SEQUENCE LISTING

<110> Astellas Pharma Inc.

<120> Nucleic acid for treatment of mite allergy

<130> A19002A00

<150> JP2018-091963
<151> 2018-05-11

<160> 3

<170> PatentIn version 3.5

<210> 1
<211> 3123
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid encoding a chimeric protein

<220>
<221> CDS
<222> (1)..(3123)

<400> 1

```
atg gcg ccc cgc agc gcc cgg cga ccc ctg ctg ctg cta ctg ctg ttg        48
Met Ala Pro Arg Ser Ala Arg Arg Pro Leu Leu Leu Leu Leu Leu Leu
1               5                   10                  15

ctg ctg ctc ggc ctc atg cat tgt gcg tca gca gca atg ttt atg gtg        96
Leu Leu Leu Gly Leu Met His Cys Ala Ser Ala Ala Met Phe Met Val
            20                  25                  30

aaa aat ggc aac ggg acc gcg tgc ata atg gcc aac ttc tct gct gcc       144
Lys Asn Gly Asn Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala Ala
        35                  40                  45

ttc tca gtg aac tac gac acc aag agt ggc cct aag aac atg acc ctt       192
Phe Ser Val Asn Tyr Asp Thr Lys Ser Gly Pro Lys Asn Met Thr Leu
    50                  55                  60

gac ctg cca tca gat gcc aca gtg gtg ctc aac cgc agc tcc tgt gga       240
Asp Leu Pro Ser Asp Ala Thr Val Val Leu Asn Arg Ser Ser Cys Gly
65                  70                  75                  80

aaa gag aac act tct gac ccc agt ctc gtg att gct ttt gga aga gga       288
Lys Glu Asn Thr Ser Asp Pro Ser Leu Val Ile Ala Phe Gly Arg Gly
                85                  90                  95

cat aca ctc act ctc aat ttc acg aga aat gca aca cgt tac agc gtc       336
His Thr Leu Thr Leu Asn Phe Thr Arg Asn Ala Thr Arg Tyr Ser Val
            100                 105                 110
```

```
cag ctc atg agt ttt gtt tat aac ttg tca gac aca cac ctt ttc ccc        384
Gln Leu Met Ser Phe Val Tyr Asn Leu Ser Asp Thr His Leu Phe Pro
        115                 120                 125

aat gcg agc tcc aaa gaa atc aag act gtg gaa tct ata act gac atc        432
Asn Ala Ser Ser Lys Glu Ile Lys Thr Val Glu Ser Ile Thr Asp Ile
    130                 135                 140

agg gca gat ata gat aaa aaa tac aga tgt gtt agt ggc acc cag gtc        480
Arg Ala Asp Ile Asp Lys Lys Tyr Arg Cys Val Ser Gly Thr Gln Val
145                 150                 155                 160

cac atg aac aac gtg acc gta acg ctc cat gat gcc acc atc cag gcg        528
His Met Asn Asn Val Thr Val Thr Leu His Asp Ala Thr Ile Gln Ala
                165                 170                 175

tac ctt tcc aac agc agc ttc agc cgg gga gag aca cgc tgt gaa caa        576
Tyr Leu Ser Asn Ser Ser Phe Ser Arg Gly Glu Thr Arg Cys Glu Gln
            180                 185                 190

gac agg cct tcc cca acc aca gcg ccc cct gcg cca ccc agc ccc tcg        624
Asp Arg Pro Ser Pro Thr Thr Ala Pro Pro Ala Pro Pro Ser Pro Ser
        195                 200                 205

ccc tca ccc gtg ccc aag agc ccc tct gtg gac aag tac aac gtg agc        672
Pro Ser Pro Val Pro Lys Ser Pro Ser Val Asp Lys Tyr Asn Val Ser
    210                 215                 220

ggc acc aac ggg acc tgc ctg ctg gcc agc atg ggg ctg cag ctg aac        720
Gly Thr Asn Gly Thr Cys Leu Leu Ala Ser Met Gly Leu Gln Leu Asn
225                 230                 235                 240

ctc acc tat gag agg aag gac aac acg acg gtg aca agg ctt ctc aac        768
Leu Thr Tyr Glu Arg Lys Asp Asn Thr Thr Val Thr Arg Leu Leu Asn
                245                 250                 255

atc aac ccc aac aag acc tcg gcc agc ggg agc tgc ggc gcc cac ctg        816
Ile Asn Pro Asn Lys Thr Ser Ala Ser Gly Ser Cys Gly Ala His Leu
            260                 265                 270

gtg act ctg gag ctg cac agc gag ggc acc acc gtc ctg ctc ttc cag        864
Val Thr Leu Glu Leu His Ser Glu Gly Thr Thr Val Leu Leu Phe Gln
        275                 280                 285

ttc ggg atg aat gca agt tct agc cgg ttt ttc cta caa gga atc cag        912
Phe Gly Met Asn Ala Ser Ser Ser Arg Phe Phe Leu Gln Gly Ile Gln
    290                 295                 300

ttg aat aca att ctt cct gac gcc aga gac cct gcc ttt aaa gct gcc        960
Leu Asn Thr Ile Leu Pro Asp Ala Arg Asp Pro Ala Phe Lys Ala Ala
305                 310                 315                 320

aac ggc tcc ctg cga gcg ctg cag gcc aca gtc ggc aat tcc tac aag       1008
Asn Gly Ser Leu Arg Ala Leu Gln Ala Thr Val Gly Asn Ser Tyr Lys
