SEQUENCE LISTING

<110> National University of Singapore

<120> BIOSYNTHESIS OF CANNABINOIDS FROM CANNABIGEROLIC ACID USING NOVEL CANNABINOID SYNTHASES

<130> 218005-0108PCT

<150> US 62/913,991
<151> 2019-10-11

<160> 135

<170> PatentIn version 3.5

<210> 1
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Strep Tag

<220>
<221> CDS
<222> (1)..(24)

<400> 1
tgg tca cat cca caa ttt gaa aag 24
Trp Ser His Pro Gln Phe Glu Lys
1 5

<210> 2
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

Trp Ser His Pro Gln Phe Glu Lys
1 5

<210> 3
<211> 57
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<220>
<223>  truncated alpha factor

<220>
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<222>  (1)..(57)

<400>  3
atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc  48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca ctt gca                                                      57
Ala Leu Ala

<210>  4
<211>  19
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  4

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

Ala Leu Ala

<210>  5
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<220>
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<220>
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atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc  48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

```
gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct                                    267
Ser Leu Glu Lys Arg Glu Ala Glu Ala
                85
```

<210>  6
<211>  89
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  6

```
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15


Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30


Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45


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


Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80


Ser Leu Glu Lys Arg Glu Ala Glu Ala
                85
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<210> 7
<211> 1431
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS1-D7MMG9

<220>
<221> CDS
<222> (1)..(1431)

<400> 7
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atg aac cac aac acc gtt gaa tcc aag gtt att cat acc tcc aag gac         48
Met Asn His Asn Thr Val Glu Ser Lys Val Ile His Thr Ser Lys Asp
1               5                   10                  15

tct tca ttc ttc tcc att ttg gac tcc tct att cag aac cca aga ttc         96
Ser Ser Phe Phe Ser Ile Leu Asp Ser Ser Ile Gln Asn Pro Arg Phe
            20                  25                  30

tct gtt tct gaa act cca aag cca gtt tcc att att act cca gtt aag        144
Ser Val Ser Glu Thr Pro Lys Pro Val Ser Ile Ile Thr Pro Val Lys
        35                  40                  45

gcc tct gat gtt caa acc gtt att aga tgt gct aga ttg cat ggt atc        192
Ala Ser Asp Val Gln Thr Val Ile Arg Cys Ala Arg Leu His Gly Ile
    50                  55                  60

cac gtt aga act aga tct gct ggt cat tgc tat gaa ggc ttg tct tat        240
His Val Arg Thr Arg Ser Ala Gly His Cys Tyr Glu Gly Leu Ser Tyr
65                  70                  75                  80

att gct tac aac aag cca ttc gtc gtc atc gac att aga aac ttg caa        288
Ile Ala Tyr Asn Lys Pro Phe Val Val Ile Asp Ile Arg Asn Leu Gln
                85                  90                  95

tcc atc tcc ttg gat gtt gat aat aga act ggt tgg gtt caa act ggt        336
Ser Ile Ser Leu Asp Val Asp Asn Arg Thr Gly Trp Val Gln Thr Gly
            100                 105                 110

gct act gct ggt gaa cta tat tac gaa att ggt aag act cca aag acc        384
Ala Thr Ala Gly Glu Leu Tyr Tyr Glu Ile Gly Lys Thr Pro Lys Thr
        115                 120                 125

ttg gct ttt cca gct ggt att cat cca act gtt gct gcc gat aac att        432
Leu Ala Phe Pro Ala Gly Ile His Pro Thr Val Ala Ala Asp Asn Ile
    130                 135                 140

att gat gct ttg gtt gtt gat gcc tcc ggt aga att ttg gat aga caa        480
Ile Asp Ala Leu Val Val Asp Ala Ser Gly Arg Ile Leu Asp Arg Gln
145                 150                 155                 160
```

```
gct atg ggt gaa gag tac tac ttt tgg gct att tgc ggt ggt ggt ggt        528
Ala Met Gly Glu Glu Tyr Tyr Phe Trp Ala Ile Cys Gly Gly Gly Gly
                165                 170                 175

tct tct ttt ggt att atc ttg tcc tgg aag atc aag ttg gtt gat gtt        576
Ser Ser Phe Gly Ile Ile Leu Ser Trp Lys Ile Lys Leu Val Asp Val
            180                 185                 190

cca tct acc atc act gtt ttc aag gtt aag agg acc tct aag aaa gaa        624
Pro Ser Thr Ile Thr Val Phe Lys Val Lys Arg Thr Ser Lys Lys Glu
        195                 200                 205

gcc gtt aga atc att aac aag tgg caa tac gtt gcc gat aag gtt cca        672
Ala Val Arg Ile Ile Asn Lys Trp Gln Tyr Val Ala Asp Lys Val Pro
    210                 215                 220

gat gat ttg ttc att aga acc acc ttg gaa agg tct aac aag aat gct        720
Asp Asp Leu Phe Ile Arg Thr Thr Leu Glu Arg Ser Asn Lys Asn Ala
225                 230                 235                 240

gtt cat gct ttg ttt acc ggc ttg tat ttg ggt cca gct aac aat ttg        768
Val His Ala Leu Phe Thr Gly Leu Tyr Leu Gly Pro Ala Asn Asn Leu
                245                 250                 255

ttg gcc ttg atg gaa gaa aag ttc cca gaa ttg ggt tta gaa aag gat        816
Leu Ala Leu Met Glu Glu Lys Phe Pro Glu Leu Gly Leu Glu Lys Asp
            260                 265                 270

ggt tgt act gaa atg tcc tgg gtt gaa tct gtt ttg tgg ttt gct gat        864
Gly Cys Thr Glu Met Ser Trp Val Glu Ser Val Leu Trp Phe Ala Asp
        275                 280                 285

ttc cac aag ggt gaa tct ttg gat gat gtt ttg acc aac aga gaa agg        912
Phe His Lys Gly Glu Ser Leu Asp Asp Val Leu Thr Asn Arg Glu Arg
    290                 295                 300

acc tct ttg tct tac aaa ggt aag gat gat ttc gtg caa gag cca att        960
Thr Ser Leu Ser Tyr Lys Gly Lys Asp Asp Phe Val Gln Glu Pro Ile
305                 310                 315                 320

cca gaa gct gct att caa gaa ctt tgg aga aga ttg gat gct cca gaa       1008
Pro Glu Ala Ala Ile Gln Glu Leu Trp Arg Arg Leu Asp Ala Pro Glu
                325                 330                 335

gca aga ttg gcc aag att att ttg act cca ttt ggt ggt aag atg tcc       1056
Ala Arg Leu Ala Lys Ile Ile Leu Thr Pro Phe Gly Gly Lys Met Ser
            340                 345                 350

gaa att gct gaa cac gaa act ttg ttc cca cat aga gaa ggt aac ttg       1104
Glu Ile Ala Glu His Glu Thr Leu Phe Pro His Arg Glu Gly Asn Leu
        355                 360                 365

tac gaa att caa tac gtc gcc tat tgg aga gaa gaa gag gat aag aat       1152
```

```
Tyr Glu Ile Gln Tyr Val Ala Tyr Trp Arg Glu Glu Glu Asp Lys Asn
    370                 375                 380

atg act ggc acc aac aaa tac ttg aag tgg gtt gat tca gtc tac gaa       1200
Met Thr Gly Thr Asn Lys Tyr Leu Lys Trp Val Asp Ser Val Tyr Glu
385                 390                 395                 400

ttg atg act cca tac gtt tct aaa tct cca aga ggt gct tac gtt aac       1248
Leu Met Thr Pro Tyr Val Ser Lys Ser Pro Arg Gly Ala Tyr Val Asn
                405                 410                 415

ttc gtt gat atg gat ttg ggt atg tac ctg ggt aag aaa aag acc aaa       1296
Phe Val Asp Met Asp Leu Gly Met Tyr Leu Gly Lys Lys Lys Thr Lys
            420                 425                 430

tac gaa gag ggt aaa tcc tgg ggt gtt aag tac ttt aag aac aac ttc       1344
Tyr Glu Glu Gly Lys Ser Trp Gly Val Lys Tyr Phe Lys Asn Asn Phe
        435                 440                 445

gaa aga ctg gtc aga gtc aag act tct gtt gat cca act gat ttc ttc       1392
Glu Arg Leu Val Arg Val Lys Thr Ser Val Asp Pro Thr Asp Phe Phe
    450                 455                 460

tgc gac gaa caa tct att ccc ttg ttg aac aaa gtc act                   1431
Cys Asp Glu Gln Ser Ile Pro Leu Leu Asn Lys Val Thr
465                 470                 475
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<210> 8
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 8

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Met Asn His Asn Thr Val Glu Ser Lys Val Ile His Thr Ser Lys Asp
1               5                   10                  15

Ser Ser Phe Phe Ser Ile Leu Asp Ser Ser Ile Gln Asn Pro Arg Phe
            20                  25                  30

Ser Val Ser Glu Thr Pro Lys Pro Val Ser Ile Ile Thr Pro Val Lys
        35                  40                  45

Ala Ser Asp Val Gln Thr Val Ile Arg Cys Ala Arg Leu His Gly Ile
    50                  55                  60
```

```
His Val Arg Thr Arg Ser Ala Gly His Cys Tyr Glu Gly Leu Ser Tyr
65                  70                  75                  80

Ile Ala Tyr Asn Lys Pro Phe Val Val Ile Asp Ile Arg Asn Leu Gln
                85                  90                  95

Ser Ile Ser Leu Asp Val Asp Asn Arg Thr Gly Trp Val Gln Thr Gly
            100                 105                 110

Ala Thr Ala Gly Glu Leu Tyr Tyr Glu Ile Gly Lys Thr Pro Lys Thr
        115                 120                 125

Leu Ala Phe Pro Ala Gly Ile His Pro Thr Val Ala Ala Asp Asn Ile
    130                 135                 140

Ile Asp Ala Leu Val Val Asp Ala Ser Gly Arg Ile Leu Asp Arg Gln
145                 150                 155                 160

Ala Met Gly Glu Glu Tyr Tyr Phe Trp Ala Ile Cys Gly Gly Gly Gly
                165                 170                 175

Ser Ser Phe Gly Ile Ile Leu Ser Trp Lys Ile Lys Leu Val Asp Val
            180                 185                 190

Pro Ser Thr Ile Thr Val Phe Lys Val Lys Arg Thr Ser Lys Lys Glu
        195                 200                 205

Ala Val Arg Ile Ile Asn Lys Trp Gln Tyr Val Ala Asp Lys Val Pro
    210                 215                 220

Asp Asp Leu Phe Ile Arg Thr Thr Leu Glu Arg Ser Asn Lys Asn Ala
225                 230                 235                 240

Val His Ala Leu Phe Thr Gly Leu Tyr Leu Gly Pro Ala Asn Asn Leu
                245                 250                 255

Leu Ala Leu Met Glu Glu Lys Phe Pro Glu Leu Gly Leu Glu Lys Asp
            260                 265                 270

Gly Cys Thr Glu Met Ser Trp Val Glu Ser Val Leu Trp Phe Ala Asp
        275                 280                 285
```

```
Phe His Lys Gly Glu Ser Leu Asp Asp Val Leu Thr Asn Arg Glu Arg
    290                 295                 300

Thr Ser Leu Ser Tyr Lys Gly Lys Asp Asp Phe Val Gln Glu Pro Ile
305                 310                 315                 320

Pro Glu Ala Ala Ile Gln Glu Leu Trp Arg Arg Leu Asp Ala Pro Glu
                325                 330                 335

Ala Arg Leu Ala Lys Ile Ile Leu Thr Pro Phe Gly Gly Lys Met Ser
            340                 345                 350

Glu Ile Ala Glu His Glu Thr Leu Phe Pro His Arg Glu Gly Asn Leu
        355                 360                 365

Tyr Glu Ile Gln Tyr Val Ala Tyr Trp Arg Glu Glu Glu Asp Lys Asn
    370                 375                 380

Met Thr Gly Thr Asn Lys Tyr Leu Lys Trp Val Asp Ser Val Tyr Glu
385                 390                 395                 400

Leu Met Thr Pro Tyr Val Ser Lys Ser Pro Arg Gly Ala Tyr Val Asn
                405                 410                 415

Phe Val Asp Met Asp Leu Gly Met Tyr Leu Gly Lys Lys Lys Thr Lys
            420                 425                 430

Tyr Glu Glu Gly Lys Ser Trp Gly Val Lys Tyr Phe Lys Asn Asn Phe
        435                 440                 445

Glu Arg Leu Val Arg Val Lys Thr Ser Val Asp Pro Thr Asp Phe Phe
    450                 455                 460

Cys Asp Glu Gln Ser Ile Pro Leu Leu Asn Lys Val Thr
465                 470                 475
```

<210> 9
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223>  CBS1-D7MMG9-strep-Tag

<220>
<221>  CDS
<222>  (1)..(1455)

<400>  9
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Met Asn His Asn Thr Val Glu Ser Lys Val Ile His Thr Ser Lys Asp
1               5                   10                  15

tct tca ttc ttc tcc att ttg gac tcc tct att cag aac cca aga ttc         96
Ser Ser Phe Phe Ser Ile Leu Asp Ser Ser Ile Gln Asn Pro Arg Phe
            20                  25                  30

tct gtt tct gaa act cca aag cca gtt tcc att att act cca gtt aag        144
Ser Val Ser Glu Thr Pro Lys Pro Val Ser Ile Ile Thr Pro Val Lys
        35                  40                  45

gcc tct gat gtt caa acc gtt att aga tgt gct aga ttg cat ggt atc        192
Ala Ser Asp Val Gln Thr Val Ile Arg Cys Ala Arg Leu His Gly Ile
    50                  55                  60

cac gtt aga act aga tct gct ggt cat tgc tat gaa ggc ttg tct tat        240
His Val Arg Thr Arg Ser Ala Gly His Cys Tyr Glu Gly Leu Ser Tyr
65                  70                  75                  80

att gct tac aac aag cca ttc gtc gtc atc gac att aga aac ttg caa        288
Ile Ala Tyr Asn Lys Pro Phe Val Val Ile Asp Ile Arg Asn Leu Gln
                85                  90                  95

tcc atc tcc ttg gat gtt gat aat aga act ggt tgg gtt caa act ggt        336
Ser Ile Ser Leu Asp Val Asp Asn Arg Thr Gly Trp Val Gln Thr Gly
            100                 105                 110

gct act gct ggt gaa cta tat tac gaa att ggt aag act cca aag acc        384
Ala Thr Ala Gly Glu Leu Tyr Tyr Glu Ile Gly Lys Thr Pro Lys Thr
        115                 120                 125

ttg gct ttt cca gct ggt att cat cca act gtt gct gcc gat aac att        432
Leu Ala Phe Pro Ala Gly Ile His Pro Thr Val Ala Ala Asp Asn Ile
    130                 135                 140

att gat gct ttg gtt gtt gat gcc tcc ggt aga att ttg gat aga caa        480
Ile Asp Ala Leu Val Val Asp Ala Ser Gly Arg Ile Leu Asp Arg Gln
145                 150                 155                 160

gct atg ggt gaa gag tac tac ttt tgg gct att tgc ggt ggt ggt ggt        528
Ala Met Gly Glu Glu Tyr Tyr Phe Trp Ala Ile Cys Gly Gly Gly Gly
                165                 170                 175
```

