gtggggacaa gggcgggggt ttgaatctac ttcataaaac    540

ctttttatat tataagtcag tcataaggtg acattctata acctacattt taataaaggt    600

ataaaaaata tattctgctt tttttgggtt aattttgtgt gaaatgtcca aataaaaaaa    660

atggcaacac aaaacaatgc tgtcactaag gtgacagttg gttcagtcga cggacttgat    720

gccttcttcg tgacgtgagg acatttatgc caaacaaacg ccaataaaca tctaaaatat    780

ggaaaagaaa aggtcaaagc catctggtgc ccaatttaga aagaaaagaa aagaagaaga    840

ggagaaaaga gataaagaaa agggtaagtc ctcacagctt gatgcatgtt ttttctaaat    900

tctaatgcta cctgccctac aacaacgttg ccgatgaaaa ctttattttg gtcgatgacc    960

aacactgaat taggcccaaa tgttgcaaat agcgtcattt ttttttttt ttttagattt   1020

tattcttaaa aatttgctct gccttaactt gtaacattag ttatgattca tgtgtctgtc   1080
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tgctctgctg taacacaaag gttttgttgg gttttgctgt tgtatactag ctcataatgt 1140

taaaaaagct gtgatggtta cacagcatgc tggtgctgcc ataagatgct aatggggcaa 1200

ataatttgag attggtcatt aatttaataa tcatttgtgg cagcctaaac gttttcacaa 1260

tgtttttttg acatttaact ggggatttag gggttaattt tgagcctgca tatgaagttt 1320

atttttatt tgttttacaa atgtgggatt atatttttag ccaatagaat ttccataaat 1380

ctgtaggtag ttttaaaaat gaatatttac catttactgc aactctatgg ggacaaaaca 1440

taatgtaaca ggtcataact aaaaatgtgc caatcaaagg attgaagacg gaaaacatga 1500

gttaattttt cttctctgaa gtagagatcg atatagaaca tgacaattta aatttccaat 1560

tcataaatgt ttttaaaata tttattttat attatttatt taacattgag tttgattcaa 1620

tattttctta gctaactgta tttttgccat gcttatggtc ttttatttt tgtgttctga 1680

taacttttat aatgcttttc agaattttga catcttttgt atccacttct taatttcaat 1740

gacaataaaa catttcagtt gacgaagaca aacaaagttc tgttgtgact atgggggggg 1800

ggggcgcctg gggatggtct cgcccgggga gtaattcagg gtagaaccgc cactg 1855

<210> 14
<211> 200
<212> DNA
<213> artificial

<220>
<223> Tol1-L transposon sequence

<400> 14
cagtagcggt tctaggcacg ggccgtccgg gcggtggcct ggggcggaaa actgaagggg 60

ggcggcaccg gcggctcagc cctttgtaat atattaatat gcaccactat tggtttactt 120

atgtcacagt ttgtaagttt gtaacagcct gaacctggcc gcgccgccgc cctcgccccg 180

cagctgcgct ctcctgtctt 200

<210> 15
<211> 505
<212> DNA
<213> artificial

<220>
<223> Tol1-R transoposon sequence

<400> 15
atatttttag ccaatagaat ttccataaat ctgtaggtag ttttaaaaat gaatatttac 60

catttactgc aactctatgg ggacaaaaca taatgtaaca ggtcataact aaaaatgtgc 120

caatcaaagg attgaagacg gaaaacatga gttaattttt cttctctgaa gtagagatcg 180

atatagaaca tgacaattta aatttccaat tcataaatgt ttttaaaata tttattttat 240

attatttatt taacattgag tttgattcaa tattttctta gctaactgta tttttgccat 300

gcttatggtc ttttatttt tgtgttctga taacttttat aatgcttttc agaattttga 360

catcttttgt atccacttct taatttcaat gacaataaaa catttcagtt gacgaagaca 420

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aacaaagttc tgttgtgact atgggggggg ggggcgcctg gggatggtct cgcccgggga    480

gtaattcagg gtagaaccgc cactg                                          505


<210>  16
<211>  2745
<212>  DNA
<213>  Oryzias latipes


<220>
<221>  CDS
<222>  (30)..(2585)

<400>  16
gccaaacaaa cgccaaaaac atctaaaat atg gag aaa aaa agg tca aag cca       53
                                   Met Glu Lys Lys Arg Ser Lys Pro
                                   1               5

tct ggt gcc caa ttt aga aag aaa aga aaa gaa gaa gag gag aaa aga      101
Ser Gly Ala Gln Phe Arg Lys Lys Arg Lys Glu Glu Glu Glu Lys Arg
    10                  15                  20

gat aaa gaa aag ggg gca ctt cta aga tat ttt gga tcg tct acc act      149
Asp Lys Glu Lys Gly Ala Leu Leu Arg Tyr Phe Gly Ser Ser Thr Thr
25                  30                  35                  40

gct caa gat gag aca tct acc tcc ctg cca gct atc tca tca gcc aca      197
Ala Gln Asp Glu Thr Ser Thr Ser Leu Pro Ala Ile Ser Ser Ala Thr
                45                  50                  55

gtc aca gtc tca ccc cct cag gat gag cta cca tct aca tcc tct gct      245
Val Thr Val Ser Pro Pro Gln Asp Glu Leu Pro Ser Thr Ser Ser Ala
            60                  65                  70

act cat gta gtt cca cag ttg tta cct gag caa agt ttt gat agt gag      293
Thr His Val Val Pro Gln Leu Leu Pro Glu Gln Ser Phe Asp Ser Glu
        75                  80                  85

gct gaa gac gtt gtt cca tct acg tct acc cag ctt gag act tca gaa      341
Ala Glu Asp Val Val Pro Ser Thr Ser Thr Gln Leu Glu Thr Ser Glu
    90                  95                  100

atg cct ggt gat gaa acc cca ctg acc ccg act gct gag gac cag cct      389
Met Pro Gly Asp Glu Thr Pro Leu Thr Pro Thr Ala Glu Asp Gln Pro
105                 110                 115                 120

cta cca act gac cct gca aag tgg ccc tca cct ctg act gac agg ata      437
Leu Pro Thr Asp Pro Ala Lys Trp Pro Ser Pro Leu Thr Asp Arg Ile
                125                 130                 135

cgg atg gag ctg gtt cga aga gga cca agt agc ata cca cct gac ttt      485
Arg Met Glu Leu Val Arg Arg Gly Pro Ser Ser Ile Pro Pro Asp Phe
            140                 145                 150

gtt ttc cca aga aat gac agt gat ggg aga agt tgt cat cac cac tat      533
Val Phe Pro Arg Asn Asp Ser Asp Gly Arg Ser Cys His His His Tyr
        155                 160                 165

ttc agg aag aca cta gta agt ggt gaa aaa ata gca aga act tgg ttg      581
Phe Arg Lys Thr Leu Val Ser Gly Glu Lys Ile Ala Arg Thr Trp Leu
    170                 175                 180

atg tat tca aaa gtg aag aac agc ctc ttt tgc ttt tgt tgc aaa ttg      629
Met Tyr Ser Lys Val Lys Asn Ser Leu Phe Cys Phe Cys Cys Lys Leu
185                 190                 195                 200
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ttt tcc aac aaa aac att aat tta aca act tct ggt aca gca aac tgg      677
Phe Ser Asn Lys Asn Ile Asn Leu Thr Thr Ser Gly Thr Ala Asn Trp
                205                 210                 215

aaa cat gca agc aca tac ctc aca gca cac gaa aaa agc cca gaa cac      725
Lys His Ala Ser Thr Tyr Leu Thr Ala His Glu Lys Ser Pro Glu His
            220                 225                 230

ctc aat tgt atg aaa gca tgg aag gaa ctg tca ggg agg atc aga agt      773
Leu Asn Cys Met Lys Ala Trp Lys Glu Leu Ser Gly Arg Ile Arg Ser
        235                 240                 245

ggg aaa aca att gat aag cag gag atg gca ctt ctg gaa gag gag cgg      821
Gly Lys Thr Ile Asp Lys Gln Glu Met Ala Leu Leu Glu Glu Glu Arg
    250                 255                 260

gtg aga tgg aga gca gtg cta acc cgt ctc att gct att gtg cag tca      869
Val Arg Trp Arg Ala Val Leu Thr Arg Leu Ile Ala Ile Val Gln Ser
265                 270                 275                 280

ctg gca gtt cgg aat ttg gct cta agg gga cac aca gaa aca ctg ttc      917
Leu Ala Val Arg Asn Leu Ala Leu Arg Gly His Thr Glu Thr Leu Phe
                285                 290                 295

aca tca tca aat ggg aat ttt ttg aaa gag gtt gaa ctg atg gcc agg      965
Thr Ser Ser Asn Gly Asn Phe Leu Lys Glu Val Glu Leu Met Ala Arg
            300                 305                 310

ttt gat ccc ata atg aaa gat cat ctt aac cgt gta tta aga gga aca     1013
Phe Asp Pro Ile Met Lys Asp His Leu Asn Arg Val Leu Arg Gly Thr
        315                 320                 325

gca agt cac aac agc tac ata ggc cat cat gtg cag aat gaa ctt att     1061
Ala Ser His Asn Ser Tyr Ile Gly His His Val Gln Asn Glu Leu Ile
    330                 335                 340

gat ttg ttg agc agc aaa atc cta tcc gct ata gtg gat gac atc aaa     1109
Asp Leu Leu Ser Ser Lys Ile Leu Ser Ala Ile Val Asp Asp Ile Lys
345                 350                 355                 360

aag gca aaa tat ttt tca ata att ctg gac tgc act ctg gat ata agc     1157
Lys Ala Lys Tyr Phe Ser Ile Ile Leu Asp Cys Thr Leu Asp Ile Ser
                365                 370                 375

cac aca gaa cag ttg tca gtt ata att aga gtg gtg tca ctg atg gag     1205
His Thr Glu Gln Leu Ser Val Ile Ile Arg Val Val Ser Leu Met Glu
            380                 385                 390

aag cct cag atc agg gaa cat ttt atg ggg ttt ttg gag gca gag gag     1253
Lys Pro Gln Ile Arg Glu His Phe Met Gly Phe Leu Glu Ala Glu Glu
        395                 400                 405

tcc aca ggc cag cac ttg gca tcc atg atc tta aac aga ctt gag gag     1301
Ser Thr Gly Gln His Leu Ala Ser Met Ile Leu Asn Arg Leu Glu Glu
    410                 415                 420

tta gga att tct ttt gaa gac tgc aga gga caa tca tat gat aat ggg     1349
Leu Gly Ile Ser Phe Glu Asp Cys Arg Gly Gln Ser Tyr Asp Asn Gly
425                 430                 435                 440

gca aat atg aaa ggc aaa aat aag gga gta caa gcc agg ctc tta gaa     1397
Ala Asn Met Lys Gly Lys Asn Lys Gly Val Gln Ala Arg Leu Leu Glu
                445                 450                 455

aag aat ccc cgt gct ctg ttt ttg cca tgc ggt gca cac aca ttg aat     1445
Lys Asn Pro Arg Ala Leu Phe Leu Pro Cys Gly Ala His Thr Leu Asn
            460                 465                 470
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tta gtt gtg tgt gat gct gct aag aga tct gtt gat gct atg agc tac     1493
Leu Val Val Cys Asp Ala Ala Lys Arg Ser Val Asp Ala Met Ser Tyr
        475                 480                 485

ttt ggt gtc ctg caa aag ctt tac act tta ttt tca gcc tct gcc caa     1541
Phe Gly Val Leu Gln Lys Leu Tyr Thr Leu Phe Ser Ala Ser Ala Gln
    490                 495                 500