                325                 330                 335

tgc aac gcg gag gag cac gtc cgt gtc acg aag gcg ttt tca gtc aat       1056
```

```
Cys Asn Ala Glu Glu His Val Arg Val Thr Lys Ala Phe Ser Val Asn
            340                 345                 350

ata ttc aaa gtg tgg gtc cag gct ttc aag gtg gaa ggt ggc cag ttt      1104
Ile Phe Lys Val Trp Val Gln Ala Phe Lys Val Glu Gly Gly Gln Phe
        355                 360                 365

ggc tct gtg gag gag tgt ctg ctg gac gag aac agc ctc gag act aac      1152
Gly Ser Val Glu Glu Cys Leu Leu Asp Glu Asn Ser Leu Glu Thr Asn
    370                 375                 380

gca tgc tcc att aac ggt aat gct ccc gcc gag att gat ctg cgc caa      1200
Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln
385                 390                 395                 400

atg aga acc gtt aca ccc ata agg tca gga gta gcc gct acg gaa tca      1248
Met Arg Thr Val Thr Pro Ile Arg Ser Gly Val Ala Ala Thr Glu Ser
                405                 410                 415

gca tac ctg gct tac aga aac cag tct ctg gac ctt gca gaa cag gaa      1296
Ala Tyr Leu Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu
            420                 425                 430

ctg gtg gac tgc gca tca cag cac aac gga tgt cac ggg gac acc ata      1344
Leu Val Asp Cys Ala Ser Gln His Asn Gly Cys His Gly Asp Thr Ile
        435                 440                 445

ccc aga ggg atc gag tat atc cag cac aat ggc gta gtg cag gaa agc      1392
Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser
    450                 455                 460

tac tat agg tat gtc gcg cga gag caa agc tgt agg cgc cct aac gca      1440
Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala
465                 470                 475                 480

cag cgt ttc gga atc tcc aat tac tgc cag atc tat ccg caa aac gtt      1488
Gln Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Gln Asn Val
                485                 490                 495

aac aaa atc cgt gaa gca ctg gcc caa acc cat agc gcc ata gct gtc      1536
Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val
            500                 505                 510

atc atc ggt atc aaa gat ctg gat gcc ttt cgg cac tac gat gga agg      1584
Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg
        515                 520                 525

act att ata cag cgc gac aat ggg tac cag ccc aat tat cac gca gtg      1632
Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val
    530                 535                 540

aac att gtg gga tat agc aat gcg caa ggt gtc gat tac tgg atc gtc      1680
Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val
545                 550                 555                 560

cgc aac tcc tgg gac aca aat tgg ggc gac aat ggc tat ggc tac ttt      1728
Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe
```

```
                565                 570                 575

gct gcc aat att gac ctc atg atg ata gag gag tat ccg tac gtc gtg      1776
Ala Ala Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val
            580                 585                 590

atc ctt ggc ggc ggc gga gat cag gta gac gtt aag gat tgc gct aac      1824
Ile Leu Gly Gly Gly Gly Asp Gln Val Asp Val Lys Asp Cys Ala Asn
        595                 600                 605

cat gag atc aag aaa gtc ttg gtg cca ggc tgt cat ggc tct gag cct      1872
His Glu Ile Lys Lys Val Leu Val Pro Gly Cys His Gly Ser Glu Pro
    610                 615                 620

tgc att atc cat cgc ggg aag cct ttt cag ctt gaa gcc gtc ttt gaa      1920
Cys Ile Ile His Arg Gly Lys Pro Phe Gln Leu Glu Ala Val Phe Glu
625                 630                 635                 640

gcc aac cag aac acc aag acg gcc aaa atc gag atc aag gct agc att      1968
Ala Asn Gln Asn Thr Lys Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile
                645                 650                 655

gat ggg ctg gaa gtc gac gtt cca ggc att gac cca aac gcc tgt cac      2016
Asp Gly Leu Glu Val Asp Val Pro Gly Ile Asp Pro Asn Ala Cys His
            660                 665                 670

tac atg aag tgc cct ctg gtg aaa ggg cag cag tac gac ata aag tac      2064
Tyr Met Lys Cys Pro Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr
        675                 680                 685