```
tct tct ttt ggt att atc ttg tcc tgg aag atc aag ttg gtt gat gtt        576
Ser Ser Phe Gly Ile Ile Leu Ser Trp Lys Ile Lys Leu Val Asp Val
            180                 185                 190

cca tct acc atc act gtt ttc aag gtt aag agg acc tct aag aaa gaa        624
Pro Ser Thr Ile Thr Val Phe Lys Val Lys Arg Thr Ser Lys Lys Glu
        195                 200                 205

gcc gtt aga atc att aac aag tgg caa tac gtt gcc gat aag gtt cca        672
Ala Val Arg Ile Ile Asn Lys Trp Gln Tyr Val Ala Asp Lys Val Pro
    210                 215                 220

gat gat ttg ttc att aga acc acc ttg gaa agg tct aac aag aat gct        720
Asp Asp Leu Phe Ile Arg Thr Thr Leu Glu Arg Ser Asn Lys Asn Ala
225                 230                 235                 240

gtt cat gct ttg ttt acc ggc ttg tat ttg ggt cca gct aac aat ttg        768
Val His Ala Leu Phe Thr Gly Leu Tyr Leu Gly Pro Ala Asn Asn Leu
                245                 250                 255

ttg gcc ttg atg gaa gaa aag ttc cca gaa ttg ggt tta gaa aag gat        816
Leu Ala Leu Met Glu Glu Lys Phe Pro Glu Leu Gly Leu Glu Lys Asp
            260                 265                 270

ggt tgt act gaa atg tcc tgg gtt gaa tct gtt ttg tgg ttt gct gat        864
Gly Cys Thr Glu Met Ser Trp Val Glu Ser Val Leu Trp Phe Ala Asp
        275                 280                 285

ttc cac aag ggt gaa tct ttg gat gat gtt ttg acc aac aga gaa agg        912
Phe His Lys Gly Glu Ser Leu Asp Asp Val Leu Thr Asn Arg Glu Arg
    290                 295                 300

acc tct ttg tct tac aaa ggt aag gat gat ttc gtg caa gag cca att        960
Thr Ser Leu Ser Tyr Lys Gly Lys Asp Asp Phe Val Gln Glu Pro Ile
305                 310                 315                 320

cca gaa gct gct att caa gaa ctt tgg aga aga ttg gat gct cca gaa       1008
Pro Glu Ala Ala Ile Gln Glu Leu Trp Arg Arg Leu Asp Ala Pro Glu
                325                 330                 335

gca aga ttg gcc aag att att ttg act cca ttt ggt ggt aag atg tcc       1056
Ala Arg Leu Ala Lys Ile Ile Leu Thr Pro Phe Gly Gly Lys Met Ser
            340                 345                 350

gaa att gct gaa cac gaa act ttg ttc cca cat aga gaa ggt aac ttg       1104
Glu Ile Ala Glu His Glu Thr Leu Phe Pro His Arg Glu Gly Asn Leu
        355                 360                 365

tac gaa att caa tac gtc gcc tat tgg aga gaa gaa gag gat aag aat       1152
Tyr Glu Ile Gln Tyr Val Ala Tyr Trp Arg Glu Glu Glu Asp Lys Asn
    370                 375                 380

atg act ggc acc aac aaa tac ttg aag tgg gtt gat tca gtc tac gaa       1200
Met Thr Gly Thr Asn Lys Tyr Leu Lys Trp Val Asp Ser Val Tyr Glu
```

```
385                 390                 395                 400

ttg atg act cca tac gtt tct aaa tct cca aga ggt gct tac gtt aac       1248
Leu Met Thr Pro Tyr Val Ser Lys Ser Pro Arg Gly Ala Tyr Val Asn
                405                 410                 415

ttc gtt gat atg gat ttg ggt atg tac ctg ggt aag aaa aag acc aaa       1296
Phe Val Asp Met Asp Leu Gly Met Tyr Leu Gly Lys Lys Lys Thr Lys
            420                 425                 430

tac gaa gag ggt aaa tcc tgg ggt gtt aag tac ttt aag aac aac ttc       1344
Tyr Glu Glu Gly Lys Ser Trp Gly Val Lys Tyr Phe Lys Asn Asn Phe
        435                 440                 445

gaa aga ctg gtc aga gtc aag act tct gtt gat cca act gat ttc ttc       1392
Glu Arg Leu Val Arg Val Lys Thr Ser Val Asp Pro Thr Asp Phe Phe
    450                 455                 460

tgc gac gaa caa tct att ccc ttg ttg aac aaa gtc act tgg tca cat       1440
Cys Asp Glu Gln Ser Ile Pro Leu Leu Asn Lys Val Thr Trp Ser His
465                 470                 475                 480

cca caa ttt gaa aag                                                  1455
Pro Gln Phe Glu Lys
                485
```

<210> 10
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 10

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Met Asn His Asn Thr Val Glu Ser Lys Val Ile His Thr Ser Lys Asp
1               5                   10                  15


Ser Ser Phe Phe Ser Ile Leu Asp Ser Ser Ile Gln Asn Pro Arg Phe
            20                  25                  30


Ser Val Ser Glu Thr Pro Lys Pro Val Ser Ile Ile Thr Pro Val Lys
        35                  40                  45


Ala Ser Asp Val Gln Thr Val Ile Arg Cys Ala Arg Leu His Gly Ile
    50                  55                  60


His Val Arg Thr Arg Ser Ala Gly His Cys Tyr Glu Gly Leu Ser Tyr
```

```
65                  70                  75                  80

Ile Ala Tyr Asn Lys Pro Phe Val Val Ile Asp Ile Arg Asn Leu Gln
                85                  90                  95

Ser Ile Ser Leu Asp Val Asp Asn Arg Thr Gly Trp Val Gln Thr Gly
            100                 105                 110

Ala Thr Ala Gly Glu Leu Tyr Tyr Glu Ile Gly Lys Thr Pro Lys Thr
        115                 120                 125

Leu Ala Phe Pro Ala Gly Ile His Pro Thr Val Ala Ala Asp Asn Ile
    130                 135                 140

Ile Asp Ala Leu Val Val Asp Ala Ser Gly Arg Ile Leu Asp Arg Gln
145                 150                 155                 160

Ala Met Gly Glu Glu Tyr Tyr Phe Trp Ala Ile Cys Gly Gly Gly Gly
                165                 170                 175

Ser Ser Phe Gly Ile Ile Leu Ser Trp Lys Ile Lys Leu Val Asp Val
            180                 185                 190

Pro Ser Thr Ile Thr Val Phe Lys Val Lys Arg Thr Ser Lys Lys Glu
        195                 200                 205

Ala Val Arg Ile Ile Asn Lys Trp Gln Tyr Val Ala Asp Lys Val Pro
    210                 215                 220

Asp Asp Leu Phe Ile Arg Thr Thr Leu Glu Arg Ser Asn Lys Asn Ala
225                 230                 235                 240

Val His Ala Leu Phe Thr Gly Leu Tyr Leu Gly Pro Ala Asn Asn Leu
                245                 250                 255

Leu Ala Leu Met Glu Glu Lys Phe Pro Glu Leu Gly Leu Glu Lys Asp
            260                 265                 270

Gly Cys Thr Glu Met Ser Trp Val Glu Ser Val Leu Trp Phe Ala Asp
        275                 280                 285
```

```
Phe His Lys Gly Glu Ser Leu Asp Asp Val Leu Thr Asn Arg Glu Arg
    290                 295                 300

Thr Ser Leu Ser Tyr Lys Gly Lys Asp Asp Phe Val Gln Glu Pro Ile
305                 310                 315                 320

Pro Glu Ala Ala Ile Gln Glu Leu Trp Arg Arg Leu Asp Ala Pro Glu
                325                 330                 335

Ala Arg Leu Ala Lys Ile Ile Leu Thr Pro Phe Gly Gly Lys Met Ser
            340                 345                 350

Glu Ile Ala Glu His Glu Thr Leu Phe Pro His Arg Glu Gly Asn Leu
        355                 360                 365

Tyr Glu Ile Gln Tyr Val Ala Tyr Trp Arg Glu Glu Glu Asp Lys Asn
    370                 375                 380

Met Thr Gly Thr Asn Lys Tyr Leu Lys Trp Val Asp Ser Val Tyr Glu
385                 390                 395                 400

Leu Met Thr Pro Tyr Val Ser Lys Ser Pro Arg Gly Ala Tyr Val Asn
                405                 410                 415

Phe Val Asp Met Asp Leu Gly Met Tyr Leu Gly Lys Lys Lys Thr Lys
            420                 425                 430

Tyr Glu Glu Gly Lys Ser Trp Gly Val Lys Tyr Phe Lys Asn Asn Phe
        435                 440                 445

Glu Arg Leu Val Arg Val Lys Thr Ser Val Asp Pro Thr Asp Phe Phe
    450                 455                 460

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

Pro Gln Phe Glu Lys
                485
```

<210>  11

<211> 1512
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS1-D7MMG9- truncated alpha factor strep Tag

<220>
<221> CDS
<222> (1)..(1512)

<400> 11
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atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                  10                  15

gca ctt gca atg aac cac aac acc gtt gaa tcc aag gtt att cat acc         96
Ala Leu Ala Met Asn His Asn Thr Val Glu Ser Lys Val Ile His Thr
            20                  25                  30

tcc aag gac tct tca ttc ttc tcc att ttg gac tcc tct att cag aac        144
Ser Lys Asp Ser Ser Phe Phe Ser Ile Leu Asp Ser Ser Ile Gln Asn
        35                  40                  45

cca aga ttc tct gtt tct gaa act cca aag cca gtt tcc att att act        192
Pro Arg Phe Ser Val Ser Glu Thr Pro Lys Pro Val Ser Ile Ile Thr
    50                  55                  60

cca gtt aag gcc tct gat gtt caa acc gtt att aga tgt gct aga ttg        240
Pro Val Lys Ala Ser Asp Val Gln Thr Val Ile Arg Cys Ala Arg Leu
65                  70                  75                  80

cat ggt atc cac gtt aga act aga tct gct ggt cat tgc tat gaa ggc        288
His Gly Ile His Val Arg Thr Arg Ser Ala Gly His Cys Tyr Glu Gly
                85                  90                  95

ttg tct tat att gct tac aac aag cca ttc gtc gtc atc gac att aga        336
Leu Ser Tyr Ile Ala Tyr Asn Lys Pro Phe Val Val Ile Asp Ile Arg
            100                 105                 110

aac ttg caa tcc atc tcc ttg gat gtt gat aat aga act ggt tgg gtt        384
Asn Leu Gln Ser Ile Ser Leu Asp Val Asp Asn Arg Thr Gly Trp Val
        115                 120                 125

caa act ggt gct act gct ggt gaa cta tat tac gaa att ggt aag act        432
Gln Thr Gly Ala Thr Ala Gly Glu Leu Tyr Tyr Glu Ile Gly Lys Thr
    130                 135                 140

cca aag acc ttg gct ttt cca gct ggt att cat cca act gtt gct gcc        480
Pro Lys Thr Leu Ala Phe Pro Ala Gly Ile His Pro Thr Val Ala Ala
145                 150                 155                 160

gat aac att att gat gct ttg gtt gtt gat gcc tcc ggt aga att ttg        528
```

```
Asp Asn Ile Ile Asp Ala Leu Val Val Asp Ala Ser Gly Arg Ile Leu
                165                 170                 175

gat aga caa gct atg ggt gaa gag tac tac ttt tgg gct att tgc ggt        576
Asp Arg Gln Ala Met Gly Glu Glu Tyr Tyr Phe Trp Ala Ile Cys Gly
            180                 185                 190

ggt ggt ggt tct tct ttt ggt att atc ttg tcc tgg aag atc aag ttg        624
Gly Gly Gly Ser Ser Phe Gly Ile Ile Leu Ser Trp Lys Ile Lys Leu
        195                 200                 205

gtt gat gtt cca tct acc atc act gtt ttc aag gtt aag agg acc tct        672
Val Asp Val Pro Ser Thr Ile Thr Val Phe Lys Val Lys Arg Thr Ser
    210                 215                 220

aag aaa gaa gcc gtt aga atc att aac aag tgg caa tac gtt gcc gat        720
Lys Lys Glu Ala Val Arg Ile Ile Asn Lys Trp Gln Tyr Val Ala Asp
225                 230                 235                 240

aag gtt cca gat gat ttg ttc att aga acc acc ttg gaa agg tct aac        768
Lys Val Pro Asp Asp Leu Phe Ile Arg Thr Thr Leu Glu Arg Ser Asn
                245                 250                 255

aag aat gct gtt cat gct ttg ttt acc ggc ttg tat ttg ggt cca gct        816
Lys Asn Ala Val His Ala Leu Phe Thr Gly Leu Tyr Leu Gly Pro Ala
            260                 265                 270

aac aat ttg ttg gcc ttg atg gaa gaa aag ttc cca gaa ttg ggt tta        864
Asn Asn Leu Leu Ala Leu Met Glu Glu Lys Phe Pro Glu Leu Gly Leu
        275                 280                 285

gaa aag gat ggt tgt act gaa atg tcc tgg gtt gaa tct gtt ttg tgg        912
Glu Lys Asp Gly Cys Thr Glu Met Ser Trp Val Glu Ser Val Leu Trp
    290                 295                 300

ttt gct gat ttc cac aag ggt gaa tct ttg gat gat gtt ttg acc aac        960
Phe Ala Asp Phe His Lys Gly Glu Ser Leu Asp Asp Val Leu Thr Asn
305                 310                 315                 320

aga gaa agg acc tct ttg tct tac aaa ggt aag gat gat ttc gtg caa       1008
Arg Glu Arg Thr Ser Leu Ser Tyr Lys Gly Lys Asp Asp Phe Val Gln
                325                 330                 335

gag cca att cca gaa gct gct att caa gaa ctt tgg aga aga ttg gat       1056
Glu Pro Ile Pro Glu Ala Ala Ile Gln Glu Leu Trp Arg Arg Leu Asp
            340                 345                 350

gct cca gaa gca aga ttg gcc aag att att ttg act cca ttt ggt ggt       1104
Ala Pro Glu Ala Arg Leu Ala Lys Ile Ile Leu Thr Pro Phe Gly Gly
        355                 360                 365

aag atg tcc gaa att gct gaa cac gaa act ttg ttc cca cat aga gaa       1152
Lys Met Ser Glu Ile Ala Glu His Glu Thr Leu Phe Pro His Arg Glu
    370                 375                 380
```