cga tgg gcc ata ctg aag agt cag gtg agc atc act cta aag tcg tgg     1589
Arg Trp Ala Ile Leu Lys Ser Gln Val Ser Ile Thr Leu Lys Ser Trp
505                 510                 515                 520

aca gaa aca agg tgg gag agc aaa atc aaa agc atc gag ccc atg agg     1637
Thr Glu Thr Arg Trp Glu Ser Lys Ile Lys Ser Ile Glu Pro Met Arg
                525                 530                 535

tac cag gga gct gca gtg aga gag gct tta ata gaa gtg aga gac aag     1685
Tyr Gln Gly Ala Ala Val Arg Glu Ala Leu Ile Glu Val Arg Asp Lys
            540                 545                 550

acc aaa gac cca gtt ata aag gct gag gcc cag tct ttg tct gaa gag     1733
Thr Lys Asp Pro Val Ile Lys Ala Glu Ala Gln Ser Leu Ser Glu Glu
        555                 560                 565

gta ggg tcg tac cgc ttc aac atc tgc aca gtc gta tgg cat gac att     1781
Val Gly Ser Tyr Arg Phe Asn Ile Cys Thr Val Val Trp His Asp Ile
    570                 575                 580

cta tct aca ata aag cat gtc agc aaa ctc atg cag tct cca aat atg     1829
Leu Ser Thr Ile Lys His Val Ser Lys Leu Met Gln Ser Pro Asn Met
585                 590                 595                 600

cat gtg gac cta gct gtg agt ctt ttg aag aag act gaa caa agt ctc     1877
His Val Asp Leu Ala Val Ser Leu Leu Lys Lys Thr Glu Gln Ser Leu
                605                 610                 615

cag agc tac agg gca aat ggc ttt gtg aat gca cag atg gca gcc aaa     1925
Gln Ser Tyr Arg Ala Asn Gly Phe Val Asn Ala Gln Met Ala Ala Lys
            620                 625                 630

gaa atg tgc aag gaa atg aat gtc gag gct att ttg aaa caa aaa aga     1973
Glu Met Cys Lys Glu Met Asn Val Glu Ala Ile Leu Lys Gln Lys Arg
        635                 640                 645

ata aga tcc aca aag tgc caa ttc tcg tat gaa tca cac gat gag cct     2021
Ile Arg Ser Thr Lys Cys Gln Phe Ser Tyr Glu Ser His Asp Glu Pro
    650                 655                 660

ttc agt gac gca ctt aaa aag ttg gag gtt gaa ttt ttc aat gtt gtt     2069
Phe Ser Asp Ala Leu Lys Lys Leu Glu Val Glu Phe Phe Asn Val Val
665                 670                 675                 680

gtt gat gaa gcc ttg tca gcc atc gcg gag agg ttt tcc aca ttg gaa     2117
Val Asp Glu Ala Leu Ser Ala Ile Ala Glu Arg Phe Ser Thr Leu Glu
                685                 690                 695

gtt gta caa aac aga ttt ggg gtt ttg acc aat ttc cca agc ctt gga     2165
Val Val Gln Asn Arg Phe Gly Val Leu Thr Asn Phe Pro Ser Leu Gly
            700                 705                 710

gac gag gag ctg acg gag caa tgc gag gca cta ggc aac ata ctc cat     2213
Asp Glu Glu Leu Thr Glu Gln Cys Glu Ala Leu Gly Asn Ile Leu His
        715                 720                 725

ttt gag aag aac tgg gat ttg gac agt aga gag ctt gtt cag gaa atc     2261
Phe Glu Lys Asn Trp Asp Leu Asp Ser Arg Glu Leu Val Gln Glu Ile
    730                 735                 740
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aag aac ttg cct aac tta cca tca acg act cca agt ctc ctt gag ctc     2309
Lys Asn Leu Pro Asn Leu Pro Ser Thr Thr Pro Ser Leu Leu Glu Leu
745                 750                 755                 760

atc tct ttc atg tct gat aag gat cta tca gaa atc tat ccg aac ttt     2357
Ile Ser Phe Met Ser Asp Lys Asp Leu Ser Glu Ile Tyr Pro Asn Phe
                765                 770                 775

tgg act gct ctc agg att gca ctc acc ttg cca gtc act gtg gct caa     2405
Trp Thr Ala Leu Arg Ile Ala Leu Thr Leu Pro Val Thr Val Ala Gln
            780                 785                 790

gca gag agg agc ttt tca aaa cta aaa ttg atc aag tcg tac ctg agg     2453
Ala Glu Arg Ser Phe Ser Lys Leu Lys Leu Ile Lys Ser Tyr Leu Arg
        795                 800                 805

tca aca atg tca cag gag cga ctc act aac ctt gcc gtt gtt agc atc     2501
Ser Thr Met Ser Gln Glu Arg Leu Thr Asn Leu Ala Val Val Ser Ile
    810                 815                 820

aat cac tca gta ggg gag cag ata tca tat gat gat gtt att gac gag     2549
Asn His Ser Val Gly Glu Gln Ile Ser Tyr Asp Asp Val Ile Asp Glu
825                 830                 835                 840

ttt gca tca aga aag gct agg aag gtt agg ttt tag ttggtgtttt          2595
Phe Ala Ser Arg Lys Ala Arg Lys Val Arg Phe
                845                 850

ctgttattgt attggtgctg cagttatatt tattttagcg tgtcatttgt gtgataaaag   2655

gtttgtgctt tataatattt attttatatt atttattcaa tattgagttt gattcaatat   2715

tttcttagct aactgtattt ttgccatgct                                   2745
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<210> 17
<211> 851
<212> PRT
<213> Oryzias latipes

<400> 17

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Met Glu Lys Lys Arg Ser Lys Pro Ser Gly Ala Gln Phe Arg Lys Lys
1               5                   10                  15

Arg Lys Glu Glu Glu Glu Lys Arg Asp Lys Glu Lys Gly Ala Leu Leu
            20                  25                  30

Arg Tyr Phe Gly Ser Ser Thr Thr Ala Gln Asp Glu Thr Ser Thr Ser
        35                  40                  45

Leu Pro Ala Ile Ser Ser Ala Thr Val Thr Val Ser Pro Pro Gln Asp
    50                  55                  60

Glu Leu Pro Ser Thr Ser Ser Ala Thr His Val Val Pro Gln Leu Leu
65                  70                  75                  80

Pro Glu Gln Ser Phe Asp Ser Glu Ala Glu Asp Val Val Pro Ser Thr
                85                  90                  95

Ser Thr Gln Leu Glu Thr Ser Glu Met Pro Gly Asp Glu Thr Pro Leu
            100                 105                 110
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Thr Pro Thr Ala Glu Asp Gln Pro Leu Pro Thr Asp Pro Ala Lys Trp
        115                 120                 125

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

Pro Ser Ser Ile Pro Pro Asp Phe Val Phe Pro Arg Asn Asp Ser Asp
145                 150                 155                 160

Gly Arg Ser Cys His His His Tyr Phe Arg Lys Thr Leu Val Ser Gly
                165                 170                 175

Glu Lys Ile Ala Arg Thr Trp Leu Met Tyr Ser Lys Val Lys Asn Ser
            180                 185                 190

Leu Phe Cys Phe Cys Cys Lys Leu Phe Ser Asn Lys Asn Ile Asn Leu
        195                 200                 205

Thr Thr Ser Gly Thr Ala Asn Trp Lys His Ala Ser Thr Tyr Leu Thr
    210                 215                 220

Ala His Glu Lys Ser Pro Glu His Leu Asn Cys Met Lys Ala Trp Lys
225                 230                 235                 240

Glu Leu Ser Gly Arg Ile Arg Ser Gly Lys Thr Ile Asp Lys Gln Glu
                245                 250                 255

Met Ala Leu Leu Glu Glu Glu Arg Val Arg Trp Arg Ala Val Leu Thr
            260                 265                 270

Arg Leu Ile Ala Ile Val Gln Ser Leu Ala Val Arg Asn Leu Ala Leu
        275                 280                 285

Arg Gly His Thr Glu Thr Leu Phe Thr Ser Ser Asn Gly Asn Phe Leu
    290                 295                 300

Lys Glu Val Glu Leu Met Ala Arg Phe Asp Pro Ile Met Lys Asp His
305                 310                 315                 320

Leu Asn Arg Val Leu Arg Gly Thr Ala Ser His Asn Ser Tyr Ile Gly
                325                 330                 335

His His Val Gln Asn Glu Leu Ile Asp Leu Leu Ser Ser Lys Ile Leu
            340                 345                 350

Ser Ala Ile Val Asp Asp Ile Lys Lys Ala Lys Tyr Phe Ser Ile Ile
        355                 360                 365

Leu Asp Cys Thr Leu Asp Ile Ser His Thr Glu Gln Leu Ser Val Ile
    370                 375                 380
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Ile Arg Val Val Ser Leu Met Glu Lys Pro Gln Ile Arg Glu His Phe
385                 390                 395                 400

Met Gly Phe Leu Glu Ala Glu Glu Ser Thr Gly Gln His Leu Ala Ser
                405                 410                 415

Met Ile Leu Asn Arg Leu Glu Glu Leu Gly Ile Ser Phe Glu Asp Cys
            420                 425                 430

Arg Gly Gln Ser Tyr Asp Asn Gly Ala Asn Met Lys Gly Lys Asn Lys
        435                 440                 445

Gly Val Gln Ala Arg Leu Leu Glu Lys Asn Pro Arg Ala Leu Phe Leu
    450                 455                 460

Pro Cys Gly Ala His Thr Leu Asn Leu Val Val Cys Asp Ala Ala Lys
465                 470                 475                 480

Arg Ser Val Asp Ala Met Ser Tyr Phe Gly Val Leu Gln Lys Leu Tyr
                485                 490                 495

Thr Leu Phe Ser Ala Ser Ala Gln Arg Trp Ala Ile Leu Lys Ser Gln
            500                 505                 510

Val Ser Ile Thr Leu Lys Ser Trp Thr Glu Thr Arg Trp Glu Ser Lys
        515                 520                 525

Ile Lys Ser Ile Glu Pro Met Arg Tyr Gln Gly Ala Ala Val Arg Glu
    530                 535                 540

Ala Leu Ile Glu Val Arg Asp Lys Thr Lys Asp Pro Val Ile Lys Ala
545                 550                 555                 560

Glu Ala Gln Ser Leu Ser Glu Glu Val Gly Ser Tyr Arg Phe Asn Ile
                565                 570                 575

Cys Thr Val Val Trp His Asp Ile Leu Ser Thr Ile Lys His Val Ser
            580                 585                 590

Lys Leu Met Gln Ser Pro Asn Met His Val Asp Leu Ala Val Ser Leu
        595                 600                 605

Leu Lys Lys Thr Glu Gln Ser Leu Gln Ser Tyr Arg Ala Asn Gly Phe
    610                 615                 620

Val Asn Ala Gln Met Ala Ala Lys Glu Met Cys Lys Glu Met Asn Val
625                 630                 635                 640

Glu Ala Ile Leu Lys Gln Lys Arg Ile Arg Ser Thr Lys Cys Gln Phe
                645                 650                 655
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Ser Tyr Glu Ser His Asp Glu Pro Phe Ser Asp Ala Leu Lys Lys Leu
            660                 665                 670

Glu Val Glu Phe Phe Asn Val Val Val Asp Glu Ala Leu Ser Ala Ile
        675                 680                 685

Ala Glu Arg Phe Ser Thr Leu Glu Val Val Gln Asn Arg Phe Gly Val
    690                 695                 700

Leu Thr Asn Phe Pro Ser Leu Gly Asp Glu Glu Leu Thr Glu Gln Cys
705                 710                 715                 720

Glu Ala Leu Gly Asn Ile Leu His Phe Glu Lys Asn Trp Asp Leu Asp
                725                 730                 735