acc tgg aat gtg cct aaa atc gcc cca aaa tct gag aat gtg gtg gtt      2112
Thr Trp Asn Val Pro Lys Ile Ala Pro Lys Ser Glu Asn Val Val Val
    690                 695                 700

aca gtg aaa gtg atg ggc gat gac gga gtt ttg gcc tgt gcc ata gca      2160
Thr Val Lys Val Met Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala
705                 710                 715                 720

acc cat gct aag att agg gac ggc ggt ggt ggg gcg aat gat aac gat      2208
Thr His Ala Lys Ile Arg Asp Gly Gly Gly Gly Ala Asn Asp Asn Asp
                725                 730                 735

gac gac ccc aca act act gta cat cct acc acc aca gaa caa ccg gat      2256
Asp Asp Pro Thr Thr Thr Val His Pro Thr Thr Thr Glu Gln Pro Asp
            740                 745                 750

gat aag ttt gaa tgc cca agc aga ttc ggt tat ttc gcg gat cca aag      2304
Asp Lys Phe Glu Cys Pro Ser Arg Phe Gly Tyr Phe Ala Asp Pro Lys
        755                 760                 765

gat cct cac aag ttc tac att tgc tca aac tgg gag gca gtg cat aaa      2352
Asp Pro His Lys Phe Tyr Ile Cys Ser Asn Trp Glu Ala Val His Lys
    770                 775                 780

gac tgt ccc ggc aat act cgg tgg aat gag gac gag gaa act tgt acc      2400
Asp Cys Pro Gly Asn Thr Arg Trp Asn Glu Asp Glu Glu Thr Cys Thr
785                 790                 795                 800
```

```
ggc ggt gga gga gat cca atc cac tat gac aag ata aca gaa gaa atc       2448
Gly Gly Gly Gly Asp Pro Ile His Tyr Asp Lys Ile Thr Glu Glu Ile
                805                 810                 815

aat aag gct gtg gat gag gct gtt gcc gcc atc gaa aag tcc gag aca       2496
Asn Lys Ala Val Asp Glu Ala Val Ala Ala Ile Glu Lys Ser Glu Thr
            820                 825                 830

ttc gat ccc atg aaa gtc ccc gac cac agc gac aag ttt gaa cgg cac       2544
Phe Asp Pro Met Lys Val Pro Asp His Ser Asp Lys Phe Glu Arg His
        835                 840                 845

att gga att atc gac ctg aaa ggg gaa ctc gac atg cgg aac att cag       2592
Ile Gly Ile Ile Asp Leu Lys Gly Glu Leu Asp Met Arg Asn Ile Gln
    850                 855                 860

gtt aga ggc ctc aaa cag atg aaa cga gtt ggg gat gct aat gtg aag       2640
Val Arg Gly Leu Lys Gln Met Lys Arg Val Gly Asp Ala Asn Val Lys
865                 870                 875                 880

agt gag gat ggg gtg gtg aag gca cat ctg ctc gta ggg gtc cat gac       2688
Ser Glu Asp Gly Val Val Lys Ala His Leu Leu Val Gly Val His Asp
                885                 890                 895

gat gtg gtc agt atg gag tat gat ctg gcc tac aaa ctc ggt gat ttg       2736
Asp Val Val Ser Met Glu Tyr Asp Leu Ala Tyr Lys Leu Gly Asp Leu
            900                 905                 910

cac ccc aat aca cac gta atc agt gac att cag gac ttt gtg gtg gag       2784
His Pro Asn Thr His Val Ile Ser Asp Ile Gln Asp Phe Val Val Glu
        915                 920                 925

ctg tct ctg gaa gtt tcc gag gag gga aac atg acc ctg act tcc ttc       2832
Leu Ser Leu Glu Val Ser Glu Glu Gly Asn Met Thr Leu Thr Ser Phe
    930                 935                 940

gag gtg cga cag ttc gca aac gtc gtg aat cac att gga ggc ctg tct       2880
Glu Val Arg Gln Phe Ala Asn Val Val Asn His Ile Gly Gly Leu Ser
945                 950                 955                 960

att ctg gat cct atc ttt gcc gtg ttg agt gac gtg ctg aca gcg atc       2928
Ile Leu Asp Pro Ile Phe Ala Val Leu Ser Asp Val Leu Thr Ala Ile
                965                 970                 975

ttc caa gac acg gtc aga gcc gag atg acc aaa gtg ctc gct cca gcc       2976
Phe Gln Asp Thr Val Arg Ala Glu Met Thr Lys Val Leu Ala Pro Ala
            980                 985                 990

ttc aag aag gag ctt gag cgg aac  aac cag gaa ttc acg  ctg atc ccc     3024
Phe Lys Lys Glu Leu Glu Arg Asn  Asn Gln Glu Phe Thr  Leu Ile Pro
        995                 1000                1005

atc gct  gtg ggt ggt gcc ctg  gcg ggg ctg gtc ctc  atc gtc ctc       3069
Ile Ala  Val Gly Gly Ala Leu  Ala Gly Leu Val Leu  Ile Val Leu
    1010                1015                1020
```

```
atc gcc  tac ctc gtc ggc agg  aag agg agt cac gca  ggc tac cag        3114
Ile Ala  Tyr Leu Val Gly Arg  Lys Arg Ser His Ala  Gly Tyr Gln
    1025                 1030                 1035

act atc  tag                                                        3123
Thr Ile
    1040
```