```
ggt aac ttg tac gaa att caa tac gtc gcc tat tgg aga gaa gaa gag       1200
Gly Asn Leu Tyr Glu Ile Gln Tyr Val Ala Tyr Trp Arg Glu Glu Glu
385                 390                 395                 400

gat aag aat atg act ggc acc aac aaa tac ttg aag tgg gtt gat tca       1248
Asp Lys Asn Met Thr Gly Thr Asn Lys Tyr Leu Lys Trp Val Asp Ser
                405                 410                 415

gtc tac gaa ttg atg act cca tac gtt tct aaa tct cca aga ggt gct       1296
Val Tyr Glu Leu Met Thr Pro Tyr Val Ser Lys Ser Pro Arg Gly Ala
            420                 425                 430

tac gtt aac ttc gtt gat atg gat ttg ggt atg tac ctg ggt aag aaa       1344
Tyr Val Asn Phe Val Asp Met Asp Leu Gly Met Tyr Leu Gly Lys Lys
        435                 440                 445

aag acc aaa tac gaa gag ggt aaa tcc tgg ggt gtt aag tac ttt aag       1392
Lys Thr Lys Tyr Glu Glu Gly Lys Ser Trp Gly Val Lys Tyr Phe Lys
    450                 455                 460

aac aac ttc gaa aga ctg gtc aga gtc aag act tct gtt gat cca act       1440
Asn Asn Phe Glu Arg Leu Val Arg Val Lys Thr Ser Val Asp Pro Thr
465                 470                 475                 480

gat ttc ttc tgc gac gaa caa tct att ccc ttg ttg aac aaa gtc act       1488
Asp Phe Phe Cys Asp Glu Gln Ser Ile Pro Leu Leu Asn Lys Val Thr
                485                 490                 495

tgg tca cat cca caa ttt gaa aag                                      1512
Trp Ser His Pro Gln Phe Glu Lys
            500
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<210> 12
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

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


Ala Leu Ala Met Asn His Asn Thr Val Glu Ser Lys Val Ile His Thr
            20                  25                  30


Ser Lys Asp Ser Ser Phe Phe Ser Ile Leu Asp Ser Ser Ile Gln Asn
        35                  40                  45
```

```
Pro Arg Phe Ser Val Ser Glu Thr Pro Lys Pro Val Ser Ile Ile Thr
    50                  55                  60

Pro Val Lys Ala Ser Asp Val Gln Thr Val Ile Arg Cys Ala Arg Leu
65                  70                  75                  80

His Gly Ile His Val Arg Thr Arg Ser Ala Gly His Cys Tyr Glu Gly
                85                  90                  95

Leu Ser Tyr Ile Ala Tyr Asn Lys Pro Phe Val Val Ile Asp Ile Arg
            100                 105                 110

Asn Leu Gln Ser Ile Ser Leu Asp Val Asp Asn Arg Thr Gly Trp Val
        115                 120                 125

Gln Thr Gly Ala Thr Ala Gly Glu Leu Tyr Tyr Glu Ile Gly Lys Thr
    130                 135                 140

Pro Lys Thr Leu Ala Phe Pro Ala Gly Ile His Pro Thr Val Ala Ala
145                 150                 155                 160

Asp Asn Ile Ile Asp Ala Leu Val Val Asp Ala Ser Gly Arg Ile Leu
                165                 170                 175

Asp Arg Gln Ala Met Gly Glu Glu Tyr Tyr Phe Trp Ala Ile Cys Gly
            180                 185                 190

Gly Gly Gly Ser Ser Phe Gly Ile Ile Leu Ser Trp Lys Ile Lys Leu
        195                 200                 205

Val Asp Val Pro Ser Thr Ile Thr Val Phe Lys Val Lys Arg Thr Ser
    210                 215                 220

Lys Lys Glu Ala Val Arg Ile Ile Asn Lys Trp Gln Tyr Val Ala Asp
225                 230                 235                 240

Lys Val Pro Asp Asp Leu Phe Ile Arg Thr Thr Leu Glu Arg Ser Asn
                245                 250                 255
```

```
Lys Asn Ala Val His Ala Leu Phe Thr Gly Leu Tyr Leu Gly Pro Ala
            260                 265                 270

Asn Asn Leu Leu Ala Leu Met Glu Glu Lys Phe Pro Glu Leu Gly Leu
        275                 280                 285

Glu Lys Asp Gly Cys Thr Glu Met Ser Trp Val Glu Ser Val Leu Trp
    290                 295                 300

Phe Ala Asp Phe His Lys Gly Glu Ser Leu Asp Asp Val Leu Thr Asn
305                 310                 315                 320

Arg Glu Arg Thr Ser Leu Ser Tyr Lys Gly Lys Asp Asp Phe Val Gln
                325                 330                 335

Glu Pro Ile Pro Glu Ala Ala Ile Gln Glu Leu Trp Arg Arg Leu Asp
            340                 345                 350

Ala Pro Glu Ala Arg Leu Ala Lys Ile Ile Leu Thr Pro Phe Gly Gly
        355                 360                 365

Lys Met Ser Glu Ile Ala Glu His Glu Thr Leu Phe Pro His Arg Glu
    370                 375                 380

Gly Asn Leu Tyr Glu Ile Gln Tyr Val Ala Tyr Trp Arg Glu Glu Glu
385                 390                 395                 400

Asp Lys Asn Met Thr Gly Thr Asn Lys Tyr Leu Lys Trp Val Asp Ser
                405                 410                 415

Val Tyr Glu Leu Met Thr Pro Tyr Val Ser Lys Ser Pro Arg Gly Ala
            420                 425                 430

Tyr Val Asn Phe Val Asp Met Asp Leu Gly Met Tyr Leu Gly Lys Lys
        435                 440                 445

Lys Thr Lys Tyr Glu Glu Gly Lys Ser Trp Gly Val Lys Tyr Phe Lys
    450                 455                 460

Asn Asn Phe Glu Arg Leu Val Arg Val Lys Thr Ser Val Asp Pro Thr
465                 470                 475                 480
```

```
Asp Phe Phe Cys Asp Glu Gln Ser Ile Pro Leu Leu Asn Lys Val Thr
                485                 490                 495


Trp Ser His Pro Gln Phe Glu Lys
            500


<210>  13
<211>  1722
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS1-D7MMG9-full alpha factor -strep Tag


<220>
<221>  CDS
<222>  (1)..(1722)

<400>  13
atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg aac cac aac acc gtt gaa        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Asn His Asn Thr Val Glu
                85                  90                  95

tcc aag gtt att cat acc tcc aag gac tct tca ttc ttc tcc att ttg        336
Ser Lys Val Ile His Thr Ser Lys Asp Ser Ser Phe Phe Ser Ile Leu
            100                 105                 110

gac tcc tct att cag aac cca aga ttc tct gtt tct gaa act cca aag        384
Asp Ser Ser Ile Gln Asn Pro Arg Phe Ser Val Ser Glu Thr Pro Lys
```

```
        115                 120                 125

cca gtt tcc att att act cca gtt aag gcc tct gat gtt caa acc gtt        432
Pro Val Ser Ile Ile Thr Pro Val Lys Ala Ser Asp Val Gln Thr Val
    130                 135                 140

att aga tgt gct aga ttg cat ggt atc cac gtt aga act aga tct gct        480
Ile Arg Cys Ala Arg Leu His Gly Ile His Val Arg Thr Arg Ser Ala
145                 150                 155                 160

ggt cat tgc tat gaa ggc ttg tct tat att gct tac aac aag cca ttc        528
Gly His Cys Tyr Glu Gly Leu Ser Tyr Ile Ala Tyr Asn Lys Pro Phe
                165                 170                 175

gtc gtc atc gac att aga aac ttg caa tcc atc tcc ttg gat gtt gat        576
Val Val Ile Asp Ile Arg Asn Leu Gln Ser Ile Ser Leu Asp Val Asp
            180                 185                 190

aat aga act ggt tgg gtt caa act ggt gct act gct ggt gaa cta tat        624
Asn Arg Thr Gly Trp Val Gln Thr Gly Ala Thr Ala Gly Glu Leu Tyr
        195                 200                 205

tac gaa att ggt aag act cca aag acc ttg gct ttt cca gct ggt att        672
Tyr Glu Ile Gly Lys Thr Pro Lys Thr Leu Ala Phe Pro Ala Gly Ile
    210                 215                 220

cat cca act gtt gct gcc gat aac att att gat gct ttg gtt gtt gat        720
His Pro Thr Val Ala Ala Asp Asn Ile Ile Asp Ala Leu Val Val Asp
225                 230                 235                 240

gcc tcc ggt aga att ttg gat aga caa gct atg ggt gaa gag tac tac        768
Ala Ser Gly Arg Ile Leu Asp Arg Gln Ala Met Gly Glu Glu Tyr Tyr
                245                 250                 255

ttt tgg gct att tgc ggt ggt ggt ggt tct tct ttt ggt att atc ttg        816
Phe Trp Ala Ile Cys Gly Gly Gly Gly Ser Ser Phe Gly Ile Ile Leu
            260                 265                 270

tcc tgg aag atc aag ttg gtt gat gtt cca tct acc atc act gtt ttc        864
Ser Trp Lys Ile Lys Leu Val Asp Val Pro Ser Thr Ile Thr Val Phe
        275                 280                 285

aag gtt aag agg acc tct aag aaa gaa gcc gtt aga atc att aac aag        912
Lys Val Lys Arg Thr Ser Lys Lys Glu Ala Val Arg Ile Ile Asn Lys
    290                 295                 300

tgg caa tac gtt gcc gat aag gtt cca gat gat ttg ttc att aga acc        960
Trp Gln Tyr Val Ala Asp Lys Val Pro Asp Asp Leu Phe Ile Arg Thr
305                 310                 315                 320

acc ttg gaa agg tct aac aag aat gct gtt cat gct ttg ttt acc ggc       1008
Thr Leu Glu Arg Ser Asn Lys Asn Ala Val His Ala Leu Phe Thr Gly
                325                 330                 335
```

```
ttg tat ttg ggt cca gct aac aat ttg ttg gcc ttg atg gaa gaa aag       1056
Leu Tyr Leu Gly Pro Ala Asn Asn Leu Leu Ala Leu Met Glu Glu Lys
            340                 345                 350

ttc cca gaa ttg ggt tta gaa aag gat ggt tgt act gaa atg tcc tgg       1104
Phe Pro Glu Leu Gly Leu Glu Lys Asp Gly Cys Thr Glu Met Ser Trp
        355                 360                 365

gtt gaa tct gtt ttg tgg ttt gct gat ttc cac aag ggt gaa tct ttg       1152
Val Glu Ser Val Leu Trp Phe Ala Asp Phe His Lys Gly Glu Ser Leu
    370                 375                 380

gat gat gtt ttg acc aac aga gaa agg acc tct ttg tct tac aaa ggt       1200
Asp Asp Val Leu Thr Asn Arg Glu Arg Thr Ser Leu Ser Tyr Lys Gly
385                 390                 395                 400

aag gat gat ttc gtg caa gag cca att cca gaa gct gct att caa gaa       1248
Lys Asp Asp Phe Val Gln Glu Pro Ile Pro Glu Ala Ala Ile Gln Glu
                405                 410                 415

ctt tgg aga aga ttg gat gct cca gaa gca aga ttg gcc aag att att       1296
Leu Trp Arg Arg Leu Asp Ala Pro Glu Ala Arg Leu Ala Lys Ile Ile
            420                 425                 430

ttg act cca ttt ggt ggt aag atg tcc gaa att gct gaa cac gaa act       1344
Leu Thr Pro Phe Gly Gly Lys Met Ser Glu Ile Ala Glu His Glu Thr
        435                 440                 445

ttg ttc cca cat aga gaa ggt aac ttg tac gaa att caa tac gtc gcc       1392
Leu Phe Pro His Arg Glu Gly Asn Leu Tyr Glu Ile Gln Tyr Val Ala
    450                 455                 460

tat tgg aga gaa gaa gag gat aag aat atg act ggc acc aac aaa tac       1440
Tyr Trp Arg Glu Glu Glu Asp Lys Asn Met Thr Gly Thr Asn Lys Tyr
465                 470                 475                 480

ttg aag tgg gtt gat tca gtc tac gaa ttg atg act cca tac gtt tct       1488
Leu Lys Trp Val Asp Ser Val Tyr Glu Leu Met Thr Pro Tyr Val Ser
                485                 490                 495

aaa tct cca aga ggt gct tac gtt aac ttc gtt gat atg gat ttg ggt       1536
Lys Ser Pro Arg Gly Ala Tyr Val Asn Phe Val Asp Met Asp Leu Gly
            500                 505                 510

atg tac ctg ggt aag aaa aag acc aaa tac gaa gag ggt aaa tcc tgg       1584
Met Tyr Leu Gly Lys Lys Lys Thr Lys Tyr Glu Glu Gly Lys Ser Trp
        515                 520                 525

ggt gtt aag tac ttt aag aac aac ttc gaa aga ctg gtc aga gtc aag       1632
Gly Val Lys Tyr Phe Lys Asn Asn Phe Glu Arg Leu Val Arg Val Lys
    530                 535                 540

act tct gtt gat cca act gat ttc ttc tgc gac gaa caa tct att ccc       1680
Thr Ser Val Asp Pro Thr Asp Phe Phe Cys Asp Glu Gln Ser Ile Pro
```

```
545                 550                 555                 560

ttg ttg aac aaa gtc act tgg tca cat cca caa ttt gaa aag              1722
Leu Leu Asn Lys Val Thr Trp Ser His Pro Gln Phe Glu Lys
                565                 570
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<210> 14
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14

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


Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30


Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45


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


Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80


Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Asn His Asn Thr Val Glu
                85                  90                  95


Ser Lys Val Ile His Thr Ser Lys Asp Ser Ser Phe Phe Ser Ile Leu
            100                 105                 110


Asp Ser Ser Ile Gln Asn Pro Arg Phe Ser Val Ser Glu Thr Pro Lys
        115                 120                 125


Pro Val Ser Ile Ile Thr Pro Val Lys Ala Ser Asp Val Gln Thr Val
    130                 135                 140


Ile Arg Cys Ala Arg Leu His Gly Ile His Val Arg Thr Arg Ser Ala
```

```
145                 150                 155                 160

Gly His Cys Tyr Glu Gly Leu Ser Tyr Ile Ala Tyr Asn Lys Pro Phe
                165                 170                 175

Val Val Ile Asp Ile Arg Asn Leu Gln Ser Ile Ser Leu Asp Val Asp
            180                 185                 190

Asn Arg Thr Gly Trp Val Gln Thr Gly Ala Thr Ala Gly Glu Leu Tyr
        195                 200                 205

Tyr Glu Ile Gly Lys Thr Pro Lys Thr Leu Ala Phe Pro Ala Gly Ile
    210                 215                 220

His Pro Thr Val Ala Ala Asp Asn Ile Ile Asp Ala Leu Val Val Asp
225                 230                 235                 240

Ala Ser Gly Arg Ile Leu Asp Arg Gln Ala Met Gly Glu Glu Tyr Tyr
                245                 250                 255