Ser Arg Glu Leu Val Gln Glu Ile Lys Asn Leu Pro Asn Leu Pro Ser
            740                 745                 750

Thr Thr Pro Ser Leu Leu Glu Leu Ile Ser Phe Met Ser Asp Lys Asp
        755                 760                 765

Leu Ser Glu Ile Tyr Pro Asn Phe Trp Thr Ala Leu Arg Ile Ala Leu
    770                 775                 780

Thr Leu Pro Val Thr Val Ala Gln Ala Glu Arg Ser Phe Ser Lys Leu
785                 790                 795                 800

Lys Leu Ile Lys Ser Tyr Leu Arg Ser Thr Met Ser Gln Glu Arg Leu
                805                 810                 815

Thr Asn Leu Ala Val Val Ser Ile Asn His Ser Val Gly Glu Gln Ile
            820                 825                 830

Ser Tyr Asp Asp Val Ile Asp Glu Phe Ala Ser Arg Lys Ala Arg Lys
        835                 840                 845

Val Arg Phe
    850
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<210> 18
<211> 417
<212> DNA
<213> Artificial

<220>
<223> Description of the artificial sequence: VH region of anti-CD98 antibody

<220>
<221> CDS
<222> (1)..(417)

<400> 18
atg aag cac ctg tgg ttc ttc ctc ctg ctg gtg gcg gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtc ctg tcc cag ctg cag ctg cag gag tcg ggc cca gga ctg gtg aag 96
Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
20 25 30

cct tcg gag acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc 144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
35 40 45

agc agt agt agt tac tac tgg ggc tgg atc cgc cag ccc cca ggg aag 192
Ser Ser Ser Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

ggg ctg gag tgg att ggg agt atc tat tat agt ggg agt acc tac tac 240
Gly Leu Glu Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr
65 70 75 80

aac ccg tcc ctc aag agt cga gtc acc ata tcc gta gac acg tcc aag 288
Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
85 90 95

aac cag ttc tcc ctg aag ctg agc tct gtg acc gcc gca gac acg gct 336
Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

gtg tat tac tgt gcg aga caa ggg acg ggg ctc gcc cta ttt gac tac 384
Val Tyr Tyr Cys Ala Arg Gln Gly Thr Gly Leu Ala Leu Phe Asp Tyr
115 120 125

tgg ggc cag gga acc ctg gtc acc gtc tcc tca 417
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 19
<211> 139
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 19

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

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

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

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

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

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

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

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

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

<210> 20
<211> 120
<212> PRT
<213> Artificial

<220>
<223> Description of the artificial sequence: VH region of anti-CD98 antibody

<400> 20

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 21
<211> 387
<212> DNA
<213> Artificial

<220>
<223> Description of the artificial sequence: VL region of anti-CD98 antibody

<220>
<221> CDS
<222> (1)..(387)

<400> 21
atg gaa acc cca gcg cag ctt ctc ttc ctc ctg cta ctc tgg ctc cca 48
Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

gat acc acc gga gaa att gtg ttg acg cag tct cca ggc acc ctg tct 96
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
20 25 30

ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt 144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

gtt agc agc agc ttc tta gcc tgg tac cag cag aaa cct ggc cag gct 192
Val Ser Ser Ser Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

ccc agg ctc ctc atc tat ggt gca tcc agc agg gcc act ggc atc cca 240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
65 70 75 80

gac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc 288
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

agc aga ctg gag cct gaa gat ttc gca gtg tat tac tgt cag cag tat 336
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
100 105 110

ggt agc tca cct cta ttc act ttc ggc cct ggg acc aaa gtg gat atc 384
Gly Ser Ser Pro Leu Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
115 120 125

aaa 387
Lys

<210> 22
<211> 129
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 22

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

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

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

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

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

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

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

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

Lys

<210> 23
<211> 109
<212> PRT
<213> Artificial

<220>
<223> Description of the artificial sequence: VL region of anti-CD98 antibody

<400> 23

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

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

Leu Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 24
<211> 420
<212> DNA
<213> Artificial

<220>
<223> Description of the artificial sequence: VH region of anti-TNF alpha antibody

<220>
<221> CDS
<222> (1)..(420)

<400> 24
atg gag ttg gga ctg agc tgg att ttc ctt ttg gct att tta aaa ggt 48
Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu Ala Ile Leu Lys Gly
1 5 10 15

gtc cag tgt gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag 96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

ccc ggc agg tcc ctg aga ctc tcc tgt gcg gcc tct gga ttc acc ttt 144
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

gat gat tat gcc atg cac tgg gtc cgg caa gct cca ggg aag ggc ctg 192
Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gaa tgg gtc tca gct atc act tgg aat agt ggt cac ata gac tat gcg 240
Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala
65 70 75 80

gac tct gtg gag ggc cga ttc acc atc tcc aga gac aac gcc aag aac 288
Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

tcc ctg tat ctg caa atg aac agt ctg aga gct gag gat acg gcc gta 336
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

tat tac tgt gcg aaa gtc tcg tac ctt agc acc gcg tcc tcc ctt gac 384
Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp
115 120 125

tat tgg ggc caa ggt acc ctg gtc acc gtc tcg tca 420
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

<210> 25
<211> 140
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 25

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

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

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

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

```
Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala
65                  70                  75                  80


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


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


Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp
        115                 120                 125


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


<210>  26
<211>  121
<212>  PRT
<213>  Artificial

<220>
<223>  Description of the artificial sequence: VH region of anti-TNF
       alpha antibody

<400>  26

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


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30


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


Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
    50                  55                  60


Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


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


Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  27
<211>  387
<212>  DNA
```

<213> Artificial

<220>
<223> Description of the artificial sequence: VL region of anti-TNF alpha antibody

<220>
<221> CDS
<222> (1)..(387)

<400> 27
atg gac atg agg gtc ccc gct cag ctc ctg ggg ctt ctg ctg ctc tgg 48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

ctc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tcc tcc 96
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

ctg tct gca tct gta ggg gac aga gtc acc atc act tgt cgg gca agt 144
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

cag ggc atc aga aat tac tta gcc tgg tat cag caa aaa cca ggg aaa 192
Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

gcc cct aag ctc ctg atc tat gct gca tcc act ttg caa tca ggg gtc 240
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
65 70 75 80

cca tct cgg ttc agt ggc agt gga tct ggg aca gat ttc act ctc acc 288
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95

atc agc agc cta cag cct gaa gat gtt gca act tat tac tgt caa agg 336
Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg
100 105 110

tat aac cgt gca ccg tat act ttt ggc cag ggg acc aaa gtg gag atc 384
Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
115 120 125

aaa 387
Lys

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

<220>
<223> Synthetic Construct

<400> 28

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

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

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

35 40 45

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

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

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

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

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

Lys

<210> 29
<211> 107
<212> PRT
<213> Artificial

<220>
<223> Description of the artificial sequence: VL region of anti-TNF alpha antibody

<400> 29

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

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

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

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

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

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

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

<210> 30
<211> 420

<212> DNA
<213> Artificial

<220>
<223> Description of the artificial sequence: VH region of anti-CD20 antibody

<220>
<221> CDS
<222> (1)..(420)

<400> 30
atg ggt tgg agc ctc atc ttg ctc ttc ctt gtc gct gtt gct acg cgt 48
Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
1 5 10 15

gtc ctg tcc cag gta caa ctg cag cag cct ggg gct gag ctg gtg aag 96
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
20 25 30

cct ggg gcc tca gtg aag atg tcc tgc aag gct tct ggc tac aca ttt 144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

acc agt tac aat atg cac tgg gta aaa cag aca cct ggt cgg ggc ctg 192
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
50 55 60

gaa tgg att gga gct att tat ccc gga aat ggt gat act tcc tac aat 240
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65 70 75 80

cag aag ttc aaa ggc aag gcc aca ttg act gca gac aaa tcc tcc agc 288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

aca gcc tac atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc 336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

tat tac tgt gca aga tcg act tac tac ggc ggt gac tgg tac ttc aat 384
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
115 120 125

gtc tgg ggc gca ggg acc acg gtc acc gtc tct gca 420
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
130 135 140

<210> 31
<211> 140
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 31

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
1 5 10 15

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

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

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

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

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95

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

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

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
    130                 135                 140
```

<210> 32
<211> 121
<212> PRT
<213> Artificial

<220>
<223> Description of the artificial sequence: VH region of anti-CD20 antibody

<400> 32

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

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

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

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

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

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

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

Ala Gly Thr Thr Val Thr Val Ser Ala
```

115 120

<210> 33
<211> 384
<212> DNA
<213> Artificial

<220>
<223> Description of the artificial sequence: VL region of anti-CD20 antibody

<220>
<221> CDS
<222> (1)..(384)

<400> 33
atg gat ttt cag gtg cag att atc agc ttc ctg cta atc agt gct tca 48
Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

gtc ata atg tcc aga gga caa att gtt ctc tcc cag tct cca gca atc 96
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30

ctg tct gca tct cca ggg gag aag gtc aca atg act tgc agg gcc agc 144
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45

tca agt gta agt tac atc cac tgg ttc cag cag aag cca gga tcc tcc 192
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
50 55 60

ccc aaa ccc tgg att tat gcc aca tcc aac ctg gct tct gga gtc cct 240
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

gtt cgc ttc agt ggc agt ggg tct ggg act tct tac tct ctc aca atc 288
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95

agc aga gtg gag gct gaa gat gct gcc act tat tac tgc cag cag tgg 336
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110

act agt aac cca ccc acg ttc gga ggg ggg acc aag ctg gaa atc aaa 384
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
115 120 125

<210> 34
<211> 128
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 34

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30

```
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
        35                  40                  45

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

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

Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
                85                  90                  95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
            100                 105                 110

Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
        115                 120                 125
```

<210> 35
<211> 106
<212> PRT
<213> Artificial

<220>
<223> Description of the artificial sequence: VL region of anti-CD20 antibody

<400> 35

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

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

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

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

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

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

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

<210> 36
<211> 795
<212> DNA
<213> unknown

<220>
<223> wild type neomycin resistant gene

<220>
<221> CDS
<222> (1)..(795)

<400> 36
atg att gaa caa gat gga ttg cac gca ggt tct ccg gcc gct tgg gtg 48
Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1   5   10   15

gag agg cta ttc ggc tat gac tgg gca caa cag aca atc ggc tgc tct 96
Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
            20   25   30

gat gcc gcc gtg ttc cgg ctg tca gcg cag ggg cgc ccg gtt ctt ttt 144
Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
        35   40   45

gtc aag acc gac ctg tcc ggt gcc ctg aat gaa ctg cag gac gag gca 192
Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
    50   55   60

gcg cgg cta tcg tgg ctg gcc acg acg ggc gtt cct tgc gca gct gtg 240
Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65   70   75   80

ctc gac gtt gtc act gaa gcg gga agg gac tgg ctg cta ttg ggc gaa 288
Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
                85   90   95

gtg ccg ggg cag gat ctc ctg tca tct cac ctt gct cct gcc gag aaa 336
Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
            100   105   110

gta tcc atc atg gct gat gca atg cgg cgg ctg cat acg ctt gat ccg 384
Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
        115   120   125

gct acc tgc cca ttc gac cac caa gcg aaa cat cgc atc gag cga gca 432
Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
    130   135   140

cgt act cgg atg gaa gcc ggt ctt gtc gat cag gat gat ctg gac gaa 480
Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145   150   155   160

gag cat cag ggg ctc gcg cca gcc gaa ctg ttc gcc agg ctc aag gcg 528
Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
                165   170   175

cgc atg ccc gac ggc gag gat ctc gtc gtg acc cat ggc gat gcc tgc 576
Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
            180   185   190

ttg ccg aat atc atg gtg gaa aat ggc cgc ttt tct gga ttc atc gac 624
Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
        195   200   205

tgt ggc cgg ctg ggt gtg gcg gac cgc tat cag gac ata gcg ttg gct 672
Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
    210   215   220

acc cgt gat att gct gaa gag ctt ggc ggc gaa tgg gct gac cgc ttc 720
Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225   230   235   240

```
ctc gtg ctt tac ggt atc gcc gct ccc gat tcg cag cgc atc gcc ttc      768
Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
                245                 250                 255

tat cgc ctt ctt gac gag ttc ttc tga                                  795
Tyr Arg Leu Leu Asp Glu Phe Phe
            260
```