<210> 2
<211> 1040
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

```
Met Ala Pro Arg Ser Ala Arg Arg Pro Leu Leu Leu Leu Leu Leu Leu
1               5                  10                  15

Leu Leu Leu Gly Leu Met His Cys Ala Ser Ala Ala Met Phe Met Val
            20                  25                  30

Lys Asn Gly Asn Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala Ala
        35                  40                  45

Phe Ser Val Asn Tyr Asp Thr Lys Ser Gly Pro Lys Asn Met Thr Leu
    50                  55                  60

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

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

His Thr Leu Thr Leu Asn Phe Thr Arg Asn Ala Thr Arg Tyr Ser Val
            100                 105                 110

Gln Leu Met Ser Phe Val Tyr Asn Leu Ser Asp Thr His Leu Phe Pro
        115                 120                 125

Asn Ala Ser Ser Lys Glu Ile Lys Thr Val Glu Ser Ile Thr Asp Ile
    130                 135                 140

Arg Ala Asp Ile Asp Lys Lys Tyr Arg Cys Val Ser Gly Thr Gln Val
145                 150                 155                 160
```

```
His Met Asn Asn Val Thr Val Thr Leu His Asp Ala Thr Ile Gln Ala
                165                 170                 175

Tyr Leu Ser Asn Ser Ser Phe Ser Arg Gly Glu Thr Arg Cys Glu Gln
            180                 185                 190

Asp Arg Pro Ser Pro Thr Thr Ala Pro Pro Ala Pro Pro Ser Pro Ser
        195                 200                 205

Pro Ser Pro Val Pro Lys Ser Pro Ser Val Asp Lys Tyr Asn Val Ser
    210                 215                 220

Gly Thr Asn Gly Thr Cys Leu Leu Ala Ser Met Gly Leu Gln Leu Asn
225                 230                 235                 240

Leu Thr Tyr Glu Arg Lys Asp Asn Thr Thr Val Thr Arg Leu Leu Asn
                245                 250                 255

Ile Asn Pro Asn Lys Thr Ser Ala Ser Gly Ser Cys Gly Ala His Leu
            260                 265                 270

Val Thr Leu Glu Leu His Ser Glu Gly Thr Thr Val Leu Leu Phe Gln
        275                 280                 285

Phe Gly Met Asn Ala Ser Ser Ser Arg Phe Phe Leu Gln Gly Ile Gln
    290                 295                 300

Leu Asn Thr Ile Leu Pro Asp Ala Arg Asp Pro Ala Phe Lys Ala Ala
305                 310                 315                 320

Asn Gly Ser Leu Arg Ala Leu Gln Ala Thr Val Gly Asn Ser Tyr Lys
                325                 330                 335

Cys Asn Ala Glu Glu His Val Arg Val Thr Lys Ala Phe Ser Val Asn
            340                 345                 350

Ile Phe Lys Val Trp Val Gln Ala Phe Lys Val Glu Gly Gly Gln Phe
        355                 360                 365

Gly Ser Val Glu Glu Cys Leu Leu Asp Glu Asn Ser Leu Glu Thr Asn
    370                 375                 380
```

Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln
385 390 395 400

Met Arg Thr Val Thr Pro Ile Arg Ser Gly Val Ala Ala Thr Glu Ser
405 410 415

Ala Tyr Leu Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu
420 425 430

Leu Val Asp Cys Ala Ser Gln His Asn Gly Cys His Gly Asp Thr Ile
435 440 445

Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser
450 455 460

Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala
465 470 475 480

Gln Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Gln Asn Val
485 490 495

Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val
500 505 510

Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg
515 520 525

Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val
530 535 540

Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val
545 550 555 560

Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe
565 570 575

Ala Ala Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val
580 585 590

Ile Leu Gly Gly Gly Gly Asp Gln Val Asp Val Lys Asp Cys Ala Asn
595 600 605

```
His Glu Ile Lys Lys Val Leu Val Pro Gly Cys His Gly Ser Glu Pro
    610                 615                 620

Cys Ile Ile His Arg Gly Lys Pro Phe Gln Leu Glu Ala Val Phe Glu
625                 630                 635                 640

Ala Asn Gln Asn Thr Lys Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile
                645                 650                 655

Asp Gly Leu Glu Val Asp Val Pro Gly Ile Asp Pro Asn Ala Cys His
            660                 665                 670

Tyr Met Lys Cys Pro Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr
        675                 680                 685

Thr Trp Asn Val Pro Lys Ile Ala Pro Lys Ser Glu Asn Val Val Val
    690                 695                 700

Thr Val Lys Val Met Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala
705                 710                 715                 720

Thr His Ala Lys Ile Arg Asp Gly Gly Gly Gly Ala Asn Asp Asn Asp
                725                 730                 735

Asp Asp Pro Thr Thr Thr Val His Pro Thr Thr Thr Glu Gln Pro Asp
            740                 745                 750

Asp Lys Phe Glu Cys Pro Ser Arg Phe Gly Tyr Phe Ala Asp Pro Lys
        755                 760                 765

Asp Pro His Lys Phe Tyr Ile Cys Ser Asn Trp Glu Ala Val His Lys
    770                 775                 780

Asp Cys Pro Gly Asn Thr Arg Trp Asn Glu Asp Glu Glu Thr Cys Thr
785                 790                 795                 800

Gly Gly Gly Gly Asp Pro Ile His Tyr Asp Lys Ile Thr Glu Glu Ile
                805                 810                 815

Asn Lys Ala Val Asp Glu Ala Val Ala Ala Ile Glu Lys Ser Glu Thr
            820                 825                 830

Phe Asp Pro Met Lys Val Pro Asp His Ser Asp Lys Phe Glu Arg His
```