Phe Trp Ala Ile Cys Gly Gly Gly Gly Ser Ser Phe Gly Ile Ile Leu
            260                 265                 270

Ser Trp Lys Ile Lys Leu Val Asp Val Pro Ser Thr Ile Thr Val Phe
        275                 280                 285

Lys Val Lys Arg Thr Ser Lys Lys Glu Ala Val Arg Ile Ile Asn Lys
    290                 295                 300

Trp Gln Tyr Val Ala Asp Lys Val Pro Asp Asp Leu Phe Ile Arg Thr
305                 310                 315                 320

Thr Leu Glu Arg Ser Asn Lys Asn Ala Val His Ala Leu Phe Thr Gly
                325                 330                 335

Leu Tyr Leu Gly Pro Ala Asn Asn Leu Leu Ala Leu Met Glu Glu Lys
            340                 345                 350

Phe Pro Glu Leu Gly Leu Glu Lys Asp Gly Cys Thr Glu Met Ser Trp
        355                 360                 365
```

```
Val Glu Ser Val Leu Trp Phe Ala Asp Phe His Lys Gly Glu Ser Leu
    370                 375                 380

Asp Asp Val Leu Thr Asn Arg Glu Arg Thr Ser Leu Ser Tyr Lys Gly
385                 390                 395                 400

Lys Asp Asp Phe Val Gln Glu Pro Ile Pro Glu Ala Ala Ile Gln Glu
                405                 410                 415

Leu Trp Arg Arg Leu Asp Ala Pro Glu Ala Arg Leu Ala Lys Ile Ile
            420                 425                 430

Leu Thr Pro Phe Gly Gly Lys Met Ser Glu Ile Ala Glu His Glu Thr
        435                 440                 445

Leu Phe Pro His Arg Glu Gly Asn Leu Tyr Glu Ile Gln Tyr Val Ala
    450                 455                 460

Tyr Trp Arg Glu Glu Glu Asp Lys Asn Met Thr Gly Thr Asn Lys Tyr
465                 470                 475                 480

Leu Lys Trp Val Asp Ser Val Tyr Glu Leu Met Thr Pro Tyr Val Ser
                485                 490                 495

Lys Ser Pro Arg Gly Ala Tyr Val Asn Phe Val Asp Met Asp Leu Gly
            500                 505                 510

Met Tyr Leu Gly Lys Lys Lys Thr Lys Tyr Glu Glu Gly Lys Ser Trp
        515                 520                 525

Gly Val Lys Tyr Phe Lys Asn Asn Phe Glu Arg Leu Val Arg Val Lys
    530                 535                 540

Thr Ser Val Asp Pro Thr Asp Phe Phe Cys Asp Glu Gln Ser Ile Pro
545                 550                 555                 560

Leu Leu Asn Lys Val Thr Trp Ser His Pro Gln Phe Glu Lys
                565                 570
```

<210>  15

<211> 1011
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS5-M4DIE5

<220>
<221> CDS
<222> (1)..(1011)

<400> 15

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atg agg aag tac ggt ttg acc gtt gat aat gtt gtt gat gcc ttg atc         48
Met Arg Lys Tyr Gly Leu Thr Val Asp Asn Val Val Asp Ala Leu Ile
1               5                   10                  15

gtt gat gtt aac ggc aag ttg ttg aac aga tct act atg ggt gaa gat         96
Val Asp Val Asn Gly Lys Leu Leu Asn Arg Ser Thr Met Gly Glu Asp
            20                  25                  30

ttg ttc tgg gct att aga ggt ggt ggt ggc ggt tct ttt ggt gtt att        144
Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly Val Ile
        35                  40                  45

ttg tct tgg aag atc aac ttg gtt gac gtc cca gaa att ttg act gtt        192
Leu Ser Trp Lys Ile Asn Leu Val Asp Val Pro Glu Ile Leu Thr Val
    50                  55                  60

ttc aga gtt aac aag acc ttg gaa caa ggt ggt att gac gtc ttg tac        240
Phe Arg Val Asn Lys Thr Leu Glu Gln Gly Gly Ile Asp Val Leu Tyr
65                  70                  75                  80

aaa tgg caa ttg gtg tcc tct aag ttg ttg gat ggt ttg ttt ttg aga        288
Lys Trp Gln Leu Val Ser Ser Lys Leu Leu Asp Gly Leu Phe Leu Arg
                85                  90                  95

gcc ttg tct caa gtt gtc aac aga act atc acc gtt gaa ttt tac gct        336
Ala Leu Ser Gln Val Val Asn Arg Thr Ile Thr Val Glu Phe Tyr Ala
            100                 105                 110

cag ttt ttg ggt aga gcc gat gaa ttg gtt gct atc gtt aat caa tct        384
Gln Phe Leu Gly Arg Ala Asp Glu Leu Val Ala Ile Val Asn Gln Ser
        115                 120                 125

ttg cca gag ttg ggt ttg aag aga caa gat tgc ttg gaa atg tct tgg        432
Leu Pro Glu Leu Gly Leu Lys Arg Gln Asp Cys Leu Glu Met Ser Trp
    130                 135                 140

ttg aac act acc ttg ttt tgg gaa gat ttg cca gtt ggt act cca act        480
Leu Asn Thr Thr Leu Phe Trp Glu Asp Leu Pro Val Gly Thr Pro Thr
145                 150                 155                 160

tct gtt ttg ttg gat aga cca tct aag cca gag aag ttc ttc aag tct        528
```

```
Ser Val Leu Leu Asp Arg Pro Ser Lys Pro Glu Lys Phe Phe Lys Ser
                165                 170                 175

aaa tcc gat tac gtc aag aag ccc att cca aaa gag ggt att aag aaa        576
Lys Ser Asp Tyr Val Lys Lys Pro Ile Pro Lys Glu Gly Ile Lys Lys
            180                 185                 190

ttg tgg gaa gcc ttg ttg gag ttt aac aac aac aat atc gtc tac atg        624
Leu Trp Glu Ala Leu Leu Glu Phe Asn Asn Asn Asn Ile Val Tyr Met
        195                 200                 205

cag tgg aat cca tac ggt ggt gtt atg gat act gtt cca gct gct gct        672
Gln Trp Asn Pro Tyr Gly Gly Val Met Asp Thr Val Pro Ala Ala Ala
    210                 215                 220

act cca ttt cca cat aga aaa ggt aac ttg ttc gaa gtc cag tac tac        720
Thr Pro Phe Pro His Arg Lys Gly Asn Leu Phe Glu Val Gln Tyr Tyr
225                 230                 235                 240

act tct tgg ttg gat gct aat gct aca atg ggt tct ttg gac atg atg        768
Thr Ser Trp Leu Asp Ala Asn Ala Thr Met Gly Ser Leu Asp Met Met
                245                 250                 255

aag aag ttg tac gaa gtt gct gaa ccc tac gtt tct tct aat cca aga        816
Lys Lys Leu Tyr Glu Val Ala Glu Pro Tyr Val Ser Ser Asn Pro Arg
            260                 265                 270

gaa gcc ttt ttg aac tac aga gac atc gac att ggt agc aat cca tct        864
Glu Ala Phe Leu Asn Tyr Arg Asp Ile Asp Ile Gly Ser Asn Pro Ser
        275                 280                 285

aac gaa act aat gtt gaa gaa gcc gaa atc tac ggc tct aag tac ttt        912
Asn Glu Thr Asn Val Glu Glu Ala Glu Ile Tyr Gly Ser Lys Tyr Phe
    290                 295                 300

gtt ggt aac ttg aag aga ttg atg gaa gtc aag gct aag tac gat cca        960
Val Gly Asn Leu Lys Arg Leu Met Glu Val Lys Ala Lys Tyr Asp Pro
305                 310                 315                 320

gaa aac ttt ttc aag aac gag caa tct att cca cca gcc aga gtt aag       1008
Glu Asn Phe Phe Lys Asn Glu Gln Ser Ile Pro Pro Ala Arg Val Lys
                325                 330                 335

caa                                                                  1011
Gln
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<210> 16
<211> 337
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 16

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Met Arg Lys Tyr Gly Leu Thr Val Asp Asn Val Val Asp Ala Leu Ile
1               5                  10                  15


Val Asp Val Asn Gly Lys Leu Leu Asn Arg Ser Thr Met Gly Glu Asp
            20                  25                  30


Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly Val Ile
        35                  40                  45


Leu Ser Trp Lys Ile Asn Leu Val Asp Val Pro Glu Ile Leu Thr Val
    50                  55                  60


Phe Arg Val Asn Lys Thr Leu Glu Gln Gly Gly Ile Asp Val Leu Tyr
65                  70                  75                  80


Lys Trp Gln Leu Val Ser Ser Lys Leu Leu Asp Gly Leu Phe Leu Arg
                85                  90                  95


Ala Leu Ser Gln Val Val Asn Arg Thr Ile Thr Val Glu Phe Tyr Ala
            100                 105                 110


Gln Phe Leu Gly Arg Ala Asp Glu Leu Val Ala Ile Val Asn Gln Ser
        115                 120                 125


Leu Pro Glu Leu Gly Leu Lys Arg Gln Asp Cys Leu Glu Met Ser Trp
    130                 135                 140


Leu Asn Thr Thr Leu Phe Trp Glu Asp Leu Pro Val Gly Thr Pro Thr
145                 150                 155                 160


Ser Val Leu Leu Asp Arg Pro Ser Lys Pro Glu Lys Phe Phe Lys Ser
                165                 170                 175


Lys Ser Asp Tyr Val Lys Lys Pro Ile Pro Lys Glu Gly Ile Lys Lys
            180                 185                 190


Leu Trp Glu Ala Leu Leu Glu Phe Asn Asn Asn Asn Ile Val Tyr Met
        195                 200                 205
```

```
Gln Trp Asn Pro Tyr Gly Gly Val Met Asp Thr Val Pro Ala Ala Ala
    210                 215                 220

Thr Pro Phe Pro His Arg Lys Gly Asn Leu Phe Glu Val Gln Tyr Tyr
225                 230                 235                 240

Thr Ser Trp Leu Asp Ala Asn Ala Thr Met Gly Ser Leu Asp Met Met
                245                 250                 255

Lys Lys Leu Tyr Glu Val Ala Glu Pro Tyr Val Ser Ser Asn Pro Arg
            260                 265                 270

Glu Ala Phe Leu Asn Tyr Arg Asp Ile Asp Ile Gly Ser Asn Pro Ser
        275                 280                 285

Asn Glu Thr Asn Val Glu Glu Ala Glu Ile Tyr Gly Ser Lys Tyr Phe
    290                 295                 300

Val Gly Asn Leu Lys Arg Leu Met Glu Val Lys Ala Lys Tyr Asp Pro
305                 310                 315                 320

Glu Asn Phe Phe Lys Asn Glu Gln Ser Ile Pro Pro Ala Arg Val Lys
                325                 330                 335

Gln
```

<210>  17
<211>  1035
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS5-M4DIE5 strep Tag

<220>
<221>  CDS
<222>  (1)..(1035)

<400>  17

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atg agg aag tac ggt ttg acc gtt gat aat gtt gtt gat gcc ttg atc         48
Met Arg Lys Tyr Gly Leu Thr Val Asp Asn Val Val Asp Ala Leu Ile
```

```
1               5                   10                  15

gtt gat gtt aac ggc aag ttg ttg aac aga tct act atg ggt gaa gat         96
Val Asp Val Asn Gly Lys Leu Leu Asn Arg Ser Thr Met Gly Glu Asp
            20                  25                  30

ttg ttc tgg gct att aga ggt ggt ggt ggc ggt tct ttt ggt gtt att        144
Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ser Phe Gly Val Ile
        35                  40                  45

ttg tct tgg aag atc aac ttg gtt gac gtc cca gaa att ttg act gtt        192
Leu Ser Trp Lys Ile Asn Leu Val Asp Val Pro Glu Ile Leu Thr Val
    50                  55                  60

ttc aga gtt aac aag acc ttg gaa caa ggt ggt att gac gtc ttg tac        240
Phe Arg Val Asn Lys Thr Leu Glu Gln Gly Gly Ile Asp Val Leu Tyr
65                  70                  75                  80

aaa tgg caa ttg gtg tcc tct aag ttg ttg gat ggt ttg ttt ttg aga        288
Lys Trp Gln Leu Val Ser Ser Lys Leu Leu Asp Gly Leu Phe Leu Arg
                85                  90                  95

gcc ttg tct caa gtt gtc aac aga act atc acc gtt gaa ttt tac gct        336
Ala Leu Ser Gln Val Val Asn Arg Thr Ile Thr Val Glu Phe Tyr Ala
            100                 105                 110

cag ttt ttg ggt aga gcc gat gaa ttg gtt gct atc gtt aat caa tct        384
Gln Phe Leu Gly Arg Ala Asp Glu Leu Val Ala Ile Val Asn Gln Ser
        115                 120                 125

ttg cca gag ttg ggt ttg aag aga caa gat tgc ttg gaa atg tct tgg        432
Leu Pro Glu Leu Gly Leu Lys Arg Gln Asp Cys Leu Glu Met Ser Trp
    130                 135                 140

ttg aac act acc ttg ttt tgg gaa gat ttg cca gtt ggt act cca act        480
Leu Asn Thr Thr Leu Phe Trp Glu Asp Leu Pro Val Gly Thr Pro Thr
145                 150                 155                 160

tct gtt ttg ttg gat aga cca tct aag cca gag aag ttc ttc aag tct        528
Ser Val Leu Leu Asp Arg Pro Ser Lys Pro Glu Lys Phe Phe Lys Ser
                165                 170                 175

aaa tcc gat tac gtc aag aag ccc att cca aaa gag ggt att aag aaa        576
Lys Ser Asp Tyr Val Lys Lys Pro Ile Pro Lys Glu Gly Ile Lys Lys
            180                 185                 190

ttg tgg gaa gcc ttg ttg gag ttt aac aac aac aat atc gtc tac atg        624
Leu Trp Glu Ala Leu Leu Glu Phe Asn Asn Asn Asn Ile Val Tyr Met
        195                 200                 205

cag tgg aat cca tac ggt ggt gtt atg gat act gtt cca gct gct gct        672
Gln Trp Asn Pro Tyr Gly Gly Val Met Asp Thr Val Pro Ala Ala Ala
    210                 215                 220
```