<210> 37
<211> 795
<212> DNA
<213> Artificial

<220>
<223> modified neomycin resistant gene

<220>
<221> CDS
<222> (1)..(795)

<400> 37

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atg att gaa caa gat gga ttg cac gca ggt tct ccg gcc gct tgg gtg       48
Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1               5                   10                  15

gag agg cta ttc ggc tat gac tgg gca caa cag aca atc ggc tgc tct       96
Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
            20                  25                  30

gat gcc gcc gtg ttc cgg ctg tca gcg cag ggg cgc ccg gtt ctt ttt      144
Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
        35                  40                  45

gtc aag acc gac ctg tcc ggt gcc ctg aat gaa ctg caa gat gaa gcg      192
Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
    50                  55                  60

gcg cga tta tcg tgg tta gcg acg acg ggg gta ccg tgt gcg gcg gta      240
Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65                  70                  75                  80

tta gat gta gta acg gaa gcg ggg cga gat tgg tta tta tta ggg gaa      288
Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
                85                  90                  95

gta ccg ggg caa gat tta tta tcg tcg cat tta gcg ccg gcg gaa aaa      336
Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
            100                 105                 110

gta tcg ata atg gcg gat gcg atg cga cga tta cat acg tta gat ccg      384
Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
        115                 120                 125

gcg acg tgt ccg ttt gat cat caa gcg aaa cat cga ata gaa cga gcg      432
Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
    130                 135                 140

cga acg cga atg gaa gcg ggg tta gta gat caa gat gat tta gat gaa      480
Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145                 150                 155                 160

gaa cat caa ggg tta gcg ccg gcg gaa tta ttt gcg cga tta aaa gcg      528
Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
                165                 170                 175

cga atg ccg gat ggg gaa gat tta gta gta acg cat ggg gat gcg tgt      576
```

```
Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
            180                 185                 190

tta ccg aat ata atg gta gaa aat ggg cga ttt tcg ggg ttt ata gat      624
Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
        195                 200                 205

tgt ggg cga tta ggg gta gcg gat cgt tat caa gat ata gcg tta gcg      672
Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
    210                 215                 220

acg cga gat ata gcg gaa gaa tta ggg ggg gaa tgg gcg gat cga ttt      720
Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225                 230                 235                 240

tta gta tta tat ggg ata gcg gcg ccg gat tcg caa cga ata gcg ttt      768
Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
                245                 250                 255

tat cga tta tta gat gaa ttt ttt tga                                  795
Tyr Arg Leu Leu Asp Glu Phe Phe
            260

<210>  38
<211>  795
<212>  DNA
<213>  artificial

<220>
<223>  modified neomycin resistant gene


<220>
<221>  CDS
<222>  (1)..(795)

<400>  38
atg att gaa caa gat gga ttg cac gca ggt tct ccg gcc gct tgg gtg       48
Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1               5                   10                  15

gag agg cta ttc ggc tat gac tgg gca caa cag aca atc ggc tgc tct       96
Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
            20                  25                  30

gat gcc gcc gtg ttc cgg ctg tca gcg cag ggg cgc ccg gtt ctt ttt      144
Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
        35                  40                  45

gta aaa acg gat tta tcg ggg gcg tta aat gaa tta caa gat gaa gcg      192
Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
    50                  55                  60

gcg cga tta tcg tgg tta gcg acg acg ggg gta ccg tgt gcg gcg gta      240
Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65                  70                  75                  80

tta gat gta gta acg gaa gcg ggg cga gat tgg tta tta tta ggg gaa      288
Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
                85                  90                  95

gta ccg ggg caa gat tta tta tcg tcg cat tta gcg ccg gcg gaa aaa      336
Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
            100                 105                 110

gta tcg ata atg gcg gat gcg atg cga cga tta cat acg tta gat ccg      384
Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
        115                 120                 125
```

```
gcg acg tgt ccg ttt gat cat caa gcg aaa cat cga ata gaa cga gcg      432
Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
    130                 135                 140

cga acg cga atg gaa gcg ggg tta gta gat caa gat gat tta gat gaa      480
Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145                 150                 155                 160

gaa cat caa ggg tta gcg ccg gcg gaa tta ttt gcg cga tta aaa gcg      528
Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
                165                 170                 175

cga atg ccg gat ggg gaa gat tta gta gta acg cat ggg gat gcg tgt      576
Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
            180                 185                 190

tta ccg aat ata atg gta gaa aat ggg cga ttt tcg ggg ttt ata gat      624
Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
        195                 200                 205

tgt ggg cga tta ggg gta gcg gat cgt tat caa gat ata gcg tta gcg      672
Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
    210                 215                 220

acg cga gat ata gcg gaa gaa tta ggg ggg gaa tgg gcg gat cga ttt      720
Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225                 230                 235                 240

tta gta tta tat ggg ata gcg gcg ccg gat tcg caa cga ata gcg ttt      768
Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
                245                 250                 255

tat cga tta tta gat gaa ttt ttt tga                                  795
Tyr Arg Leu Leu Asp Glu Phe Phe
            260
```

<210> 39
<211> 795
<212> DNA
<213> artificial

<220>
<223> modified neomycin resistant gene

<220>
<221> CDS
<222> (1)..(795)

<400> 39

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atg att gaa caa gat gga ttg cac gca ggt tct ccg gcc gct tgg gtg       48
Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1               5                   10                  15

gag agg cta ttt ggg tat gat tgg gcg caa caa acg ata ggg tgt tcg       96
Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
            20                  25                  30

gat gcg gcg gta ttt cga tta tcg gcg caa ggg cga ccg gta tta ttt      144
Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
        35                  40                  45

gta aaa acg gat tta tcg ggg gcg tta aat gaa tta caa gat gaa gcg      192
Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
    50                  55                  60

gcg cga tta tcg tgg tta gcg acg acg ggg gta ccg tgt gcg gcg gta      240
```

```
Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65                  70                  75                  80

tta gat gta gta acg gaa gcg ggg cga gat tgg tta tta tta ggg gaa      288
Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
                85                  90                  95

gta ccg ggg caa gat tta tta tcg tcg cat tta gcg ccg gcg gaa aaa      336
Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
            100                 105                 110

gta tcg ata atg gcg gat gcg atg cga cga tta cat acg tta gat ccg      384
Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
        115                 120                 125

gcg acg tgt ccg ttt gat cat caa gcg aaa cat cga ata gaa cga gcg      432
Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
    130                 135                 140

cga acg cga atg gaa gcg ggg tta gta gat caa gat gat tta gat gaa      480
Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145                 150                 155                 160

gaa cat caa ggg tta gcg ccg gcg gaa tta ttt gcg cga tta aaa gcg      528
Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
                165                 170                 175

cga atg ccg gat ggg gaa gat tta gta gta acg cat ggg gat gcg tgt      576
Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
            180                 185                 190

tta ccg aat ata atg gta gaa aat ggg cga ttt tcg ggg ttt ata gat      624
Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
        195                 200                 205

tgt ggg cga tta ggg gta gcg gat cgt tat caa gat ata gcg tta gcg      672
Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
    210                 215                 220

acg cga gat ata gcg gaa gaa tta ggg ggg gaa tgg gcg gat cga ttt      720
Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225                 230                 235                 240

tta gta tta tat ggg ata gcg gcg ccg gat tcg caa cga ata gcg ttt      768
Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
                245                 250                 255

tat cga tta tta gat gaa ttt ttt tga                                  795
Tyr Arg Leu Leu Asp Glu Phe Phe
            260
```