835 840 845

Ile Gly Ile Ile Asp Leu Lys Gly Glu Leu Asp Met Arg Asn Ile Gln
850 855 860

Val Arg Gly Leu Lys Gln Met Lys Arg Val Gly Asp Ala Asn Val Lys
865 870 875 880

Ser Glu Asp Gly Val Val Lys Ala His Leu Leu Val Gly Val His Asp
885 890 895

Asp Val Val Ser Met Glu Tyr Asp Leu Ala Tyr Lys Leu Gly Asp Leu
900 905 910

His Pro Asn Thr His Val Ile Ser Asp Ile Gln Asp Phe Val Val Glu
915 920 925

Leu Ser Leu Glu Val Ser Glu Glu Gly Asn Met Thr Leu Thr Ser Phe
930 935 940

Glu Val Arg Gln Phe Ala Asn Val Val Asn His Ile Gly Gly Leu Ser
945 950 955 960

Ile Leu Asp Pro Ile Phe Ala Val Leu Ser Asp Val Leu Thr Ala Ile
965 970 975

Phe Gln Asp Thr Val Arg Ala Glu Met Thr Lys Val Leu Ala Pro Ala
980 985 990

Phe Lys Lys Glu Leu Glu Arg Asn Asn Gln Glu Phe Thr Leu Ile Pro
995 1000 1005

Ile Ala Val Gly Gly Ala Leu Ala Gly Leu Val Leu Ile Val Leu
1010 1015 1020

Ile Ala Tyr Leu Val Gly Arg Lys Arg Ser His Ala Gly Tyr Gln
1025 1030 1035

Thr Ile
1040

<210> 3
<211> 6127

<212> DNA
<213> Artificial Sequence

<220>
<223> A vector comprising nucleic acid encoding a chimeric protein

<400> 3
ccgcctaatg agcgggcttt tttttcttag ggtgcaaaag gagagcctgt aagcgggcac 60

tcttccgtgg tctggtggat aaattcgcaa gggtatcatg gcggacgacc ggggttcgag 120

ccccgtatcc ggccgtccgc cgtgatccat gcggttaccg cccgcgtgtc gaacccaggt 180

gtgcgacgtc agacaacggg ggagtgctcc ttttggcttc cttcccctc ttccgcttcc 240

tcgctcactg actcgctgcg ctcggtcgtt cggctgcggc gagcggtatc agctcactca 300

aaggcggtaa tacggttatc cacagaatca ggggataacg caggaaagaa catgtgagca 360

aaaggccagc aaaaggccag gaaccgtaaa aaggccgcgt tgctggcgtt tttccatagg 420

ctccgccccc ctgacgagca tcacaaaaat cgacgctcaa gtcagaggtg gcgaaacccg 480

acaggactat aaagatacca ggcgtttccc cctggaagct ccctcgtgcg ctctcctgtt 540

ccgaccctgc cgcttaccgg atacctgtcc gcctttctcc cttcgggaag cgtggcgctt 600

tctcatagct cacgctgtag gtatctcagt tcggtgtagg tcgttcgctc caagctgggc 660

tgtgtgcacg aacccccccgt tcagcccgac cgctgcgcct tatccggtaa ctatcgtctt 720

gagtccaacc cggtaagaca cgacttatcg ccactggcag cagccactgg taacaggatt 780

agcagagcga ggtatgtagg cggtgctaca gagttcttga agtggtggcc taactacggc 840

tacactagaa gaacagtatt tggtatctgc gctctgctga agccagttac cttcggaaaa 900

agagttggta gctcttgatc cggcaaacaa accaccgctg gtagcggtgg ttttttgtt 960

tgcaagcagc agattacgcg cagaaaaaaa ggatctcaag aagatccttt gatcttttct 1020

acggggtctg acgctcagtg gaacgaaaac tcacgttaag ggattttggt catgagatta 1080

tcaaaaagga tcttcaccta gatcctttta aattaaaaat gaagttttaa atcaatctaa 1140

agtatatatg agtaaacttg gtctgacagt taccaatgct taatcagtga ggcacctatc 1200

tcagcgatct gtctatttcg ttcatccata gttgcctgac tcctgcaaac cacgttgtgg 1260

tagaattggt aaagagagtc gtgtaaaata tcgagttcgc acatcttgtt gtctgattat 1320

tgatttttgg cgaaaccatt tgatcatatg acaagatgtg tatctacctt aacttaatga 1380

ttttgataaa aatcattagg taccccggct ctagatggca tgacattaac ctataaaaat 1440