```
act cca ttt cca cat aga aaa ggt aac ttg ttc gaa gtc cag tac tac        720
Thr Pro Phe Pro His Arg Lys Gly Asn Leu Phe Glu Val Gln Tyr Tyr
225                 230                 235                 240

act tct tgg ttg gat gct aat gct aca atg ggt tct ttg gac atg atg        768
Thr Ser Trp Leu Asp Ala Asn Ala Thr Met Gly Ser Leu Asp Met Met
                245                 250                 255

aag aag ttg tac gaa gtt gct gaa ccc tac gtt tct tct aat cca aga        816
Lys Lys Leu Tyr Glu Val Ala Glu Pro Tyr Val Ser Ser Asn Pro Arg
            260                 265                 270

gaa gcc ttt ttg aac tac aga gac atc gac att ggt agc aat cca tct        864
Glu Ala Phe Leu Asn Tyr Arg Asp Ile Asp Ile Gly Ser Asn Pro Ser
        275                 280                 285

aac gaa act aat gtt gaa gaa gcc gaa atc tac ggc tct aag tac ttt        912
Asn Glu Thr Asn Val Glu Glu Ala Glu Ile Tyr Gly Ser Lys Tyr Phe
    290                 295                 300

gtt ggt aac ttg aag aga ttg atg gaa gtc aag gct aag tac gat cca        960
Val Gly Asn Leu Lys Arg Leu Met Glu Val Lys Ala Lys Tyr Asp Pro
305                 310                 315                 320

gaa aac ttt ttc aag aac gag caa tct att cca cca gcc aga gtt aag       1008
Glu Asn Phe Phe Lys Asn Glu Gln Ser Ile Pro Pro Ala Arg Val Lys
                325                 330                 335

caa tgg tca cat cca caa ttt gaa aag                                  1035
Gln Trp Ser His Pro Gln Phe Glu Lys
            340                 345
```

<210> 18
<211> 345
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18

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Met Arg Lys Tyr Gly Leu Thr Val Asp Asn Val Val Asp Ala Leu Ile
1               5                   10                  15


Val Asp Val Asn Gly Lys Leu Leu Asn Arg Ser Thr Met Gly Glu Asp
            20                  25                  30


Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly Val Ile
        35                  40                  45
```

```
Leu Ser Trp Lys Ile Asn Leu Val Asp Val Pro Glu Ile Leu Thr Val
    50                  55                  60

Phe Arg Val Asn Lys Thr Leu Glu Gln Gly Gly Ile Asp Val Leu Tyr
65                  70                  75                  80

Lys Trp Gln Leu Val Ser Ser Lys Leu Leu Asp Gly Leu Phe Leu Arg
                85                  90                  95

Ala Leu Ser Gln Val Val Asn Arg Thr Ile Thr Val Glu Phe Tyr Ala
            100                 105                 110

Gln Phe Leu Gly Arg Ala Asp Glu Leu Val Ala Ile Val Asn Gln Ser
        115                 120                 125

Leu Pro Glu Leu Gly Leu Lys Arg Gln Asp Cys Leu Glu Met Ser Trp
    130                 135                 140

Leu Asn Thr Thr Leu Phe Trp Glu Asp Leu Pro Val Gly Thr Pro Thr
145                 150                 155                 160

Ser Val Leu Leu Asp Arg Pro Ser Lys Pro Glu Lys Phe Phe Lys Ser
                165                 170                 175

Lys Ser Asp Tyr Val Lys Lys Pro Ile Pro Lys Glu Gly Ile Lys Lys
            180                 185                 190

Leu Trp Glu Ala Leu Leu Glu Phe Asn Asn Asn Asn Ile Val Tyr Met
        195                 200                 205

Gln Trp Asn Pro Tyr Gly Gly Val Met Asp Thr Val Pro Ala Ala Ala
    210                 215                 220

Thr Pro Phe Pro His Arg Lys Gly Asn Leu Phe Glu Val Gln Tyr Tyr
225                 230                 235                 240

Thr Ser Trp Leu Asp Ala Asn Ala Thr Met Gly Ser Leu Asp Met Met
                245                 250                 255

Lys Lys Leu Tyr Glu Val Ala Glu Pro Tyr Val Ser Ser Asn Pro Arg
```

260 265 270

Glu Ala Phe Leu Asn Tyr Arg Asp Ile Asp Ile Gly Ser Asn Pro Ser
275 280 285

Asn Glu Thr Asn Val Glu Glu Ala Glu Ile Tyr Gly Ser Lys Tyr Phe
290 295 300

Val Gly Asn Leu Lys Arg Leu Met Glu Val Lys Ala Lys Tyr Asp Pro
305 310 315 320

Glu Asn Phe Phe Lys Asn Glu Gln Ser Ile Pro Pro Ala Arg Val Lys
325 330 335

Gln Trp Ser His Pro Gln Phe Glu Lys
340 345

<210> 19
<211> 1092
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS5-M4DIE5-truncated alpha factor strep Tag

<400> 19
atgagatttc cttccatctt cacggctgtg ctatttgcag catcctccgc acttgcaatg 60

aggaagtacg gtttgaccgt tgataatgtt gttgatgcct tgatcgttga tgttaacggc 120

aagttgttga acagatctac tatgggtgaa gatttgttct gggctattag aggtggtggt 180

ggcggttctt ttggtgttat tttgtcttgg aagatcaact tggttgacgt cccagaaatt 240

ttgactgttt tcagagttaa caagaccttg gaacaaggtg gtattgacgt cttgtacaaa 300

tggcaattgg tgtcctctaa gttgttggat ggtttgtttt tgagagcctt gtctcaagtt 360

gtcaacagaa ctatcaccgt tgaattttac gctcagtttt tgggtagagc cgatgaattg 420

gttgctatcg ttaatcaatc tttgccagag ttgggtttga agagacaaga ttgcttggaa 480

atgtcttggt tgaacactac cttgttttgg gaagatttgc cagttggtac tccaacttct 540

gttttgttgg atagaccatc taagccagag aagttcttca agtctaaatc cgattacgtc 600

aagaagccca ttccaaaaga gggtattaag aaattgtggg aagccttgtt ggagtttaac 660

```
aacaacaata tcgtctacat gcagtggaat ccatacggtg gtgttatgga tactgttcca      720

gctgctgcta ctccatttcc acatagaaaa ggtaacttgt tcgaagtcca gtactacact      780

tcttggttgg atgctaatgc tacaatgggt tctttggaca tgatgaagaa gttgtacgaa      840

gttgctgaac cctacgtttc ttctaatcca agagaagcct ttttgaacta cagagacatc      900

gacattggta gcaatccatc taacgaaact aatgttgaag aagccgaaat ctacggctct      960

aagtactttg ttggtaactt gaagagattg atggaagtca aggctaagta cgatccagaa     1020

aacttttca agaacgagca atctattcca ccagccagag ttaagcaatg gtcacatcca     1080

caatttgaaa ag                                                        1092
```

<210> 20
<211> 1302
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS5-M4DIE5-nucleotide-full alpha factor strep Tag

<220>
<221> CDS
<222> (1)..(1302)

<400> 20

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atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg agg aag tac ggt ttg acc        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Arg Lys Tyr Gly Leu Thr
                85                  90                  95
```

```
gtt gat aat gtt gtt gat gcc ttg atc gtt gat gtt aac ggc aag ttg        336
Val Asp Asn Val Val Asp Ala Leu Ile Val Asp Val Asn Gly Lys Leu
            100                 105                 110

ttg aac aga tct act atg ggt gaa gat ttg ttc tgg gct att aga ggt        384
Leu Asn Arg Ser Thr Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly
        115                 120                 125

ggt ggt ggc ggt tct ttt ggt gtt att ttg tct tgg aag atc aac ttg        432
Gly Gly Gly Gly Ser Phe Gly Val Ile Leu Ser Trp Lys Ile Asn Leu
    130                 135                 140

gtt gac gtc cca gaa att ttg act gtt ttc aga gtt aac aag acc ttg        480
Val Asp Val Pro Glu Ile Leu Thr Val Phe Arg Val Asn Lys Thr Leu
145                 150                 155                 160

gaa caa ggt ggt att gac gtc ttg tac aaa tgg caa ttg gtg tcc tct        528
Glu Gln Gly Gly Ile Asp Val Leu Tyr Lys Trp Gln Leu Val Ser Ser
                165                 170                 175

aag ttg ttg gat ggt ttg ttt ttg aga gcc ttg tct caa gtt gtc aac        576
Lys Leu Leu Asp Gly Leu Phe Leu Arg Ala Leu Ser Gln Val Val Asn
            180                 185                 190

aga act atc acc gtt gaa ttt tac gct cag ttt ttg ggt aga gcc gat        624
Arg Thr Ile Thr Val Glu Phe Tyr Ala Gln Phe Leu Gly Arg Ala Asp
        195                 200                 205

gaa ttg gtt gct atc gtt aat caa tct ttg cca gag ttg ggt ttg aag        672
Glu Leu Val Ala Ile Val Asn Gln Ser Leu Pro Glu Leu Gly Leu Lys
    210                 215                 220

aga caa gat tgc ttg gaa atg tct tgg ttg aac act acc ttg ttt tgg        720
Arg Gln Asp Cys Leu Glu Met Ser Trp Leu Asn Thr Thr Leu Phe Trp
225                 230                 235                 240

gaa gat ttg cca gtt ggt act cca act tct gtt ttg ttg gat aga cca        768
Glu Asp Leu Pro Val Gly Thr Pro Thr Ser Val Leu Leu Asp Arg Pro
                245                 250                 255

tct aag cca gag aag ttc ttc aag tct aaa tcc gat tac gtc aag aag        816
Ser Lys Pro Glu Lys Phe Phe Lys Ser Lys Ser Asp Tyr Val Lys Lys
            260                 265                 270

ccc att cca aaa gag ggt att aag aaa ttg tgg gaa gcc ttg ttg gag        864
Pro Ile Pro Lys Glu Gly Ile Lys Lys Leu Trp Glu Ala Leu Leu Glu
        275                 280                 285

ttt aac aac aac aat atc gtc tac atg cag tgg aat cca tac ggt ggt        912
Phe Asn Asn Asn Asn Ile Val Tyr Met Gln Trp Asn Pro Tyr Gly Gly
    290                 295                 300

gtt atg gat act gtt cca gct gct gct act cca ttt cca cat aga aaa        960
```

```
Val Met Asp Thr Val Pro Ala Ala Ala Thr Pro Phe Pro His Arg Lys
305                 310                 315                 320

ggt aac ttg ttc gaa gtc cag tac tac act tct tgg ttg gat gct aat       1008
Gly Asn Leu Phe Glu Val Gln Tyr Tyr Thr Ser Trp Leu Asp Ala Asn
                325                 330                 335

gct aca atg ggt tct ttg gac atg atg aag aag ttg tac gaa gtt gct       1056
Ala Thr Met Gly Ser Leu Asp Met Met Lys Lys Leu Tyr Glu Val Ala
            340                 345                 350

gaa ccc tac gtt tct tct aat cca aga gaa gcc ttt ttg aac tac aga       1104
Glu Pro Tyr Val Ser Ser Asn Pro Arg Glu Ala Phe Leu Asn Tyr Arg
        355                 360                 365

gac atc gac att ggt agc aat cca tct aac gaa act aat gtt gaa gaa       1152
Asp Ile Asp Ile Gly Ser Asn Pro Ser Asn Glu Thr Asn Val Glu Glu
    370                 375                 380

gcc gaa atc tac ggc tct aag tac ttt gtt ggt aac ttg aag aga ttg       1200
Ala Glu Ile Tyr Gly Ser Lys Tyr Phe Val Gly Asn Leu Lys Arg Leu
385                 390                 395                 400

atg gaa gtc aag gct aag tac gat cca gaa aac ttt ttc aag aac gag       1248
Met Glu Val Lys Ala Lys Tyr Asp Pro Glu Asn Phe Phe Lys Asn Glu
                405                 410                 415

caa tct att cca cca gcc aga gtt aag caa tgg tca cat cca caa ttt       1296
Gln Ser Ile Pro Pro Ala Arg Val Lys Gln Trp Ser His Pro Gln Phe
            420                 425                 430