<210> 40
<211> 649
<212> PRT
<213> Oryzias latipes

<400> 40

```
Met Glu Glu Val Cys Asp Ser Ser Ala Ala Ala Ser Ser Thr Val Gln
1               5                   10                  15


Asn Gln Pro Gln Asp Gln Glu His Pro Trp Pro Tyr Leu Arg Glu Phe
            20                  25                  30


Phe Ser Leu Ser Gly Val Asn Lys Asp Ser Phe Lys Met Lys Cys Val
        35                  40                  45
```

```
Leu Cys Leu Pro Leu Asn Lys Glu Ile Ser Ala Phe Lys Ser Ser Pro
    50                  55                  60

Ser Asn Leu Arg Lys His Ile Glu Arg Met His Pro Asn Tyr Leu Lys
65                  70                  75                  80

Asn Tyr Ser Lys Leu Thr Ala Gln Lys Arg Lys Ile Gly Thr Ser Thr
                85                  90                  95

His Ala Ser Ser Ser Lys Gln Leu Lys Val Asp Ser Val Phe Pro Val
            100                 105                 110

Lys His Val Ser Pro Val Thr Val Asn Lys Ala Ile Leu Arg Tyr Ile
        115                 120                 125

Ile Gln Gly Leu His Pro Phe Ser Thr Val Asp Leu Pro Ser Phe Lys
    130                 135                 140

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

Thr Leu Arg Ser Lys Ile Ala Glu Ala Ala Leu Ile Met Lys Gln Lys
                165                 170                 175

Val Thr Ala Ala Met Ser Glu Val Glu Trp Ile Ala Thr Thr Thr Asp
            180                 185                 190

Cys Trp Thr Ala Arg Arg Lys Ser Phe Ile Gly Val Thr Ala His Trp
        195                 200                 205

Ile Asn Pro Gly Ser Leu Glu Arg His Ser Ala Ala Leu Ala Cys Lys
    210                 215                 220

Arg Leu Met Gly Ser His Thr Phe Glu Val Leu Ala Ser Ala Met Asn
225                 230                 235                 240

Asp Ile His Ser Glu Tyr Glu Ile Arg Asp Lys Val Val Cys Thr Thr
                245                 250                 255

Thr Asp Ser Gly Ser Asn Phe Met Lys Ala Phe Arg Val Phe Gly Val
            260                 265                 270

Glu Asn Asn Asp Ile Glu Thr Glu Ala Arg Arg Cys Glu Ser Asp Asp
        275                 280                 285

Thr Asp Ser Glu Gly Cys Gly Glu Gly Ser Asp Gly Val Glu Phe Gln
    290                 295                 300

Asp Ala Ser Arg Val Leu Asp Gln Asp Asp Gly Phe Glu Phe Gln Leu
305                 310                 315                 320
```

```
Pro Lys His Gln Lys Cys Ala Cys His Leu Leu Asn Leu Val Ser Ser
                325                 330                 335

Val Asp Ala Gln Lys Ala Leu Ser Asn Glu His Tyr Lys Lys Leu Tyr
            340                 345                 350

Arg Ser Val Phe Gly Lys Cys Gln Ala Leu Trp Asn Lys Ser Ser Arg
        355                 360                 365

Ser Ala Leu Ala Ala Glu Ala Val Glu Ser Glu Ser Arg Leu Gln Leu
    370                 375                 380

Leu Arg Pro Asn Gln Thr Arg Trp Asn Ser Thr Phe Met Ala Val Asp
385                 390                 395                 400

Arg Ile Leu Gln Ile Cys Lys Glu Ala Gly Glu Gly Ala Leu Arg Asn
                405                 410                 415

Ile Cys Thr Ser Leu Glu Val Pro Met Phe Asn Pro Ala Glu Met Leu
            420                 425                 430

Phe Leu Thr Glu Trp Ala Asn Thr Met Arg Pro Val Ala Lys Val Leu
        435                 440                 445

Asp Ile Leu Gln Ala Glu Thr Asn Thr Gln Leu Gly Trp Leu Leu Pro
    450                 455                 460

Ser Val His Gln Leu Ser Leu Lys Leu Gln Arg Leu His His Ser Leu
465                 470                 475                 480

Arg Tyr Cys Asp Pro Leu Val Asp Ala Leu Gln Gln Gly Ile Gln Thr
                485                 490                 495

Arg Phe Lys His Met Phe Glu Asp Pro Glu Ile Ile Ala Ala Ala Ile
            500                 505                 510

Leu Leu Pro Lys Phe Arg Thr Ser Trp Thr Asn Asp Glu Thr Ile Ile
        515                 520                 525

Lys Arg Gly Met Asp Tyr Ile Arg Val His Leu Glu Pro Leu Asp His
    530                 535                 540

Lys Lys Glu Leu Ala Asn Ser Ser Ser Asp Asp Glu Asp Phe Phe Ala
545                 550                 555                 560

Ser Leu Lys Pro Thr Thr His Glu Ala Ser Lys Glu Leu Asp Gly Tyr
                565                 570                 575

Leu Ala Cys Val Ser Asp Thr Arg Glu Ser Leu Leu Thr Phe Pro Ala
            580                 585                 590
```

```
Ile Cys Ser Leu Ser Ile Lys Thr Asn Thr Pro Leu Pro Ala Ser Ala
        595                 600                 605


Ala Cys Glu Arg Leu Phe Ser Thr Ala Gly Leu Leu Phe Ser Pro Lys
    610                 615                 620


Arg Ala Arg Leu Asp Thr Asn Asn Phe Glu Asn Gln Leu Leu Leu Lys
625                 630                 635                 640


Leu Asn Leu Arg Phe Tyr Asn Phe Glu
                645
<210>  41
<211>  600
<212>  DNA
<213>  artificial

<220>
<223>  modified puromycin resistant gene


<220>
<221>  CDS
<222>  (1)..(600)

<400>  41
atg acg gaa tat aaa ccg acg gta cgt tta gcg acg cgt gat gat gta       48
Met Thr Glu Tyr Lys Pro Thr Val Arg Leu Ala Thr Arg Asp Asp Val
1               5                   10                  15

ccg cgt gcg gta cgt acg tta gcg gcg gcg ttt gcg gat tat ccg gcg       96
Pro Arg Ala Val Arg Thr Leu Ala Ala Ala Phe Ala Asp Tyr Pro Ala
            20                  25                  30

acg cgt cat acg gta gat ccg gat cgt cat ata gaa cgt gta acg gaa      144
Thr Arg His Thr Val Asp Pro Asp Arg His Ile Glu Arg Val Thr Glu
        35                  40                  45

tta caa gaa tta ttt tta acg cgt gta ggt tta gat ata ggt aaa gta      192
Leu Gln Glu Leu Phe Leu Thr Arg Val Gly Leu Asp Ile Gly Lys Val
    50                  55                  60

tgg gta gcg gat gat ggt gcg gcg gta gcg gta tgg acg acg ccg gaa      240
Trp Val Ala Asp Asp Gly Ala Ala Val Ala Val Trp Thr Thr Pro Glu
65                  70                  75                  80

tcg gta gaa gcg ggt gcg gta ttt gcg gaa ata ggt ccg cgt atg gcg      288
Ser Val Glu Ala Gly Ala Val Phe Ala Glu Ile Gly Pro Arg Met Ala
                85                  90                  95

gaa tta tcg ggt tcg cgt tta gcg gcg caa caa caa atg gaa ggt tta      336
Glu Leu Ser Gly Ser Arg Leu Ala Ala Gln Gln Gln Met Glu Gly Leu
            100                 105                 110

tta gcg ccg cat cgt ccg aaa gaa ccg gcg tgg ttt tta gcg acg gta      384
Leu Ala Pro His Arg Pro Lys Glu Pro Ala Trp Phe Leu Ala Thr Val
        115                 120                 125

ggt gta tcg ccg gat cat caa ggt aaa ggt tta ggt tcg gcg gta gta      432
Gly Val Ser Pro Asp His Gln Gly Lys Gly Leu Gly Ser Ala Val Val
    130                 135                 140

tta ccg ggt gta gaa gcg gcg gaa cgt gcg ggt gta ccg gcg ttt tta      480
Leu Pro Gly Val Glu Ala Ala Glu Arg Ala Gly Val Pro Ala Phe Leu
```

```
145                 150                 155                 160

gaa acg tcg gcg ccg cgt aat tta ccg ttt tat gaa cgt tta ggt ttt      528
Glu Thr Ser Ala Pro Arg Asn Leu Pro Phe Tyr Glu Arg Leu Gly Phe
                165                 170                 175

acg gta acg gcg gat gta gaa gta ccg gaa ggt ccg cgt acg tgg tgt      576
Thr Val Thr Ala Asp Val Glu Val Pro Glu Gly Pro Arg Thr Trp Cys
            180                 185                 190

atg acg cgt aaa ccg ggt gcg tga                                     600
Met Thr Arg Lys Pro Gly Ala
        195

<210>  42
<211>  600
<212>  DNA
<213>  unknown

<220>
<223>  wild type puromycin resistant gene


<220>
<221>  CDS
<222>  (1)..(600)

<400>  42
atg acc gag tac aag ccc acg gtg cgc ctc gcc acc cgc gac gac gtc       48
Met Thr Glu Tyr Lys Pro Thr Val Arg Leu Ala Thr Arg Asp Asp Val
1               5                   10                  15

ccc cgg gcc gta cgc acc ctc gcc gcc gcg ttc gcc gac tac ccc gcc       96
Pro Arg Ala Val Arg Thr Leu Ala Ala Ala Phe Ala Asp Tyr Pro Ala
            20                  25                  30

acg cgc cac acc gtc gac ccg gac cgc cac atc gag cgg gtc acc gag      144
Thr Arg His Thr Val Asp Pro Asp Arg His Ile Glu Arg Val Thr Glu
        35                  40                  45

ctg caa gaa ctc ttc ctc acg cgc gtc ggg ctc gac atc ggc aag gtg      192
Leu Gln Glu Leu Phe Leu Thr Arg Val Gly Leu Asp Ile Gly Lys Val
    50                  55                  60

tgg gtc gcg gac gac ggc gcc gcg gtg gcg gtc tgg acc acg ccg gag      240
Trp Val Ala Asp Asp Gly Ala Ala Val Ala Val Trp Thr Thr Pro Glu
65                  70                  75                  80

agc gtc gaa gcg ggg gcg gtg ttc gcc gag atc ggc ccg cgc atg gcc      288
Ser Val Glu Ala Gly Ala Val Phe Ala Glu Ile Gly Pro Arg Met Ala
                85                  90                  95

gag ttg agc ggt tcc cgg ctg gcc gcg cag caa cag atg gaa ggc ctc      336
Glu Leu Ser Gly Ser Arg Leu Ala Ala Gln Gln Gln Met Glu Gly Leu
            100                 105                 110

ctg gcg ccg cac cgg ccc aag gag ccc gcg tgg ttc ctg gcc acc gtc      384
Leu Ala Pro His Arg Pro Lys Glu Pro Ala Trp Phe Leu Ala Thr Val
        115                 120                 125

ggc gtc tcg ccc gac cac cag ggc aag ggt ctg ggc agc gcc gtc gtg      432
Gly Val Ser Pro Asp His Gln Gly Lys Gly Leu Gly Ser Ala Val Val
    130                 135                 140

ctc ccc gga gtg gag gcg gcc gag cgc gcc ggg gtg ccc gcc ttc ctg      480
Leu Pro Gly Val Glu Ala Ala Glu Arg Ala Gly Val Pro Ala Phe Leu
145                 150                 155                 160
```

```
gag acc tcc gcg ccc cgc aac ctc ccc ttc tac gag cgg ctc ggc ttc      528
Glu Thr Ser Ala Pro Arg Asn Leu Pro Phe Tyr Glu Arg Leu Gly Phe
                165                 170                 175

acc gtc acc gcc gac gtc gag gtg ccc gaa gga ccg cgc acc tgg tgc      576
Thr Val Thr Ala Asp Val Glu Val Pro Glu Gly Pro Arg Thr Trp Cys
            180                 185                 190

atg acc cgc aag ccc ggt gcc tga                                     600
Met Thr Arg Lys Pro Gly Ala
        195
```

<210> 43
<211> 600
<212> DNA
<213> artificial

<220>
<223> modified puromycin resistant gene

<220>
<221> CDS
<222> (1)..(600)

<400> 43

```
atg acc gag tac aag ccc acg gta cgc tta gcg acc cgc gac gac gta       48
Met Thr Glu Tyr Lys Pro Thr Val Arg Leu Ala Thr Arg Asp Asp Val
1               5                   10                  15

ccc cgg gcg gta cgc acc tta gcg gcg gcg ttc gcg gac tac ccc gcg       96
Pro Arg Ala Val Arg Thr Leu Ala Ala Ala Phe Ala Asp Tyr Pro Ala
            20                  25                  30

acg cgc cac acc gta gac ccg gac cgc cac atc gag cgg gta acc gag      144
Thr Arg His Thr Val Asp Pro Asp Arg His Ile Glu Arg Val Thr Glu
        35                  40                  45

tta caa gaa tta ttc tta acg cgc gta ggg tta gac atc ggc aag gta      192
Leu Gln Glu Leu Phe Leu Thr Arg Val Gly Leu Asp Ile Gly Lys Val
    50                  55                  60

tgg gta gcg gac gac ggc gcg gcg gta gcg gta tgg acc acg ccg gag      240
Trp Val Ala Asp Asp Gly Ala Ala Val Ala Val Trp Thr Thr Pro Glu
65                  70                  75                  80

tcg gta gaa gcg ggg gcg gta ttc gcg gag atc ggc ccg cgc atg gcg      288
Ser Val Glu Ala Gly Ala Val Phe Ala Glu Ile Gly Pro Arg Met Ala
                85                  90                  95

gag tta tcg ggt tcg cgg tta gcg gcg cag caa cag atg gaa ggc tta      336
Glu Leu Ser Gly Ser Arg Leu Ala Ala Gln Gln Gln Met Glu Gly Leu
            100                 105                 110

tta gcg ccg cac cgg ccc aag gag ccc gcg tgg ttc tta gcg acc gta      384
Leu Ala Pro His Arg Pro Lys Glu Pro Ala Trp Phe Leu Ala Thr Val
        115                 120                 125

ggc gta tcg ccc gac cac cag ggc aag ggt tta ggc tcg gcg gta gta      432
Gly Val Ser Pro Asp His Gln Gly Lys Gly Leu Gly Ser Ala Val Val
    130                 135                 140

tta ccc gga gta gag gcg gcg gag cgc gcg ggg gta ccc gcg ttc tta      480
Leu Pro Gly Val Glu Ala Ala Glu Arg Ala Gly Val Pro Ala Phe Leu
145                 150                 155                 160

gag acc tcg gcg ccc cgc aac tta ccc ttc tac gag cgg tta ggc ttc      528
Glu Thr Ser Ala Pro Arg Asn Leu Pro Phe Tyr Glu Arg Leu Gly Phe
```

```
                165                 170                 175

acc gta acc gcg gac gta gag gta ccc gaa gga ccg cgc acc tgg tgc      576
Thr Val Thr Ala Asp Val Glu Val Pro Glu Gly Pro Arg Thr Trp Cys
            180                 185                 190

atg acc cgc aag ccc ggt gcg tga                                      600
Met Thr Arg Lys Pro Gly Ala
        195
```

<210> 44
<211> 600
<212> DNA
<213> artificial

<220>
<223> modified puromycin resistant gene

<220>
<221> CDS
<222> (1)..(600)

