SEQUENCE LISTING

<110> Kyowa Hakko Kirin Co., Ltd.
Inter-University Research Institute Corporation Research Organization of Information and Systems

<120> Protein production method

<130> WO69874

<150> JP2009-140626
<151> 2009-06-11

<150> US61/186138
<151> 2009-06-11

<160> 17

<170> PatentIn version 3.3

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<211> 2788
<212> DNA
<213> Artificial

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<223> Description of artificial sequence; nonautologus Tol2 transposon

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cgctgatgcc cagtttaatt taaatgttat ttattctgcc tatgaaaatc gttttcacat 300

tatatgaaat tggtcagaca tgttcattgg tcctttggaa gtgacgtcat gtcacatcta 360

ttaccacaat gcacagcacc ttgacctgga aattagggaa attataacag tcaatcagtg 420

gaagaaaatg gaggaagtat gtgattcatc agcagctgcg agcagcacag tccaaaatca 480

gccacaggat caagagcacc cgtggccgta tcttcgcgaa ttcttttctt taagtggtgt 540

aaataaagat tcattcaaga tgaaatgtgt cctctgtctc ccgcttaata aagaaatatc 600

gagtcattaa tgacatcttt tcatttttgg gtgaactaac cctttaatgc tgtaatcaga 2100

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aaatttttga gtacttttta cacctctg 2788

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<223> Description of artificial sequence; Tol2-L transposon sequence

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aggcttgaca ctaacaattt tgagaatcag cttctactga agttaaatct gaggttttac 180

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Met Glu Glu Val Cys Asp Ser Ser Ala
1 5

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
10 15 20 25

tgg ccg tat ctt cgc gaa ttc ttt tct tta agt ggt gta aat aaa gat 207

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Trp Pro Tyr Leu Arg Glu Phe Phe Ser Leu Ser Gly Val Asn Lys Asp
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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

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
90                  95                  100                 105

gtt gac tca gtt ttc cca gtc aaa cat gtg tct cca gtc act gtg aac      447
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
                190                 195                 200

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
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tcc gct gca ctt gcc tgc aaa aga tta atg ggc tct cat act ttt gag      783
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Ser Ala Ala Leu Ala Cys Lys Arg Leu Met Gly Ser His Thr Phe Glu
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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
        300                 305                 310

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
                350                 355                 360

tta tgg aat aaa agc agc cga tcg gct cta gca gct gaa gct gtt gaa     1215
Leu Trp Asn Lys Ser Ser Arg Ser Ala Leu Ala Ala Glu Ala Val Glu
            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
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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
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aca cct ctt ccc gca tcg gct gcc tgt gag agg ctt ttc agc act gca     1935
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Thr Pro Leu Pro Ala Ser Ala Ala Cys Glu Arg Leu Phe Ser Thr Ala
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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
        620                 625                 630

gag aat cag ctt cta ctg aag tta aat ctg agg ttt tac aac ttt gag     2031
Glu Asn Gln Leu Leu Leu Lys Leu Asn Leu Arg Phe Tyr Asn Phe Glu
    635                 640                 645

tag cgtgtactgg cattagattg tctgtcttat agtttgataa ttaaatacaa          2084

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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
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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
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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
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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

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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
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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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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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Lys Arg Gly Met Asp Tyr Ile Arg Val His Leu Glu Pro Leu Asp His
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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
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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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cattagattg tctgtcttat agtttgataa ttaaatacaa acagttctaa agcaggataa 4440

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gttttctttc ttgcttttac ttttacttcc ttaatactca agtacaattt taatggagta 4560

ctttttttact 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

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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

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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

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

<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
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
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<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

<210> 13
<211> 1855
<212> DNA
<213> artificial

<220>
<223> nonautologus Tol1 transposon

<400> 13
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

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

atttttttatt 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 ttttatttttt 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

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

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                  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

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
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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

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

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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
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<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

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
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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

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

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