gaa aag                                                              1302
Glu Lys
```

<210>  21
<211>  434
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  21

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


Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30
```

```
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

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

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Arg Lys Tyr Gly Leu Thr
                85                  90                  95

Val Asp Asn Val Val Asp Ala Leu Ile Val Asp Val Asn Gly Lys Leu
            100                 105                 110

Leu Asn Arg Ser Thr Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly
        115                 120                 125

Gly Gly Gly Gly Ser Phe Gly Val Ile Leu Ser Trp Lys Ile Asn Leu
    130                 135                 140

Val Asp Val Pro Glu Ile Leu Thr Val Phe Arg Val Asn Lys Thr Leu
145                 150                 155                 160

Glu Gln Gly Gly Ile Asp Val Leu Tyr Lys Trp Gln Leu Val Ser Ser
                165                 170                 175

Lys Leu Leu Asp Gly Leu Phe Leu Arg Ala Leu Ser Gln Val Val Asn
            180                 185                 190

Arg Thr Ile Thr Val Glu Phe Tyr Ala Gln Phe Leu Gly Arg Ala Asp
        195                 200                 205

Glu Leu Val Ala Ile Val Asn Gln Ser Leu Pro Glu Leu Gly Leu Lys
    210                 215                 220

Arg Gln Asp Cys Leu Glu Met Ser Trp Leu Asn Thr Thr Leu Phe Trp
225                 230                 235                 240

Glu Asp Leu Pro Val Gly Thr Pro Thr Ser Val Leu Leu Asp Arg Pro
                245                 250                 255
```

```
Ser Lys Pro Glu Lys Phe Phe Lys Ser Lys Ser Asp Tyr Val Lys Lys
            260                 265                 270

Pro Ile Pro Lys Glu Gly Ile Lys Lys Leu Trp Glu Ala Leu Leu Glu
        275                 280                 285

Phe Asn Asn Asn Asn Ile Val Tyr Met Gln Trp Asn Pro Tyr Gly Gly
    290                 295                 300

Val Met Asp Thr Val Pro Ala Ala Ala Thr Pro Phe Pro His Arg Lys
305                 310                 315                 320

Gly Asn Leu Phe Glu Val Gln Tyr Tyr Thr Ser Trp Leu Asp Ala Asn
                325                 330                 335

Ala Thr Met Gly Ser Leu Asp Met Met Lys Lys Leu Tyr Glu Val Ala
            340                 345                 350

Glu Pro Tyr Val Ser Ser Asn Pro Arg Glu Ala Phe Leu Asn Tyr Arg
        355                 360                 365

Asp Ile Asp Ile Gly Ser Asn Pro Ser Asn Glu Thr Asn Val Glu Glu
    370                 375                 380

Ala Glu Ile Tyr Gly Ser Lys Tyr Phe Val Gly Asn Leu Lys Arg Leu
385                 390                 395                 400

Met Glu Val Lys Ala Lys Tyr Asp Pro Glu Asn Phe Phe Lys Asn Glu
                405                 410                 415

Gln Ser Ile Pro Pro Ala Arg Val Lys Gln Trp Ser His Pro Gln Phe
            420                 425                 430

Glu Lys
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<210> 22
<211> 1641
<212> DNA
<213> Artificial Sequence

<220>
<223>  CBS17-A0A1J6KPK0


<220>
<221>  CDS
<222>  (1)..(1641)

<400>  22
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atg gcc tcc ttg aac tct atc atg gtg tct ttt ttc ttg gtc ctg ctg         48
Met Ala Ser Leu Asn Ser Ile Met Val Ser Phe Phe Leu Val Leu Leu
1               5                   10                  15

ttc tct tct tct tgt ttt gct ttg tct gat acc act cca gaa aag ttc         96
Phe Ser Ser Ser Cys Phe Ala Leu Ser Asp Thr Thr Pro Glu Lys Phe
            20                  25                  30

tac caa tgt atc tgc aag aac tcc gat ttc tct gat cca ttt tct aag        144
Tyr Gln Cys Ile Cys Lys Asn Ser Asp Phe Ser Asp Pro Phe Ser Lys
        35                  40                  45

gct ttc ttc act cca aac acc gat tct ttc aac acc gtt tta aac tct        192
Ala Phe Phe Thr Pro Asn Thr Asp Ser Phe Asn Thr Val Leu Asn Ser
    50                  55                  60

acc gct caa aac ttg aga tgt ttg atg cca act gtt cca aag cca gtt        240
Thr Ala Gln Asn Leu Arg Cys Leu Met Pro Thr Val Pro Lys Pro Val
65                  70                  75                  80

ttg att ttt act cca atg gcc gaa tct cat gtt caa gct gct gtt att        288
Leu Ile Phe Thr Pro Met Ala Glu Ser His Val Gln Ala Ala Val Ile
                85                  90                  95

tgt gcc aag caa ttg aac ttg caa ttg aga gtt aga tcc ggt ggt cat        336
Cys Ala Lys Gln Leu Asn Leu Gln Leu Arg Val Arg Ser Gly Gly His
            100                 105                 110

gat tat gaa ggt ttg tcc tac atc tcc gtt atg gat tct cca ttc gtt        384
Asp Tyr Glu Gly Leu Ser Tyr Ile Ser Val Met Asp Ser Pro Phe Val
        115                 120                 125

atc gtt gac ttg tcc aag ttg aga gag att gac gtt aac atc gaa gaa        432
Ile Val Asp Leu Ser Lys Leu Arg Glu Ile Asp Val Asn Ile Glu Glu
    130                 135                 140

aat tct gct tgg gct caa gct ggt gct act gtt ggt gaa gtt tat tac        480
Asn Ser Ala Trp Ala Gln Ala Gly Ala Thr Val Gly Glu Val Tyr Tyr
145                 150                 155                 160

aga atc tcc gag aag tct aag act cat ggt ttt cca gct ggt ttg tgt        528
Arg Ile Ser Glu Lys Ser Lys Thr His Gly Phe Pro Ala Gly Leu Cys
                165                 170                 175
```

```
acc tct tta ggt att ggt ggt cat atc act ggt ggt gct tat ggt tct        576
Thr Ser Leu Gly Ile Gly Gly His Ile Thr Gly Gly Ala Tyr Gly Ser
            180                 185                 190

atg atg aga aaa ttt ggt ttg ggt gcc gat aac gtc att gat gct aga        624
Met Met Arg Lys Phe Gly Leu Gly Ala Asp Asn Val Ile Asp Ala Arg
        195                 200                 205

atc gtt aat gcc aac ggt act atc ttg gac aga ttg tct atg ggt gaa        672
Ile Val Asn Ala Asn Gly Thr Ile Leu Asp Arg Leu Ser Met Gly Glu
    210                 215                 220

gat ttg ttc tgg gct att aga ggt ggt ggt ggc gct tct ttt ggt att        720
Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Ile
225                 230                 235                 240

atc ttg tct tgg aag ttg aag ttg gtt acc gtt cca tct gtt gtt act        768
Ile Leu Ser Trp Lys Leu Lys Leu Val Thr Val Pro Ser Val Val Thr
                245                 250                 255

gtt ttc acc gtt cca aaa acc ttg gaa gat ggt gct aca aag atc ttg        816
Val Phe Thr Val Pro Lys Thr Leu Glu Asp Gly Ala Thr Lys Ile Leu
            260                 265                 270

tac aaa tgg caa caa gtt gcc gat aag atc gat gat gat ttg ttc atg        864
Tyr Lys Trp Gln Gln Val Ala Asp Lys Ile Asp Asp Asp Leu Phe Met
        275                 280                 285

aga gtc gtt atc aac gtc gtt gac aaa aag gat aag aag ggt gaa aga        912
Arg Val Val Ile Asn Val Val Asp Lys Lys Asp Lys Lys Gly Glu Arg
    290                 295                 300

act gtt caa acc gct tac aac tct ttg ttc ttg ggt aat gtt gac agg        960
Thr Val Gln Thr Ala Tyr Asn Ser Leu Phe Leu Gly Asn Val Asp Arg
305                 310                 315                 320

ttg ttg cag atc atg aat gaa tct ttt cca gag ttg ggt ttg acc caa       1008
Leu Leu Gln Ile Met Asn Glu Ser Phe Pro Glu Leu Gly Leu Thr Gln
                325                 330                 335

aaa gat tgc act gaa atg tcc tgg atc gag tcc atc ttg tat att gct       1056
Lys Asp Cys Thr Glu Met Ser Trp Ile Glu Ser Ile Leu Tyr Ile Ala
            340                 345                 350

ggt ttc cca aca aaa acc cca cca gaa att ttg ttg caa ggt aag cca       1104
Gly Phe Pro Thr Lys Thr Pro Pro Glu Ile Leu Leu Gln Gly Lys Pro
        355                 360                 365

act ttc aag aac tac ttc aag gct aag tcc gac ttc atc aaa gaa cct       1152
Thr Phe Lys Asn Tyr Phe Lys Ala Lys Ser Asp Phe Ile Lys Glu Pro
    370                 375                 380

att cca gaa act ggt ctg gat ggt att tgg aaa aga cta ttg gaa gag       1200
Ile Pro Glu Thr Gly Leu Asp Gly Ile Trp Lys Arg Leu Leu Glu Glu
```

```
385                 390                 395                 400

gac tcc cca ttg atg ata tgg aat cca tac ggt ggt atg atg gcc aac       1248
Asp Ser Pro Leu Met Ile Trp Asn Pro Tyr Gly Gly Met Met Ala Asn
                405                 410                 415

att tct gaa tct gaa act cca ttt cca cac aga aag ggt gtt atc ttc       1296
Ile Ser Glu Ser Glu Thr Pro Phe Pro His Arg Lys Gly Val Ile Phe
            420                 425                 430

aag atc caa tac ttg act ttg tgg acc gaa cca gat caa gaa ttg gct       1344
Lys Ile Gln Tyr Leu Thr Leu Trp Thr Glu Pro Asp Gln Glu Leu Ala
        435                 440                 445

aca aaa cat gtt gac tgg atc aga aag ctg tac tct tac atg act tct       1392
Thr Lys His Val Asp Trp Ile Arg Lys Leu Tyr Ser Tyr Met Thr Ser
    450                 455                 460

tac gct tct atg ttt cca aga gaa gcc tac gtt aac tac aga gat ttg       1440
Tyr Ala Ser Met Phe Pro Arg Glu Ala Tyr Val Asn Tyr Arg Asp Leu
465                 470                 475                 480

gac ttg ggt atg aac aag aat ggc aac tct aac tcc tca ttc gtt caa       1488
Asp Leu Gly Met Asn Lys Asn Gly Asn Ser Asn Ser Ser Phe Val Gln
                485                 490                 495

gct aca gtt tgg ggt aac aag tac ttc aac aac aat ttc aac agg ctg       1536
Ala Thr Val Trp Gly Asn Lys Tyr Phe Asn Asn Asn Phe Asn Arg Leu
            500                 505                 510

gtc gaa atc aag act aag gtt gat cca gag aat ttc ttc aag ttc gaa       1584
Val Glu Ile Lys Thr Lys Val Asp Pro Glu Asn Phe Phe Lys Phe Glu
        515                 520                 525

caa tcc att cca acc ttg cca ttg act aag aaa aga aag ggt aag aag       1632
Gln Ser Ile Pro Thr Leu Pro Leu Thr Lys Lys Arg Lys Gly Lys Lys
    530                 535                 540

atc aac cat                                                          1641
Ile Asn His
545
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<210>  23
<211>  547
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  23

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Met Ala Ser Leu Asn Ser Ile Met Val Ser Phe Phe Leu Val Leu Leu
```

```
1               5                   10                  15

Phe Ser Ser Ser Cys Phe Ala Leu Ser Asp Thr Thr Pro Glu Lys Phe
            20                  25                  30

Tyr Gln Cys Ile Cys Lys Asn Ser Asp Phe Ser Asp Pro Phe Ser Lys
        35                  40                  45

Ala Phe Phe Thr Pro Asn Thr Asp Ser Phe Asn Thr Val Leu Asn Ser
    50                  55                  60

Thr Ala Gln Asn Leu Arg Cys Leu Met Pro Thr Val Pro Lys Pro Val
65                  70                  75                  80

Leu Ile Phe Thr Pro Met Ala Glu Ser His Val Gln Ala Ala Val Ile
                85                  90                  95

Cys Ala Lys Gln Leu Asn Leu Gln Leu Arg Val Arg Ser Gly Gly His
            100                 105                 110

Asp Tyr Glu Gly Leu Ser Tyr Ile Ser Val Met Asp Ser Pro Phe Val
        115                 120                 125

Ile Val Asp Leu Ser Lys Leu Arg Glu Ile Asp Val Asn Ile Glu Glu
    130                 135                 140

Asn Ser Ala Trp Ala Gln Ala Gly Ala Thr Val Gly Glu Val Tyr Tyr
145                 150                 155                 160

Arg Ile Ser Glu Lys Ser Lys Thr His Gly Phe Pro Ala Gly Leu Cys
                165                 170                 175

Thr Ser Leu Gly Ile Gly Gly His Ile Thr Gly Gly Ala Tyr Gly Ser
            180                 185                 190

Met Met Arg Lys Phe Gly Leu Gly Ala Asp Asn Val Ile Asp Ala Arg
        195                 200                 205

Ile Val Asn Ala Asn Gly Thr Ile Leu Asp Arg Leu Ser Met Gly Glu
    210                 215                 220
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Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Ile
225                 230                 235                 240

Ile Leu Ser Trp Lys Leu Lys Leu Val Thr Val Pro Ser Val Val Thr
                245                 250                 255

Val Phe Thr Val Pro Lys Thr Leu Glu Asp Gly Ala Thr Lys Ile Leu
            260                 265                 270

Tyr Lys Trp Gln Gln Val Ala Asp Lys Ile Asp Asp Asp Leu Phe Met
        275                 280                 285

Arg Val Val Ile Asn Val Val Asp Lys Lys Asp Lys Lys Gly Glu Arg
    290                 295                 300

Thr Val Gln Thr Ala Tyr Asn Ser Leu Phe Leu Gly Asn Val Asp Arg
305                 310                 315                 320

Leu Leu Gln Ile Met Asn Glu Ser Phe Pro Glu Leu Gly Leu Thr Gln
                325                 330                 335

Lys Asp Cys Thr Glu Met Ser Trp Ile Glu Ser Ile Leu Tyr Ile Ala
            340                 345                 350

Gly Phe Pro Thr Lys Thr Pro Pro Glu Ile Leu Leu Gln Gly Lys Pro
        355                 360                 365

Thr Phe Lys Asn Tyr Phe Lys Ala Lys Ser Asp Phe Ile Lys Glu Pro
    370                 375                 380

Ile Pro Glu Thr Gly Leu Asp Gly Ile Trp Lys Arg Leu Leu Glu Glu
385                 390                 395                 400

Asp Ser Pro Leu Met Ile Trp Asn Pro Tyr Gly Gly Met Met Ala Asn
                405                 410                 415

Ile Ser Glu Ser Glu Thr Pro Phe Pro His Arg Lys Gly Val Ile Phe
            420                 425                 430

Lys Ile Gln Tyr Leu Thr Leu Trp Thr Glu Pro Asp Gln Glu Leu Ala
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        435                 440                 445

Thr Lys His Val Asp Trp Ile Arg Lys Leu Tyr Ser Tyr Met Thr Ser
    450                 455                 460

Tyr Ala Ser Met Phe Pro Arg Glu Ala Tyr Val Asn Tyr Arg Asp Leu
465                 470                 475                 480

Asp Leu Gly Met Asn Lys Asn Gly Asn Ser Asn Ser Ser Phe Val Gln
                485                 490                 495

Ala Thr Val Trp Gly Asn Lys Tyr Phe Asn Asn Asn Phe Asn Arg Leu
            500                 505                 510

Val Glu Ile Lys Thr Lys Val Asp Pro Glu Asn Phe Phe Lys Phe Glu
        515                 520                 525

Gln Ser Ile Pro Thr Leu Pro Leu Thr Lys Lys Arg Lys Gly Lys Lys
    530                 535                 540

Ile Asn His
545
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<210>  24
<211>  1575
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS17-A0A1J6KPK0-no signal peptide

<220>
<221>  CDS
<222>  (1)..(1575)

<400>  24

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atg ttg tct gat acc act cca gaa aag ttc tac caa tgt atc tgc aag         48
Met Leu Ser Asp Thr Thr Pro Glu Lys Phe Tyr Gln Cys Ile Cys Lys
1               5                   10                  15

aac tcc gat ttc tct gat cca ttt tct aag gct ttc ttc act cca aac         96
Asn Ser Asp Phe Ser Asp Pro Phe Ser Lys Ala Phe Phe Thr Pro Asn
            20                  25                  30

acc gat tct ttc aac acc gtt tta aac tct acc gct caa aac ttg aga        144
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```
Thr Asp Ser Phe Asn Thr Val Leu Asn Ser Thr Ala Gln Asn Leu Arg
        35                  40                  45

tgt ttg atg cca act gtt cca aag cca gtt ttg att ttt act cca atg        192
Cys Leu Met Pro Thr Val Pro Lys Pro Val Leu Ile Phe Thr Pro Met
    50                  55                  60

gcc gaa tct cat gtt caa gct gct gtt att tgt gcc aag caa ttg aac        240
Ala Glu Ser His Val Gln Ala Ala Val Ile Cys Ala Lys Gln Leu Asn
65                  70                  75                  80

ttg caa ttg aga gtt aga tcc ggt ggt cat gat tat gaa ggt ttg tcc        288
Leu Gln Leu Arg Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser
                85                  90                  95

tac atc tcc gtt atg gat tct cca ttc gtt atc gtt gac ttg tcc aag        336
Tyr Ile Ser Val Met Asp Ser Pro Phe Val Ile Val Asp Leu Ser Lys
            100                 105                 110

ttg aga gag att gac gtt aac atc gaa gaa aat tct gct tgg gct caa        384
Leu Arg Glu Ile Asp Val Asn Ile Glu Glu Asn Ser Ala Trp Ala Gln
        115                 120                 125

gct ggt gct act gtt ggt gaa gtt tat tac aga atc tcc gag aag tct        432
Ala Gly Ala Thr Val Gly Glu Val Tyr Tyr Arg Ile Ser Glu Lys Ser
    130                 135                 140

aag act cat ggt ttt cca gct ggt ttg tgt acc tct tta ggt att ggt        480
Lys Thr His Gly Phe Pro Ala Gly Leu Cys Thr Ser Leu Gly Ile Gly
145                 150                 155                 160

ggt cat atc act ggt ggt gct tat ggt tct atg atg aga aaa ttt ggt        528
Gly His Ile Thr Gly Gly Ala Tyr Gly Ser Met Met Arg Lys Phe Gly
                165                 170                 175

ttg ggt gcc gat aac gtc att gat gct aga atc gtt aat gcc aac ggt        576
Leu Gly Ala Asp Asn Val Ile Asp Ala Arg Ile Val Asn Ala Asn Gly
            180                 185                 190

act atc ttg gac aga ttg tct atg ggt gaa gat ttg ttc tgg gct att        624
Thr Ile Leu Asp Arg Leu Ser Met Gly Glu Asp Leu Phe Trp Ala Ile
        195                 200                 205

aga ggt ggt ggt ggc gct tct ttt ggt att atc ttg tct tgg aag ttg        672
Arg Gly Gly Gly Gly Ala Ser Phe Gly Ile Ile Leu Ser Trp Lys Leu
    210                 215                 220

aag ttg gtt acc gtt cca tct gtt gtt act gtt ttc acc gtt cca aaa        720
Lys Leu Val Thr Val Pro Ser Val Val Thr Val Phe Thr Val Pro Lys
225                 230                 235                 240

acc ttg gaa gat ggt gct aca aag atc ttg tac aaa tgg caa caa gtt        768
Thr Leu Glu Asp Gly Ala Thr Lys Ile Leu Tyr Lys Trp Gln Gln Val
                245                 250                 255
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gcc gat aag atc gat gat gat ttg ttc atg aga gtc gtt atc aac gtc        816
Ala Asp Lys Ile Asp Asp Asp Leu Phe Met Arg Val Val Ile Asn Val
            260                 265                 270

gtt gac aaa aag gat aag aag ggt gaa aga act gtt caa acc gct tac        864
Val Asp Lys Lys Asp Lys Lys Gly Glu Arg Thr Val Gln Thr Ala Tyr
        275                 280                 285

aac tct ttg ttc ttg ggt aat gtt gac agg ttg ttg cag atc atg aat        912
Asn Ser Leu Phe Leu Gly Asn Val Asp Arg Leu Leu Gln Ile Met Asn