<400> 44

```
atg acg gaa tat aaa ccg acg gta cgt tta gcg acg cgt gat gat gta       48
Met Thr Glu Tyr Lys Pro Thr Val Arg Leu Ala Thr Arg Asp Asp Val
1               5                   10                  15

ccg cgt gcg gta cgt acg tta gcg gcg gcg ttt gcg gat tat ccg gcg       96
Pro Arg Ala Val Arg Thr Leu Ala Ala Ala Phe Ala Asp Tyr Pro Ala
            20                  25                  30

acg cgt cat acg gta gat ccg gat cgt cat ata gaa cgt gta acg gaa      144
Thr Arg His Thr Val Asp Pro Asp Arg His Ile Glu Arg Val Thr Glu
        35                  40                  45

tta caa gaa tta ttt tta acg cgt gta ggt tta gat ata ggt aaa gta      192
Leu Gln Glu Leu Phe Leu Thr Arg Val Gly Leu Asp Ile Gly Lys Val
    50                  55                  60

tgg gta gcg gat gat ggt gcg gcg gta gcg gta tgg acg acg ccg gaa      240
Trp Val Ala Asp Asp Gly Ala Ala Val Ala Val Trp Thr Thr Pro Glu
65                  70                  75                  80

tcg gta gaa gcg ggt gcg gta ttt gcg gaa ata ggt ccg cgt atg gcg      288
Ser Val Glu Ala Gly Ala Val Phe Ala Glu Ile Gly Pro Arg Met Ala
                85                  90                  95

gaa tta tcg ggt tcg cgt tta gcg gcg caa caa caa atg gaa ggt tta      336
Glu Leu Ser Gly Ser Arg Leu Ala Ala Gln Gln Gln Met Glu Gly Leu
            100                 105                 110

tta gcg ccg cat cgt ccg aaa gaa ccg gcg tgg ttt tta gcg acg gta      384
Leu Ala Pro His Arg Pro Lys Glu Pro Ala Trp Phe Leu Ala Thr Val
        115                 120                 125

ggt gta tcg ccg gat cat caa ggt aaa ggt tta ggt tcg gcg gta gta      432
Gly Val Ser Pro Asp His Gln Gly Lys Gly Leu Gly Ser Ala Val Val
    130                 135                 140

tta ccg ggt gta gaa gcg gcg gaa cgt gcg ggt gta ccg gcg ttt tta      480
Leu Pro Gly Val Glu Ala Ala Glu Arg Ala Gly Val Pro Ala Phe Leu
145                 150                 155                 160

gaa acg tcg gcg ccg cgt aat tta ccg ttt tat gaa cgt tta ggt ttt      528
Glu Thr Ser Ala Pro Arg Asn Leu Pro Phe Tyr Glu Arg Leu Gly Phe
                165                 170                 175
```

```
acg gta acg gcg gat gta gaa gta ccg gaa ggt ccg cgt acg tgg tgt      576
Thr Val Thr Ala Asp Val Glu Val Pro Glu Gly Pro Arg Thr Trp Cys
            180                 185                 190

atg acg cgt aaa ccg ggt gcg tga                                     600
Met Thr Arg Lys Pro Gly Ala
        195
```

<210> 45
<211> 375
<212> DNA
<213> artificial

<220>
<223> modified zeocin resistant gene

<220>
<221> CDS
<222> (1)..(375)

<400> 45

```
atg gcg aag tta acc tcg gcg gtt ccg gta tta acc gcg cgc gac gtc       48
Met Ala Lys Leu Thr Ser Ala Val Pro Val Leu Thr Ala Arg Asp Val
1               5                   10                  15

gcg gga gcg gtc gag ttc tgg acc gac cgg tta ggg ttc tcg cgg gac       96
Ala Gly Ala Val Glu Phe Trp Thr Asp Arg Leu Gly Phe Ser Arg Asp
            20                  25                  30

ttc gta gag gac gac ttc gcg ggt gta gtc cgg gac gac gta acc tta      144
Phe Val Glu Asp Asp Phe Ala Gly Val Val Arg Asp Asp Val Thr Leu
        35                  40                  45

ttc atc tcg gcg gtc cag gac cag gta gta ccg gac aac acc tta gcg      192
Phe Ile Ser Ala Val Gln Asp Gln Val Val Pro Asp Asn Thr Leu Ala
    50                  55                  60

tgg gta tgg gta cgc ggc tta gac gag tta tac gcg gag tgg tcg gag      240
Trp Val Trp Val Arg Gly Leu Asp Glu Leu Tyr Ala Glu Trp Ser Glu
65                  70                  75                  80

gtc gta tcg acg aac ttc cgg gac gcc tcg ggg ccg gcg atg acc gag      288
Val Val Ser Thr Asn Phe Arg Asp Ala Ser Gly Pro Ala Met Thr Glu
                85                  90                  95

atc ggc gag cag ccg tgg ggg cgg gag ttc gcg tta cgc gac ccg gcg      336
Ile Gly Glu Gln Pro Trp Gly Arg Glu Phe Ala Leu Arg Asp Pro Ala
            100                 105                 110

ggc aac tgc gta cac ttc gta gcg gag gag cag gac tga                  375
Gly Asn Cys Val His Phe Val Ala Glu Glu Gln Asp
        115                 120
```

<210> 46
<211> 375
<212> DNA
<213> artificial

<220>
<223> modified zeocin resistant gene

<220>
<221> CDS
<222> (1)..(375)

<400> 46

```
atg gcg aaa tta acg tcg gcg gta ccg gta tta acg gcg cgt gat gta       48
Met Ala Lys Leu Thr Ser Ala Val Pro Val Leu Thr Ala Arg Asp Val
1               5                  10                  15

gcg ggt gcg gta gaa ttt tgg acg gat cgt tta ggt ttt tcg cgt gat       96
Ala Gly Ala Val Glu Phe Trp Thr Asp Arg Leu Gly Phe Ser Arg Asp
            20                  25                  30

ttt gta gaa gat gat ttt gcg ggt gta gta cgt gat gat gta acg tta      144
Phe Val Glu Asp Asp Phe Ala Gly Val Val Arg Asp Asp Val Thr Leu
        35                  40                  45

ttt ata tcg gcg gta caa gat caa gta gta ccg gat aat acg tta gcg      192
Phe Ile Ser Ala Val Gln Asp Gln Val Val Pro Asp Asn Thr Leu Ala
    50                  55                  60

tgg gta tgg gta cgt ggt tta gat gaa tta tat gcg gaa tgg tcg gaa      240
Trp Val Trp Val Arg Gly Leu Asp Glu Leu Tyr Ala Glu Trp Ser Glu
65                  70                  75                  80

gta gta tcg acg aat ttt cgt gat gcg tcg ggt ccg gcg atg acg gaa      288
Val Val Ser Thr Asn Phe Arg Asp Ala Ser Gly Pro Ala Met Thr Glu
                85                  90                  95

ata ggt gaa caa ccg tgg ggt cgt gaa ttt gcg tta cgt gat ccg gcg      336
Ile Gly Glu Gln Pro Trp Gly Arg Glu Phe Ala Leu Arg Asp Pro Ala
            100                 105                 110

ggt aat tgt gta cat ttt gta gcg gaa gaa caa gat tga                  375
Gly Asn Cys Val His Phe Val Ala Glu Glu Gln Asp
        115                 120
```

<210> 47
<211> 1026
<212> DNA
<213> artificial

<220>
<223> modified hygromycin resistant gene

<220>
<221> CDS
<222> (1)..(1026)

<400> 47

```
atg aaa aag cct gaa tta acc gcg acg tcg gta gag aag ttt tta atc       48
Met Lys Lys Pro Glu Leu Thr Ala Thr Ser Val Glu Lys Phe Leu Ile
1               5                  10                  15

gaa aag ttc gac tcg gta tcg gac tta atg cag tta tcg gag ggc gaa       96
Glu Lys Phe Asp Ser Val Ser Asp Leu Met Gln Leu Ser Glu Gly Glu
            20                  25                  30

gaa tcg cgt gcg ttc tcg ttc gat gta gga ggg cgt gga tat gta tta      144
Glu Ser Arg Ala Phe Ser Phe Asp Val Gly Gly Arg Gly Tyr Val Leu
        35                  40                  45

cgt gta aat tcg tgc gcg gat ggt ttc tac aaa gat cgt tat gta tat      192
Arg Val Asn Ser Cys Ala Asp Gly Phe Tyr Lys Asp Arg Tyr Val Tyr
    50                  55                  60

cgt cac ttt gcg tcg gcg gcg tta ccg att ccg gaa gta tta gac att      240
Arg His Phe Ala Ser Ala Ala Leu Pro Ile Pro Glu Val Leu Asp Ile
65                  70                  75                  80

ggg gaa ttc tcg gag tcg tta acc tat tgc atc tcg cgc cgt gcg cag      288
Gly Glu Phe Ser Glu Ser Leu Thr Tyr Cys Ile Ser Arg Arg Ala Gln
```

```
                85                  90                  95

ggt gta acg ttg caa gac tta cct gaa acc gaa tta ccc gcg gta tta      336
Gly Val Thr Leu Gln Asp Leu Pro Glu Thr Glu Leu Pro Ala Val Leu
            100                 105                 110

cag ccg gta gcg gag gcg atg gat gcg atc gcg gcg gcg gat tta tcg      384
Gln Pro Val Ala Glu Ala Met Asp Ala Ile Ala Ala Ala Asp Leu Ser
        115                 120                 125

cag acg tcg ggg ttc ggc cca ttc gga ccg caa gga atc ggt caa tac      432
Gln Thr Ser Gly Phe Gly Pro Phe Gly Pro Gln Gly Ile Gly Gln Tyr
    130                 135                 140

act aca tgg cgt gat ttc ata tgc gcg att gcg gat ccc cat gta tat      480
Thr Thr Trp Arg Asp Phe Ile Cys Ala Ile Ala Asp Pro His Val Tyr
145                 150                 155                 160

cac tgg caa act gta atg gac gac acc gta tcg gcg tcg gta gcg cag      528
His Trp Gln Thr Val Met Asp Asp Thr Val Ser Ala Ser Val Ala Gln
                165                 170                 175

gcg tta gat gag tta atg tta tgg gcg gag gac tgc ccc gaa gta cgt      576
Ala Leu Asp Glu Leu Met Leu Trp Ala Glu Asp Cys Pro Glu Val Arg
            180                 185                 190

cac tta gta cac gcg gat ttc ggc tcg aac aat gta tta acg gac aat      624
His Leu Val His Ala Asp Phe Gly Ser Asn Asn Val Leu Thr Asp Asn
        195                 200                 205

ggc cgc ata aca gcg gta att gac tgg tcg gag gcg atg ttc ggg gat      672
Gly Arg Ile Thr Ala Val Ile Asp Trp Ser Glu Ala Met Phe Gly Asp
    210                 215                 220

tcg caa tac gag gta gcg aac atc ttc ttc tgg cgt ccg tgg ttg gcg      720
Ser Gln Tyr Glu Val Ala Asn Ile Phe Phe Trp Arg Pro Trp Leu Ala
225                 230                 235                 240

tgt atg gag cag cag acg cgc tac ttc gag cgt cgt cat ccg gag tta      768
Cys Met Glu Gln Gln Thr Arg Tyr Phe Glu Arg Arg His Pro Glu Leu
                245                 250                 255

gcg gga tcg ccg cgt tta cgt gcg tat atg tta cgc att ggt ctt gac      816
Ala Gly Ser Pro Arg Leu Arg Ala Tyr Met Leu Arg Ile Gly Leu Asp
            260                 265                 270

caa tta tat cag tcg ttg gta gac ggc aat ttc gat gat gcg gcg tgg      864
Gln Leu Tyr Gln Ser Leu Val Asp Gly Asn Phe Asp Asp Ala Ala Trp
        275                 280                 285

gcg cag ggt cga tgc gac gcg atc gta cga tcg gga gcg ggg act gta      912
Ala Gln Gly Arg Cys Asp Ala Ile Val Arg Ser Gly Ala Gly Thr Val
    290                 295                 300

ggg cgt aca caa atc gcg cgc cgt tcg gcg gcg gta tgg acc gat ggc      960
Gly Arg Thr Gln Ile Ala Arg Arg Ser Ala Ala Val Trp Thr Asp Gly
305                 310                 315                 320

tgt gta gaa gta tta gcg gat tcg gga aac cga cgc ccc tcg act cgt     1008
Cys Val Glu Val Leu Ala Asp Ser Gly Asn Arg Arg Pro Ser Thr Arg
                325                 330                 335

ccg cgt gcg aag gaa tag                                            1026
Pro Arg Ala Lys Glu
            340
```