aggcgtatca cgaggccctt tcgtctcgcg cgtttcggtg atgacggtga aaacctctga 1500

cacatgcagc tcccggagac ggtcacagct tgtctgtaag cggatgccgg gagcagacaa 1560

gcccgtcagg gcgcgtcagc gggtgttggc gggtgtcggg gctggcttaa ctatgcggca 1620

tcagagcaga ttgtactgag agtgcaccat atgcggtgtg aaataccgca cagatgcgta 1680

aggagaaaat accgcatcag attggctatt ggccattgca tacgttgtat ccatatcata 1740

atatgtacat ttatattggc tcatgtccaa cattaccgcc atgttgacat tgattattga 1800

ctagttatta atagtaatca attacggggt cattagttca tagcccatat atggagttcc 1860

gcgttacata acttacggta aatggcccgc ctggctgacc gcccaacgac ccccgcccat 1920

tgacgtcaat aatgacgtat gttcccatag taacgccaat agggactttc cattgacgtc 1980

aatgggtgga gtatttacgg taaactgccc acttggcagt acatcaagtg tatcatatgc 2040

caagtacgcc ccctattgac gtcaatgacg gtaaatggcc cgcctggcat tatgcccagt 2100

acatgacctt atgggacttt cctacttggc agtacatcta cgtattagtc atcgctatta 2160

ccatggtgat gcggttttgg cagtacatca atgggcgtgg atagcggttt gactcacggg 2220

gatttccaag tctccacccc attgacgtca atgggagttt gttttggcac caaaatcaac 2280

gggactttcc aaaatgtcgt aacaactccg ccccattgac gcaaatgggc ggtaggcgtg 2340

tacggtggga ggtctatata agcagagctc gtttagtgaa ccgtcagatc gcctggagac 2400

gccatccacg ctgttttgac ctccatagaa gacaccggga ccgatccagc ctccgcggct 2460

cgcatctctc cttcacgcgc ccgccgccct acctgaggcc gccatccacg ccggttgagt 2520

cgcgttctgc cgcctcccgc ctgtggtgcc tcctgaactg cgtccgccgt ctaggtaagt 2580

ttaaagctca ggtcgagacc gggcctttgt ccggcgctcc cttggagcct acctagactc 2640

agccggctct ccacgctttg cctgaccctg cttgctcaac tctagttctc tcgttaactt 2700

aatgagacag atagaaactg gtcttgtaga aacagagtag tcgcctgctt ttctgccagg 2760

tgctgacttc tctcccctgg gctttttttct ttttctcagg ttgaaaagaa gaagacgaag 2820

aagacgaaga agacaaaccg tcgtcgacat ggcgccccgc agcgcccggc gacccctgct 2880

gctgctactg ctgttgctgc tgctcggcct catgcattgt gcgtcagcag caatgtttat 2940

ggtgaaaaat ggcaacggga ccgcgtgcat aatggccaac ttctctgctg ccttctcagt 3000

gaactacgac accaagagtg gccctaagaa catgaccctt gacctgccat cagatgccac 3060

agtggtgctc aaccgcagct cctgtggaaa agagaacact tctgacccca gtctcgtgat 3120

tgcttttgga agaggacata cactcactct caatttcacg agaaatgcaa cacgttacag 3180

cgtccagctc atgagttttg tttataactt gtcagacaca cacctttcc ccaatgcgag 3240

ctccaaagaa atcaagactg tggaatctat aactgacatc agggcagata tagataaaaa 3300

atacagatgt gttagtggca cccaggtcca catgaacaac gtgaccgtaa cgctccatga 3360

tgccaccatc caggcgtacc tttccaacag cagcttcagc cggggagaga cacgctgtga 3420

acaagacagg ccttccccaa ccacagcgcc ccctgcgcca cccagcccct cgccctcacc 3480

cgtgcccaag agcccctctg tggacaagta caacgtgagc ggcaccaacg ggacctgcct 3540

gctggccagc atggggctgc agctgaacct cacctatgag aggaaggaca acacgacggt 3600

gacaaggctt ctcaacatca accccaacaa gacctcggcc agcgggagct gcggcgccca 3660

cctggtgact ctggagctgc acagcgaggg caccaccgtc ctgctcttcc agttcgggat 3720

gaatgcaagt tctagccggt ttttcctaca aggaatccag ttgaatacaa ttcttcctga 3780