    290                 295                 300

gaa tct ttt cca gag ttg ggt ttg acc caa aaa gat tgc act gaa atg        960
Glu Ser Phe Pro Glu Leu Gly Leu Thr Gln Lys Asp Cys Thr Glu Met
305                 310                 315                 320

tcc tgg atc gag tcc atc ttg tat att gct ggt ttc cca aca aaa acc       1008
Ser Trp Ile Glu Ser Ile Leu Tyr Ile Ala Gly Phe Pro Thr Lys Thr
                325                 330                 335

cca cca gaa att ttg ttg caa ggt aag cca act ttc aag aac tac ttc       1056
Pro Pro Glu Ile Leu Leu Gln Gly Lys Pro Thr Phe Lys Asn Tyr Phe
            340                 345                 350

aag gct aag tcc gac ttc atc aaa gaa cct att cca gaa act ggt ctg       1104
Lys Ala Lys Ser Asp Phe Ile Lys Glu Pro Ile Pro Glu Thr Gly Leu
        355                 360                 365

gat ggt att tgg aaa aga cta ttg gaa gag gac tcc cca ttg atg ata       1152
Asp Gly Ile Trp Lys Arg Leu Leu Glu Glu Asp Ser Pro Leu Met Ile
    370                 375                 380

tgg aat cca tac ggt ggt atg atg gcc aac att tct gaa tct gaa act       1200
Trp Asn Pro Tyr Gly Gly Met Met Ala Asn Ile Ser Glu Ser Glu Thr
385                 390                 395                 400

cca ttt cca cac aga aag ggt gtt atc ttc aag atc caa tac ttg act       1248
Pro Phe Pro His Arg Lys Gly Val Ile Phe Lys Ile Gln Tyr Leu Thr
                405                 410                 415

ttg tgg acc gaa cca gat caa gaa ttg gct aca aaa cat gtt gac tgg       1296
Leu Trp Thr Glu Pro Asp Gln Glu Leu Ala Thr Lys His Val Asp Trp
            420                 425                 430

atc aga aag ctg tac tct tac atg act tct tac gct tct atg ttt cca       1344
Ile Arg Lys Leu Tyr Ser Tyr Met Thr Ser Tyr Ala Ser Met Phe Pro
        435                 440                 445

aga gaa gcc tac gtt aac tac aga gat ttg gac ttg ggt atg aac aag       1392
Arg Glu Ala Tyr Val Asn Tyr Arg Asp Leu Asp Leu Gly Met Asn Lys
    450                 455                 460

aat ggc aac tct aac tcc tca ttc gtt caa gct aca gtt tgg ggt aac       1440
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Asn Gly Asn Ser Asn Ser Ser Phe Val Gln Ala Thr Val Trp Gly Asn
465                 470                 475                 480

aag tac ttc aac aac aat ttc aac agg ctg gtc gaa atc aag act aag       1488
Lys Tyr Phe Asn Asn Asn Phe Asn Arg Leu Val Glu Ile Lys Thr Lys
                485                 490                 495

gtt gat cca gag aat ttc ttc aag ttc gaa caa tcc att cca acc ttg       1536
Val Asp Pro Glu Asn Phe Phe Lys Phe Glu Gln Ser Ile Pro Thr Leu
            500                 505                 510

cca ttg act aag aaa aga aag ggt aag aag atc aac cat                   1575
Pro Leu Thr Lys Lys Arg Lys Gly Lys Lys Ile Asn His
        515                 520                 525


<210>  25
<211>  525
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  25

Met Leu Ser Asp Thr Thr Pro Glu Lys Phe Tyr Gln Cys Ile Cys Lys
1               5                   10                  15


Asn Ser Asp Phe Ser Asp Pro Phe Ser Lys Ala Phe Phe Thr Pro Asn
            20                  25                  30


Thr Asp Ser Phe Asn Thr Val Leu Asn Ser Thr Ala Gln Asn Leu Arg
        35                  40                  45


Cys Leu Met Pro Thr Val Pro Lys Pro Val Leu Ile Phe Thr Pro Met
    50                  55                  60


Ala Glu Ser His Val Gln Ala Ala Val Ile Cys Ala Lys Gln Leu Asn
65                  70                  75                  80


Leu Gln Leu Arg Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser
                85                  90                  95


Tyr Ile Ser Val Met Asp Ser Pro Phe Val Ile Val Asp Leu Ser Lys
            100                 105                 110
```

```
Leu Arg Glu Ile Asp Val Asn Ile Glu Glu Asn Ser Ala Trp Ala Gln
        115                 120                 125

Ala Gly Ala Thr Val Gly Glu Val Tyr Tyr Arg Ile Ser Glu Lys Ser
    130                 135                 140

Lys Thr His Gly Phe Pro Ala Gly Leu Cys Thr Ser Leu Gly Ile Gly
145                 150                 155                 160

Gly His Ile Thr Gly Gly Ala Tyr Gly Ser Met Met Arg Lys Phe Gly
                165                 170                 175

Leu Gly Ala Asp Asn Val Ile Asp Ala Arg Ile Val Asn Ala Asn Gly
            180                 185                 190

Thr Ile Leu Asp Arg Leu Ser Met Gly Glu Asp Leu Phe Trp Ala Ile
        195                 200                 205

Arg Gly Gly Gly Gly Ala Ser Phe Gly Ile Ile Leu Ser Trp Lys Leu
    210                 215                 220

Lys Leu Val Thr Val Pro Ser Val Val Thr Val Phe Thr Val Pro Lys
225                 230                 235                 240

Thr Leu Glu Asp Gly Ala Thr Lys Ile Leu Tyr Lys Trp Gln Gln Val
                245                 250                 255

Ala Asp Lys Ile Asp Asp Asp Leu Phe Met Arg Val Val Ile Asn Val
            260                 265                 270

Val Asp Lys Lys Asp Lys Lys Gly Glu Arg Thr Val Gln Thr Ala Tyr
        275                 280                 285

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

Glu Ser Phe Pro Glu Leu Gly Leu Thr Gln Lys Asp Cys Thr Glu Met
305                 310                 315                 320

Ser Trp Ile Glu Ser Ile Leu Tyr Ile Ala Gly Phe Pro Thr Lys Thr
                325                 330                 335
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Pro Pro Glu Ile Leu Leu Gln Gly Lys Pro Thr Phe Lys Asn Tyr Phe
            340                 345                 350

Lys Ala Lys Ser Asp Phe Ile Lys Glu Pro Ile Pro Glu Thr Gly Leu
        355                 360                 365

Asp Gly Ile Trp Lys Arg Leu Leu Glu Glu Asp Ser Pro Leu Met Ile
    370                 375                 380

Trp Asn Pro Tyr Gly Gly Met Met Ala Asn Ile Ser Glu Ser Glu Thr
385                 390                 395                 400

Pro Phe Pro His Arg Lys Gly Val Ile Phe Lys Ile Gln Tyr Leu Thr
                405                 410                 415

Leu Trp Thr Glu Pro Asp Gln Glu Leu Ala Thr Lys His Val Asp Trp
            420                 425                 430

Ile Arg Lys Leu Tyr Ser Tyr Met Thr Ser Tyr Ala Ser Met Phe Pro
        435                 440                 445

Arg Glu Ala Tyr Val Asn Tyr Arg Asp Leu Asp Leu Gly Met Asn Lys
    450                 455                 460

Asn Gly Asn Ser Asn Ser Ser Phe Val Gln Ala Thr Val Trp Gly Asn
465                 470                 475                 480

Lys Tyr Phe Asn Asn Asn Phe Asn Arg Leu Val Glu Ile Lys Thr Lys
                485                 490                 495

Val Asp Pro Glu Asn Phe Phe Lys Phe Glu Gln Ser Ile Pro Thr Leu
            500                 505                 510

Pro Leu Thr Lys Lys Arg Lys Gly Lys Lys Ile Asn His
        515                 520                 525
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<210> 26
<211> 1599
<212> DNA
<213> Artificial Sequence

<220>
<223>  CBS17-A0A1J6KPK0-no signal peptide-strep Tag

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tctgatccat tttctaaggc tttcttcact ccaaacaccg attctttcaa caccgtttta 120

aactctaccg ctcaaaactt gagatgtttg atgccaactg ttccaaagcc agttttgatt 180

tttactccaa tggccgaatc tcatgttcaa gctgctgtta tttgtgccaa gcaattgaac 240

ttgcaattga gagttagatc cggtggtcat gattatgaag gtttgtccta catctccgtt 300

atggattctc cattcgttat cgttgacttg tccaagttga gagagattga cgttaacatc 360

gaagaaaatt ctgcttgggc tcaagctggt gctactgttg gtgaagttta ttacagaatc 420

tccgagaagt ctaagactca tggttttcca gctggtttgt gtacctcttt aggtattggt 480

ggtcatatca ctggtggtgc ttatggttct atgatgagaa aatttggttt gggtgccgat 540

aacgtcattg atgctagaat cgttaatgcc aacggtacta tcttggacag attgtctatg 600

ggtgaagatt tgttctgggc tattagaggt ggtggtggcg cttcttttgg tattatcttg 660

tcttggaagt tgaagttggt taccgttcca tctgttgtta ctgttttcac cgttccaaaa 720

accttggaag atggtgctac aaagatcttg tacaaatggc aacaagttgc cgataagatc 780

gatgatgatt tgttcatgag agtcgttatc aacgtcgttg acaaaaagga taagaagggt 840

gaaagaactg ttcaaaccgc ttacaactct ttgttcttgg gtaatgttga caggttgttg 900

cagatcatga atgaatcttt tccagagttg ggtttgaccc aaaaagattg cactgaaatg 960

tcctggatcg agtccatctt gtatattgct ggtttcccaa caaaaacccc accagaaatt 1020

ttgttgcaag gtaagccaac tttcaagaac tacttcaagg ctaagtccga cttcatcaaa 1080

gaacctattc cagaaactgg tctggatggt atttggaaaa gactattgga agaggactcc 1140

ccattgatga tatggaatcc atacggtggt atgatggcca acatttctga atctgaaact 1200

ccatttccac acagaaaggg tgttatcttc aagatccaat acttgacttt gtggaccgaa 1260

ccagatcaag aattggctac aaaacatgtt gactggatca gaaagctgta ctcttacatg 1320

acttcttacg cttctatgtt tccaagagaa gcctacgtta actacagaga tttggacttg 1380

ggtatgaaca agaatggcaa ctctaactcc tcattcgttc aagctacagt ttggggtaac 1440

aagtacttca acaacaattt caacaggctg gtcgaaatca agactaaggt tgatccagag 1500

aatttcttca agttcgaaca atccattcca accttgccat tgactaagaa aagaaagggt 1560

aagaagatca accattggtc acatccacaa tttgaaaag 1599

<210> 27
<211> 1656
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS17-A0A1J6KPK0-truncatd alpha factor - no signal peptide-strep Tag

<400> 27
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ttgtctgata ccactccaga aaagttctac caatgtatct gcaagaactc cgatttctct 120

gatccatttt ctaaggcttt cttcactcca aacaccgatt ctttcaacac cgttttaaac 180

tctaccgctc aaaacttgag atgtttgatg ccaactgttc caaagccagt tttgattttt 240

actccaatgg ccgaatctca tgttcaagct gctgttattt gtgccaagca attgaacttg 300

caattgagag ttagatccgg tggtcatgat tatgaaggtt tgtcctacat ctccgttatg 360

gattctccat tcgttatcgt tgacttgtcc aagttgagag agattgacgt taacatcgaa 420

gaaaattctg cttgggctca agctggtgct actgttggtg aagtttatta cagaatctcc 480

gagaagtcta agactcatgg ttttccagct ggtttgtgta cctctttagg tattggtggt 540

catatcactg gtggtgctta tggttctatg atgagaaaat ttggtttggg tgccgataac 600

gtcattgatg ctagaatcgt taatgccaac ggtactatct tggacagatt gtctatgggt 660

gaagatttgt tctgggctat tagaggtggt ggtggcgctt cttttggtat tatcttgtct 720

tggaagttga agttggttac cgttccatct gttgttactg ttttcaccgt tccaaaaacc 780

ttggaagatg gtgctacaaa gatcttgtac aaatggcaac aagttgccga taagatcgat 840

gatgatttgt tcatgagagt cgttatcaac gtcgttgaca aaaaggataa gaagggtgaa 900

agaactgttc aaaccgctta caactctttg ttcttgggta atgttgacag gttgttgcag 960

atcatgaatg aatcttttcc agagttgggt ttgacccaaa aagattgcac tgaaatgtcc 1020

tggatcgagt ccatcttgta tattgctggt ttcccaacaa aaaccccacc agaaattttg 1080

ttgcaaggta agccaacttt caagaactac ttcaaggcta agtccgactt catcaaagaa 1140

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cctattccag aaactggtct ggatggtatt tggaaaagac tattggaaga ggactcccca     1200

ttgatgatat ggaatccata cggtggtatg atggccaaca tttctgaatc tgaaactcca     1260

tttccacaca gaaagggtgt tatcttcaag atccaatact tgactttgtg gaccgaacca     1320

gatcaagaat tggctacaaa acatgttgac tggatcagaa agctgtactc ttacatgact     1380

tcttacgctt ctatgtttcc aagagaagcc tacgttaact acagagattt ggacttgggt     1440

atgaacaaga atggcaactc taactcctca ttcgttcaag ctacagtttg gggtaacaag     1500

tacttcaaca acaatttcaa caggctggtc gaaatcaaga ctaaggttga tccagagaat     1560

ttcttcaagt tcgaacaatc cattccaacc ttgccattga ctaagaaaag aaagggtaag     1620

aagatcaacc attggtcaca tccacaattt gaaaag                               1656
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<210> 28
<211> 1866
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS17-A0A1J6KPK0-full alpha factor - no signal peptide-strep Tag

<220>
<221> CDS
<222> (1)..(1866)

<400> 28

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

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg ttg tct gat acc act cca        288
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```
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Leu Ser Asp Thr Thr Pro
                85                  90                  95

gaa aag ttc tac caa tgt atc tgc aag aac tcc gat ttc tct gat cca        336
Glu Lys Phe Tyr Gln Cys Ile Cys Lys Asn Ser Asp Phe Ser Asp Pro
            100                 105                 110

ttt tct aag gct ttc ttc act cca aac acc gat tct ttc aac acc gtt        384
Phe Ser Lys Ala Phe Phe Thr Pro Asn Thr Asp Ser Phe Asn Thr Val
        115                 120                 125

tta aac tct acc gct caa aac ttg aga tgt ttg atg cca act gtt cca        432
Leu Asn Ser Thr Ala Gln Asn Leu Arg Cys Leu Met Pro Thr Val Pro
    130                 135                 140

aag cca gtt ttg att ttt act cca atg gcc gaa tct cat gtt caa gct        480
Lys Pro Val Leu Ile Phe Thr Pro Met Ala Glu Ser His Val Gln Ala
145                 150                 155                 160

gct gtt att tgt gcc aag caa ttg aac ttg caa ttg aga gtt aga tcc        528
Ala Val Ile Cys Ala Lys Gln Leu Asn Leu Gln Leu Arg Val Arg Ser
                165                 170                 175

ggt ggt cat gat tat gaa ggt ttg tcc tac atc tcc gtt atg gat tct        576
Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Ile Ser Val Met Asp Ser
            180                 185                 190

cca ttc gtt atc gtt gac ttg tcc aag ttg aga gag att gac gtt aac        624
Pro Phe Val Ile Val Asp Leu Ser Lys Leu Arg Glu Ile Asp Val Asn
        195                 200                 205

atc gaa gaa aat tct gct tgg gct caa gct ggt gct act gtt ggt gaa        672
Ile Glu Glu Asn Ser Ala Trp Ala Gln Ala Gly Ala Thr Val Gly Glu
    210                 215                 220

gtt tat tac aga atc tcc gag aag tct aag act cat ggt ttt cca gct        720
Val Tyr Tyr Arg Ile Ser Glu Lys Ser Lys Thr His Gly Phe Pro Ala
225                 230                 235                 240

ggt ttg tgt acc tct tta ggt att ggt ggt cat atc act ggt ggt gct        768
Gly Leu Cys Thr Ser Leu Gly Ile Gly Gly His Ile Thr Gly Gly Ala
                245                 250                 255

tat ggt tct atg atg aga aaa ttt ggt ttg ggt gcc gat aac gtc att        816
Tyr Gly Ser Met Met Arg Lys Phe Gly Leu Gly Ala Asp Asn Val Ile
            260                 265                 270

gat gct aga atc gtt aat gcc aac ggt act atc ttg gac aga ttg tct        864
Asp Ala Arg Ile Val Asn Ala Asn Gly Thr Ile Leu Asp Arg Leu Ser
        275                 280                 285

atg ggt gaa gat ttg ttc tgg gct att aga ggt ggt ggt ggc gct tct        912
Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser
    290                 295                 300
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ttt ggt att atc ttg tct tgg aag ttg aag ttg gtt acc gtt cca tct        960
Phe Gly Ile Ile Leu Ser Trp Lys Leu Lys Leu Val Thr Val Pro Ser
305                 310                 315                 320

gtt gtt act gtt ttc acc gtt cca aaa acc ttg gaa gat ggt gct aca       1008
Val Val Thr Val Phe Thr Val Pro Lys Thr Leu Glu Asp Gly Ala Thr
                325                 330                 335

aag atc ttg tac aaa tgg caa caa gtt gcc gat aag atc gat gat gat       1056
Lys Ile Leu Tyr Lys Trp Gln Gln Val Ala Asp Lys Ile Asp Asp Asp
            340                 345                 350

ttg ttc atg aga gtc gtt atc aac gtc gtt gac aaa aag gat aag aag       1104
Leu Phe Met Arg Val Val Ile Asn Val Val Asp Lys Lys Asp Lys Lys
        355                 360                 365

ggt gaa aga act gtt caa acc gct tac aac tct ttg ttc ttg ggt aat       1152
Gly Glu Arg Thr Val Gln Thr Ala Tyr Asn Ser Leu Phe Leu Gly Asn
    370                 375                 380

gtt gac agg ttg ttg cag atc atg aat gaa tct ttt cca gag ttg ggt       1200
Val Asp Arg Leu Leu Gln Ile Met Asn Glu Ser Phe Pro Glu Leu Gly
385                 390                 395                 400

ttg acc caa aaa gat tgc act gaa atg tcc tgg atc gag tcc atc ttg       1248
Leu Thr Gln Lys Asp Cys Thr Glu Met Ser Trp Ile Glu Ser Ile Leu
                405                 410                 415

tat att gct ggt ttc cca aca aaa acc cca cca gaa att ttg ttg caa       1296
Tyr Ile Ala Gly Phe Pro Thr Lys Thr Pro Pro Glu Ile Leu Leu Gln
            420                 425                 430

ggt aag cca act ttc aag aac tac ttc aag gct aag tcc gac ttc atc       1344
Gly Lys Pro Thr Phe Lys Asn Tyr Phe Lys Ala Lys Ser Asp Phe Ile
        435                 440                 445

aaa gaa cct att cca gaa act ggt ctg gat ggt att tgg aaa aga cta       1392
Lys Glu Pro Ile Pro Glu Thr Gly Leu Asp Gly Ile Trp Lys Arg Leu
    450                 455                 460

ttg gaa gag gac tcc cca ttg atg ata tgg aat cca tac ggt ggt atg       1440
Leu Glu Glu Asp Ser Pro Leu Met Ile Trp Asn Pro Tyr Gly Gly Met
465                 470                 475                 480

atg gcc aac att tct gaa tct gaa act cca ttt cca cac aga aag ggt       1488
Met Ala Asn Ile Ser Glu Ser Glu Thr Pro Phe Pro His Arg Lys Gly
                485                 490                 495

gtt atc ttc aag atc caa tac ttg act ttg tgg acc gaa cca gat caa       1536
Val Ile Phe Lys Ile Gln Tyr Leu Thr Leu Trp Thr Glu Pro Asp Gln
            500                 505                 510

gaa ttg gct aca aaa cat gtt gac tgg atc aga aag ctg tac tct tac       1584
```

```
Glu Leu Ala Thr Lys His Val Asp Trp Ile Arg Lys Leu Tyr Ser Tyr
        515                 520                 525

atg act tct tac gct tct atg ttt cca aga gaa gcc tac gtt aac tac       1632
Met Thr Ser Tyr Ala Ser Met Phe Pro Arg Glu Ala Tyr Val Asn Tyr
    530                 535                 540

aga gat ttg gac ttg ggt atg aac aag aat ggc aac tct aac tcc tca       1680
Arg Asp Leu Asp Leu Gly Met Asn Lys Asn Gly Asn Ser Asn Ser Ser
545                 550                 555                 560

ttc gtt caa gct aca gtt tgg ggt aac aag tac ttc aac aac aat ttc       1728
Phe Val Gln Ala Thr Val Trp Gly Asn Lys Tyr Phe Asn Asn Asn Phe
                565                 570                 575

aac agg ctg gtc gaa atc aag act aag gtt gat cca gag aat ttc ttc       1776
Asn Arg Leu Val Glu Ile Lys Thr Lys Val Asp Pro Glu Asn Phe Phe
            580                 585                 590

aag ttc gaa caa tcc att cca acc ttg cca ttg act aag aaa aga aag       1824
Lys Phe Glu Gln Ser Ile Pro Thr Leu Pro Leu Thr Lys Lys Arg Lys
        595                 600                 605

ggt aag aag atc aac cat tgg tca cat cca caa ttt gaa aag               1866
Gly Lys Lys Ile Asn His Trp Ser His Pro Gln Phe Glu Lys
    610                 615                 620


<210>  29
<211>  622
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  29

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


Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30


Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45


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