<210> 48
<211> 1026

<212> DNA
<213> artificial

<220>
<223> modified hygromycin resistant gene

<220>
<221> CDS
<222> (1)..(1026)

<400> 48

```
atg aaa aaa ccg gaa tta acg gcg acg tcg gta gaa aaa ttt tta ata       48
Met Lys Lys Pro Glu Leu Thr Ala Thr Ser Val Glu Lys Phe Leu Ile
1               5                   10                  15

gaa aaa ttt gat tcg gta tcg gat tta atg caa tta tcg gaa ggt gaa       96
Glu Lys Phe Asp Ser Val Ser Asp Leu Met Gln Leu Ser Glu Gly Glu
            20                  25                  30

gaa tcg cgt gcg ttt tcg ttt gat gta ggt ggt cgt ggt tat gta tta      144
Glu Ser Arg Ala Phe Ser Phe Asp Val Gly Gly Arg Gly Tyr Val Leu
        35                  40                  45

cgt gta aat tcg tgt gcg gat ggt ttt tat aaa gat cgt tat gta tat      192
Arg Val Asn Ser Cys Ala Asp Gly Phe Tyr Lys Asp Arg Tyr Val Tyr
    50                  55                  60

cgt cat ttt gcg tcg gcg gcg tta ccg ata ccg gaa gta tta gat ata      240
Arg His Phe Ala Ser Ala Ala Leu Pro Ile Pro Glu Val Leu Asp Ile
65                  70                  75                  80

ggt gaa ttt tcg gaa tcg tta acg tat tgt ata tcg cgt cgt gcg caa      288
Gly Glu Phe Ser Glu Ser Leu Thr Tyr Cys Ile Ser Arg Arg Ala Gln
                85                  90                  95

ggt gta acg tta caa gat tta ccg gaa acg gaa tta ccg gcg gta tta      336
Gly Val Thr Leu Gln Asp Leu Pro Glu Thr Glu Leu Pro Ala Val Leu
            100                 105                 110

caa ccg gta gcg gaa gcg atg gat gcg ata gcg gcg gcg gat tta tcg      384
Gln Pro Val Ala Glu Ala Met Asp Ala Ile Ala Ala Ala Asp Leu Ser
        115                 120                 125

caa acg tcg ggt ttt ggt ccg ttt ggt ccg caa ggt ata ggt caa tat      432
Gln Thr Ser Gly Phe Gly Pro Phe Gly Pro Gln Gly Ile Gly Gln Tyr
    130                 135                 140

acg acg tgg cgt gat ttt ata tgt gcg ata gcg gat ccg cat gta tat      480
Thr Thr Trp Arg Asp Phe Ile Cys Ala Ile Ala Asp Pro His Val Tyr
145                 150                 155                 160

cat tgg caa acg gta atg gat gat acg gta tcg gcg tcg gta gcg caa      528
His Trp Gln Thr Val Met Asp Asp Thr Val Ser Ala Ser Val Ala Gln
                165                 170                 175

gcg tta gat gaa tta atg tta tgg gcg gaa gat tgt ccg gaa gta cgt      576
Ala Leu Asp Glu Leu Met Leu Trp Ala Glu Asp Cys Pro Glu Val Arg
            180                 185                 190

cat tta gta cat gcg gat ttt ggt tcg aat aat gta tta acg gat aat      624
His Leu Val His Ala Asp Phe Gly Ser Asn Asn Val Leu Thr Asp Asn
        195                 200                 205

ggt cgt ata acg gcg gta ata gat tgg tcg gaa gcg atg ttt ggt gat      672
Gly Arg Ile Thr Ala Val Ile Asp Trp Ser Glu Ala Met Phe Gly Asp
    210                 215                 220
```

```
tcg caa tat gaa gta gcg aat ata ttt ttt tgg cgt ccg tgg tta gcg      720
Ser Gln Tyr Glu Val Ala Asn Ile Phe Phe Trp Arg Pro Trp Leu Ala
225                 230                 235                 240

tgt atg gaa caa caa acg cgt tat ttt gaa cgt cgt cat ccg gaa tta      768
Cys Met Glu Gln Gln Thr Arg Tyr Phe Glu Arg Arg His Pro Glu Leu
                245                 250                 255

gcg ggt tcg ccg cgt tta cgt gcg tat atg tta cgt ata ggt tta gat      816
Ala Gly Ser Pro Arg Leu Arg Ala Tyr Met Leu Arg Ile Gly Leu Asp
            260                 265                 270

caa tta tat caa tcg tta gta gat ggt aat ttt gat gat gcg gcg tgg      864
Gln Leu Tyr Gln Ser Leu Val Asp Gly Asn Phe Asp Asp Ala Ala Trp
        275                 280                 285

gcg caa ggt cgt tgt gat gcg ata gta cgt tcg ggt gcg ggt acg gta      912
Ala Gln Gly Arg Cys Asp Ala Ile Val Arg Ser Gly Ala Gly Thr Val
    290                 295                 300

ggt cgt acg caa ata gcg cgt cgt tcg gcg gcg gta tgg acg gat ggt      960
Gly Arg Thr Gln Ile Ala Arg Arg Ser Ala Ala Val Trp Thr Asp Gly
305                 310                 315                 320

tgt gta gaa gta tta gcg gat tcg ggt aat cgt cgt ccg tcg acg cgt     1008
Cys Val Glu Val Leu Ala Asp Ser Gly Asn Arg Arg Pro Ser Thr Arg
                325                 330                 335

ccg cgt gcg aaa gaa tga                                            1026
Pro Arg Ala Lys Glu
            340
```

<210> 49
<211> 264
<212> PRT
<213> unknown

<220>
<223> Synthetic Construct

<400> 49

```
Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1               5                   10                  15

Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
            20                  25                  30

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
        35                  40                  45

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

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65                  70                  75                  80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
                85                  90                  95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
```

```
            100                 105                 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
        115                 120                 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
    130                 135                 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145                 150                 155                 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
                165                 170                 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
            180                 185                 190

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
        195                 200                 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
    210                 215                 220

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225                 230                 235                 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
                245                 250                 255

Tyr Arg Leu Leu Asp Glu Phe Phe
            260

<210>  50
<211>  264
<212>  PRT
<213>  Artificial


<220>
<223>  Synthetic Construct

<400>  50

Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1               5                   10                  15

Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
            20                  25                  30

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
        35                  40                  45

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

```
Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65                  70                  75                  80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
                85                  90                  95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
            100                 105                 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
        115                 120                 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
    130                 135                 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145                 150                 155                 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
                165                 170                 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
            180                 185                 190

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
        195                 200                 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
    210                 215                 220

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225                 230                 235                 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
                245                 250                 255

Tyr Arg Leu Leu Asp Glu Phe Phe
            260

<210>  51
<211>  264
<212>  PRT
<213>  artificial

<220>
<223>  Synthetic Construct

<400>  51

Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1               5                   10                  15

Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
```

```
            20                  25                  30

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
        35                  40                  45

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

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65                  70                  75                  80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
                85                  90                  95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
            100                 105                 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
        115                 120                 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
    130                 135                 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145                 150                 155                 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
                165                 170                 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
            180                 185                 190

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
        195                 200                 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
    210                 215                 220

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225                 230                 235                 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
                245                 250                 255

Tyr Arg Leu Leu Asp Glu Phe Phe
            260
```

<210> 52
<211> 264
<212> PRT
<213> artificial

<220>
<223> Synthetic Construct

<400> 52

Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1 5 10 15

Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
20 25 30

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
35 40 45

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

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65 70 75 80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
85 90 95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
100 105 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
115 120 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
130 135 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145 150 155 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
165 170 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
180 185 190

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
195 200 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
210 215 220

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225 230 235 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
245 250 255

Tyr Arg Leu Leu Asp Glu Phe Phe
260

<210> 53
<211> 199
<212> PRT
<213> artificial

<220>
<223> Synthetic Construct

<400> 53

Met Thr Glu Tyr Lys Pro Thr Val Arg Leu Ala Thr Arg Asp Asp Val
1 5 10 15

Pro Arg Ala Val Arg Thr Leu Ala Ala Ala Phe Ala Asp Tyr Pro Ala
20 25 30

Thr Arg His Thr Val Asp Pro Asp Arg His Ile Glu Arg Val Thr Glu
35 40 45

Leu Gln Glu Leu Phe Leu Thr Arg Val Gly Leu Asp Ile Gly Lys Val
50 55 60

Trp Val Ala Asp Asp Gly Ala Ala Val Ala Val Trp Thr Thr Pro Glu
65 70 75 80

Ser Val Glu Ala Gly Ala Val Phe Ala Glu Ile Gly Pro Arg Met Ala
85 90 95

Glu Leu Ser Gly Ser Arg Leu Ala Ala Gln Gln Gln Met Glu Gly Leu
100 105 110

Leu Ala Pro His Arg Pro Lys Glu Pro Ala Trp Phe Leu Ala Thr Val
115 120 125

Gly Val Ser Pro Asp His Gln Gly Lys Gly Leu Gly Ser Ala Val Val
130 135 140

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

Glu Thr Ser Ala Pro Arg Asn Leu Pro Phe Tyr Glu Arg Leu Gly Phe
165 170 175

Thr Val Thr Ala Asp Val Glu Val Pro Glu Gly Pro Arg Thr Trp Cys
180 185 190

Met Thr Arg Lys Pro Gly Ala
195

<210> 54
<211> 199

<212> PRT
<213> unknown

<220>
<223> Synthetic Construct

<400> 54

Met Thr Glu Tyr Lys Pro Thr Val Arg Leu Ala Thr Arg Asp Asp Val
1 5 10 15

Pro Arg Ala Val Arg Thr Leu Ala Ala Ala Phe Ala Asp Tyr Pro Ala
20 25 30

Thr Arg His Thr Val Asp Pro Asp Arg His Ile Glu Arg Val Thr Glu
35 40 45

Leu Gln Glu Leu Phe Leu Thr Arg Val Gly Leu Asp Ile Gly Lys Val
50 55 60

Trp Val Ala Asp Asp Gly Ala Ala Val Ala Val Trp Thr Thr Pro Glu
65 70 75 80

Ser Val Glu Ala Gly Ala Val Phe Ala Glu Ile Gly Pro Arg Met Ala
85 90 95

Glu Leu Ser Gly Ser Arg Leu Ala Ala Gln Gln Gln Met Glu Gly Leu
100 105 110

Leu Ala Pro His Arg Pro Lys Glu Pro Ala Trp Phe Leu Ala Thr Val
115 120 125

Gly Val Ser Pro Asp His Gln Gly Lys Gly Leu Gly Ser Ala Val Val
130 135 140

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

Glu Thr Ser Ala Pro Arg Asn Leu Pro Phe Tyr Glu Arg Leu Gly Phe
165 170 175

Thr Val Thr Ala Asp Val Glu Val Pro Glu Gly Pro Arg Thr Trp Cys
180 185 190

Met Thr Arg Lys Pro Gly Ala
195

<210> 55
<211> 199
<212> PRT
<213> artificial

<220>
<223> Synthetic Construct

<400> 55

Met Thr Glu Tyr Lys Pro Thr Val Arg Leu Ala Thr Arg Asp Asp Val
1 5 10 15

Pro Arg Ala Val Arg Thr Leu Ala Ala Ala Phe Ala Asp Tyr Pro Ala
20 25 30

Thr Arg His Thr Val Asp Pro Asp Arg His Ile Glu Arg Val Thr Glu
35 40 45

Leu Gln Glu Leu Phe Leu Thr Arg Val Gly Leu Asp Ile Gly Lys Val
50 55 60

Trp Val Ala Asp Asp Gly Ala Ala Val Ala Val Trp Thr Thr Pro Glu
65 70 75 80

Ser Val Glu Ala Gly Ala Val Phe Ala Glu Ile Gly Pro Arg Met Ala
85 90 95

Glu Leu Ser Gly Ser Arg Leu Ala Ala Gln Gln Gln Met Glu Gly Leu
100 105 110

Leu Ala Pro His Arg Pro Lys Glu Pro Ala Trp Phe Leu Ala Thr Val
115 120 125

Gly Val Ser Pro Asp His Gln Gly Lys Gly Leu Gly Ser Ala Val Val
130 135 140

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

Glu Thr Ser Ala Pro Arg Asn Leu Pro Phe Tyr Glu Arg Leu Gly Phe
165 170 175

Thr Val Thr Ala Asp Val Glu Val Pro Glu Gly Pro Arg Thr Trp Cys
180 185 190

Met Thr Arg Lys Pro Gly Ala
195

<210> 56
<211> 199
<212> PRT
<213> artificial

<220>
<223> Synthetic Construct

<400> 56

Met Thr Glu Tyr Lys Pro Thr Val Arg Leu Ala Thr Arg Asp Asp Val
1 5 10 15