cgccagagac cctgccttta aagctgccaa cggctccctg cgagcgctgc aggccacagt 3840

cggcaattcc tacaagtgca acgcggagga gcacgtccgt gtcacgaagg cgttttcagt 3900

caatatattc aaagtgtggg tccaggcttt caaggtggaa ggtggccagt ttggctctgt 3960

ggaggagtgt ctgctggacg agaacagcct cgagactaac gcatgctcca ttaacggtaa 4020

tgctcccgcc gagattgatc tgcgccaaat gagaaccgtt acacccataa ggtcaggagt 4080

agccgctacg gaatcagcat acctggctta cagaaaccag tctctggacc ttgcagaaca 4140

ggaactggtg gactgcgcat cacagcacaa cggatgtcac ggggacacca tacccagagg 4200

gatcgagtat atccagcaca atggcgtagt gcaggaaagc tactataggt atgtcgcgcg 4260

agagcaaagc tgtaggcgcc ctaacgcaca gcgtttcgga atctccaatt actgccagat 4320

ctatccgcaa aacgttaaca aaatccgtga agcactggcc caaacccata gcgccatagc 4380

tgtcatcatc ggtatcaaag atctggatgc ctttcggcac tacgatggaa ggactattat 4440

acagcgcgac aatgggtacc agcccaatta tcacgcagtg aacattgtgg gatatagcaa 4500

tgcgcaaggt gtcgattact ggatcgtccg caactcctgg gacacaaatt ggggcgacaa 4560

tggctatggc tactttgctg ccaatattga cctcatgatg atagaggagt atccgtacgt 4620

cgtgatcctt ggcggcggcg gagatcaggt agacgttaag gattgcgcta accatgagat 4680

caagaaagtc ttggtgccag gctgtcatgg ctctgagcct tgcattatcc atcgcgggaa 4740

gccttttcag cttgaagccg tctttgaagc caaccagaac accaagacgg ccaaaatcga 4800

gatcaaggct agcattgatg ggctggaagt cgacgttcca ggcattgacc caaacgcctg 4860

tcactacatg aagtgccctc tggtgaaagg gcagcagtac gacataaagt acacctggaa 4920

tgtgcctaaa atcgccccaa aatctgagaa tgtggtggtt acagtgaaag tgatgggcga 4980

tgacggagtt ttggcctgtg ccatagcaac ccatgctaag attagggacg gcggtggtgg 5040

ggcgaatgat aacgatgacg accccacaac tactgtacat cctaccacca cagaacaacc 5100

ggatgataag tttgaatgcc caagcagatt cggttatttc gcggatccaa aggatcctca 5160

caagttctac atttgctcaa actgggaggc agtgcataaa gactgtcccg gcaatactcg 5220

gtggaatgag gacgaggaaa cttgtaccgg cggtggagga gatccaatcc actatgacaa 5280

gataacagaa gaaatcaata aggctgtgga tgaggctgtt gccgccatcg aaaagtccga 5340

gacattcgat cccatgaaag tccccgacca cagcgacaag tttgaacggc acattggaat 5400

tatcgacctg aaaggggaac tcgacatgcg gaacattcag gttagaggcc tcaaacagat 5460

gaaacgagtt ggggatgcta atgtgaagag tgaggatggg gtggtgaagg cacatctgct 5520

cgtaggggtc catgacgatg tggtcagtat ggagtatgat ctggcctaca aactcggtga 5580

tttgcacccc aatacacacg taatcagtga cattcaggac tttgtggtgg agctgtctct 5640

ggaagtttcc gaggagggaa acatgaccct gacttccttc gaggtgcgac agttcgcaaa 5700

cgtcgtgaat cacattggag gcctgtctat tctggatcct atctttgccg tgttgagtga 5760

cgtgctgaca gcgatcttcc aagacacggt cagagccgag atgaccaaag tgctcgctcc 5820

agccttcaag aaggagcttg agcggaacaa ccaggaattc acgctgatcc ccatcgctgt 5880

gggtggtgcc ctggcggggc tggtcctcat cgtcctcatc gcctacctcg tcggcaggaa 5940

gaggagtcac gcaggctacc agactatcta gtaaggatct ttttccctct gccaaaaatt 6000

atggggacat catgaagccc cttgagcatc tgacttctgg ctaataaagg aaatttattt 6060

tcattgcaat agtgtgttgg aatttttgt gtctctcact cggaaggaca taagggcggc 6120

cgctagc 6127