```
Pro Arg Ala Val Arg Thr Leu Ala Ala Ala Phe Ala Asp Tyr Pro Ala
            20                  25                  30

Thr Arg His Thr Val Asp Pro Asp Arg His Ile Glu Arg Val Thr Glu
        35                  40                  45

Leu Gln Glu Leu Phe Leu Thr Arg Val Gly Leu Asp Ile Gly Lys Val
    50                  55                  60

Trp Val Ala Asp Asp Gly Ala Ala Val Ala Val Trp Thr Thr Pro Glu
65                  70                  75                  80

Ser Val Glu Ala Gly Ala Val Phe Ala Glu Ile Gly Pro Arg Met Ala
                85                  90                  95

Glu Leu Ser Gly Ser Arg Leu Ala Ala Gln Gln Gln Met Glu Gly Leu
            100                 105                 110

Leu Ala Pro His Arg Pro Lys Glu Pro Ala Trp Phe Leu Ala Thr Val
        115                 120                 125

Gly Val Ser Pro Asp His Gln Gly Lys Gly Leu Gly Ser Ala Val Val
    130                 135                 140

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

Glu Thr Ser Ala Pro Arg Asn Leu Pro Phe Tyr Glu Arg Leu Gly Phe
                165                 170                 175

Thr Val Thr Ala Asp Val Glu Val Pro Glu Gly Pro Arg Thr Trp Cys
            180                 185                 190

Met Thr Arg Lys Pro Gly Ala
        195


<210>  57
<211>  124
<212>  PRT
<213>  artificial


<220>
<223>  Synthetic Construct

<400>  57

Met Ala Lys Leu Thr Ser Ala Val Pro Val Leu Thr Ala Arg Asp Val
1               5                   10                  15

Ala Gly Ala Val Glu Phe Trp Thr Asp Arg Leu Gly Phe Ser Arg Asp
            20                  25                  30

Phe Val Glu Asp Asp Phe Ala Gly Val Val Arg Asp Asp Val Thr Leu
```

```
        35                  40                  45

Phe Ile Ser Ala Val Gln Asp Gln Val Val Pro Asp Asn Thr Leu Ala
    50                  55                  60

Trp Val Trp Val Arg Gly Leu Asp Glu Leu Tyr Ala Glu Trp Ser Glu
65                  70                  75                  80

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

Ile Gly Glu Gln Pro Trp Gly Arg Glu Phe Ala Leu Arg Asp Pro Ala
            100                 105                 110

Gly Asn Cys Val His Phe Val Ala Glu Glu Gln Asp
        115                 120
```

<210> 58
<211> 124
<212> PRT
<213> artificial

<220>
<223> Synthetic Construct

<400> 58

```
Met Ala Lys Leu Thr Ser Ala Val Pro Val Leu Thr Ala Arg Asp Val
1               5                   10                  15

Ala Gly Ala Val Glu Phe Trp Thr Asp Arg Leu Gly Phe Ser Arg Asp
            20                  25                  30

Phe Val Glu Asp Asp Phe Ala Gly Val Val Arg Asp Asp Val Thr Leu
        35                  40                  45

Phe Ile Ser Ala Val Gln Asp Gln Val Val Pro Asp Asn Thr Leu Ala
    50                  55                  60

Trp Val Trp Val Arg Gly Leu Asp Glu Leu Tyr Ala Glu Trp Ser Glu
65                  70                  75                  80

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

Ile Gly Glu Gln Pro Trp Gly Arg Glu Phe Ala Leu Arg Asp Pro Ala
            100                 105                 110

Gly Asn Cys Val His Phe Val Ala Glu Glu Gln Asp
        115                 120
```

<210> 59
<211> 341
<212> PRT

<213> artificial

<220>
<223> Synthetic Construct

<400> 59

```
Met Lys Lys Pro Glu Leu Thr Ala Thr Ser Val Glu Lys Phe Leu Ile
1               5                  10                  15

Glu Lys Phe Asp Ser Val Ser Asp Leu Met Gln Leu Ser Glu Gly Glu
            20                  25                  30

Glu Ser Arg Ala Phe Ser Phe Asp Val Gly Gly Arg Gly Tyr Val Leu
        35                  40                  45

Arg Val Asn Ser Cys Ala Asp Gly Phe Tyr Lys Asp Arg Tyr Val Tyr
    50                  55                  60

Arg His Phe Ala Ser Ala Ala Leu Pro Ile Pro Glu Val Leu Asp Ile
65                  70                  75                  80

Gly Glu Phe Ser Glu Ser Leu Thr Tyr Cys Ile Ser Arg Arg Ala Gln
                85                  90                  95

Gly Val Thr Leu Gln Asp Leu Pro Glu Thr Glu Leu Pro Ala Val Leu
            100                 105                 110

Gln Pro Val Ala Glu Ala Met Asp Ala Ile Ala Ala Ala Asp Leu Ser
        115                 120                 125

Gln Thr Ser Gly Phe Gly Pro Phe Gly Pro Gln Gly Ile Gly Gln Tyr
    130                 135                 140

Thr Thr Trp Arg Asp Phe Ile Cys Ala Ile Ala Asp Pro His Val Tyr
145                 150                 155                 160

His Trp Gln Thr Val Met Asp Asp Thr Val Ser Ala Ser Val Ala Gln
                165                 170                 175

Ala Leu Asp Glu Leu Met Leu Trp Ala Glu Asp Cys Pro Glu Val Arg
            180                 185                 190

His Leu Val His Ala Asp Phe Gly Ser Asn Asn Val Leu Thr Asp Asn
        195                 200                 205

Gly Arg Ile Thr Ala Val Ile Asp Trp Ser Glu Ala Met Phe Gly Asp
    210                 215                 220

Ser Gln Tyr Glu Val Ala Asn Ile Phe Phe Trp Arg Pro Trp Leu Ala
225                 230                 235                 240
```

Cys Met Glu Gln Gln Thr Arg Tyr Phe Glu Arg Arg His Pro Glu Leu
245 250 255

Ala Gly Ser Pro Arg Leu Arg Ala Tyr Met Leu Arg Ile Gly Leu Asp
260 265 270

Gln Leu Tyr Gln Ser Leu Val Asp Gly Asn Phe Asp Asp Ala Ala Trp
275 280 285

Ala Gln Gly Arg Cys Asp Ala Ile Val Arg Ser Gly Ala Gly Thr Val
290 295 300

Gly Arg Thr Gln Ile Ala Arg Arg Ser Ala Ala Val Trp Thr Asp Gly
305 310 315 320

Cys Val Glu Val Leu Ala Asp Ser Gly Asn Arg Arg Pro Ser Thr Arg
325 330 335

Pro Arg Ala Lys Glu
340

<210> 60
<211> 341
<212> PRT
<213> artificial

<220>
<223> Synthetic Construct

<400> 60

Met Lys Lys Pro Glu Leu Thr Ala Thr Ser Val Glu Lys Phe Leu Ile
1 5 10 15

Glu Lys Phe Asp Ser Val Ser Asp Leu Met Gln Leu Ser Glu Gly Glu
20 25 30

Glu Ser Arg Ala Phe Ser Phe Asp Val Gly Gly Arg Gly Tyr Val Leu
35 40 45

Arg Val Asn Ser Cys Ala Asp Gly Phe Tyr Lys Asp Arg Tyr Val Tyr
50 55 60

Arg His Phe Ala Ser Ala Ala Leu Pro Ile Pro Glu Val Leu Asp Ile
65 70 75 80

Gly Glu Phe Ser Glu Ser Leu Thr Tyr Cys Ile Ser Arg Arg Ala Gln
85 90 95

Gly Val Thr Leu Gln Asp Leu Pro Glu Thr Glu Leu Pro Ala Val Leu
100 105 110

Gln Pro Val Ala Glu Ala Met Asp Ala Ile Ala Ala Ala Asp Leu Ser
115 120 125

```
Gln Thr Ser Gly Phe Gly Pro Phe Gly Pro Gln Gly Ile Gly Gln Tyr
    130                 135                 140

Thr Thr Trp Arg Asp Phe Ile Cys Ala Ile Ala Asp Pro His Val Tyr
145                 150                 155                 160

His Trp Gln Thr Val Met Asp Asp Thr Val Ser Ala Ser Val Ala Gln
                165                 170                 175

Ala Leu Asp Glu Leu Met Leu Trp Ala Glu Asp Cys Pro Glu Val Arg
            180                 185                 190

His Leu Val His Ala Asp Phe Gly Ser Asn Asn Val Leu Thr Asp Asn
        195                 200                 205

Gly Arg Ile Thr Ala Val Ile Asp Trp Ser Glu Ala Met Phe Gly Asp
    210                 215                 220

Ser Gln Tyr Glu Val Ala Asn Ile Phe Phe Trp Arg Pro Trp Leu Ala
225                 230                 235                 240

Cys Met Glu Gln Gln Thr Arg Tyr Phe Glu Arg Arg His Pro Glu Leu
                245                 250                 255

Ala Gly Ser Pro Arg Leu Arg Ala Tyr Met Leu Arg Ile Gly Leu Asp
            260                 265                 270

Gln Leu Tyr Gln Ser Leu Val Asp Gly Asn Phe Asp Asp Ala Ala Trp
        275                 280                 285

Ala Gln Gly Arg Cys Asp Ala Ile Val Arg Ser Gly Ala Gly Thr Val
    290                 295                 300

Gly Arg Thr Gln Ile Ala Arg Arg Ser Ala Ala Val Trp Thr Asp Gly
305                 310                 315                 320

Cys Val Glu Val Leu Ala Asp Ser Gly Asn Arg Arg Pro Ser Thr Arg
                325                 330                 335

Pro Arg Ala Lys Glu
            340
```