```
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Leu Ser Asp Thr Thr Pro
                85                  90                  95

Glu Lys Phe Tyr Gln Cys Ile Cys Lys Asn Ser Asp Phe Ser Asp Pro
            100                 105                 110

Phe Ser Lys Ala Phe Phe Thr Pro Asn Thr Asp Ser Phe Asn Thr Val
        115                 120                 125

Leu Asn Ser Thr Ala Gln Asn Leu Arg Cys Leu Met Pro Thr Val Pro
    130                 135                 140

Lys Pro Val Leu Ile Phe Thr Pro Met Ala Glu Ser His Val Gln Ala
145                 150                 155                 160

Ala Val Ile Cys Ala Lys Gln Leu Asn Leu Gln Leu Arg Val Arg Ser
                165                 170                 175

Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Ile Ser Val Met Asp Ser
            180                 185                 190

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

Ile Glu Glu Asn Ser Ala Trp Ala Gln Ala Gly Ala Thr Val Gly Glu
    210                 215                 220

Val Tyr Tyr Arg Ile Ser Glu Lys Ser Lys Thr His Gly Phe Pro Ala
225                 230                 235                 240

Gly Leu Cys Thr Ser Leu Gly Ile Gly Gly His Ile Thr Gly Gly Ala
                245                 250                 255

Tyr Gly Ser Met Met Arg Lys Phe Gly Leu Gly Ala Asp Asn Val Ile
            260                 265                 270

Asp Ala Arg Ile Val Asn Ala Asn Gly Thr Ile Leu Asp Arg Leu Ser
        275                 280                 285
```

```
Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser
    290                 295                 300

Phe Gly Ile Ile Leu Ser Trp Lys Leu Lys Leu Val Thr Val Pro Ser
305                 310                 315                 320

Val Val Thr Val Phe Thr Val Pro Lys Thr Leu Glu Asp Gly Ala Thr
                325                 330                 335

Lys Ile Leu Tyr Lys Trp Gln Gln Val Ala Asp Lys Ile Asp Asp Asp
            340                 345                 350

Leu Phe Met Arg Val Val Ile Asn Val Val Asp Lys Lys Asp Lys Lys
        355                 360                 365

Gly Glu Arg Thr Val Gln Thr Ala Tyr Asn Ser Leu Phe Leu Gly Asn
    370                 375                 380

Val Asp Arg Leu Leu Gln Ile Met Asn Glu Ser Phe Pro Glu Leu Gly
385                 390                 395                 400

Leu Thr Gln Lys Asp Cys Thr Glu Met Ser Trp Ile Glu Ser Ile Leu
                405                 410                 415

Tyr Ile Ala Gly Phe Pro Thr Lys Thr Pro Pro Glu Ile Leu Leu Gln
            420                 425                 430

Gly Lys Pro Thr Phe Lys Asn Tyr Phe Lys Ala Lys Ser Asp Phe Ile
        435                 440                 445

Lys Glu Pro Ile Pro Glu Thr Gly Leu Asp Gly Ile Trp Lys Arg Leu
    450                 455                 460

Leu Glu Glu Asp Ser Pro Leu Met Ile Trp Asn Pro Tyr Gly Gly Met
465                 470                 475                 480

Met Ala Asn Ile Ser Glu Ser Glu Thr Pro Phe Pro His Arg Lys Gly
                485                 490                 495
```

```
Val Ile Phe Lys Ile Gln Tyr Leu Thr Leu Trp Thr Glu Pro Asp Gln
            500                 505                 510

Glu Leu Ala Thr Lys His Val Asp Trp Ile Arg Lys Leu Tyr Ser Tyr
        515                 520                 525

Met Thr Ser Tyr Ala Ser Met Phe Pro Arg Glu Ala Tyr Val Asn Tyr
    530                 535                 540

Arg Asp Leu Asp Leu Gly Met Asn Lys Asn Gly Asn Ser Asn Ser Ser
545                 550                 555                 560

Phe Val Gln Ala Thr Val Trp Gly Asn Lys Tyr Phe Asn Asn Asn Phe
                565                 570                 575

Asn Arg Leu Val Glu Ile Lys Thr Lys Val Asp Pro Glu Asn Phe Phe
            580                 585                 590

Lys Phe Glu Gln Ser Ile Pro Thr Leu Pro Leu Thr Lys Lys Arg Lys
        595                 600                 605

Gly Lys Lys Ile Asn His Trp Ser His Pro Gln Phe Glu Lys
    610                 615                 620
```

<210> 30
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS35-M5X864

<400> 30

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atgcagatca ttatcaccaa gagatcctct gcttacttct ctgctgttca atcctctatc       60

caaaacttga tcttcgttac cagaggtact tctagaccag aagctattat taccttgttg      120

catgattctc acggtgtctt gattagaatc agatctagag gtcatgacta cgaaggtcaa      180

tcttatgttg ctagagcccc attcgttatc atcgatttgt ttaacttgag gtccatcgac      240

gttgacattg aaaatggttc tgcttgggtt gaatctggtg ctactttggg tgagttgtat      300

tacagaattg ccgaaaagtc taaggcttac ggttttccag ctggttcttg tccaactatt      360

ggtgttggtg gtcatatttc tggtggtggt tttggtactt tgttcagaaa gtatggtttg      420
```

gctgctgata acgttttgga tgctaaaatc gttgatgtca acggtagagt tttggacaga 480

aaacctatgg gtgaagaatt attctgggct attagaggtg gtggtggatc ttcttttggt 540

gttattttgg cttggaagtt gaagttggtt ccagttccac catctgttac tagacatgaa 600

gatttgttct tgcactccgt tataggtgtt ggtaacaaag ctggtactaa tggtgataag 660

accattatta tcgagttcag ctccttgttt ttgggtccag ttgaaaagtt gttgccatcc 720

atgcaagata acttctccga attgtctgtt gatagatccg attgcactga aatgtcctgg 780

attgaatctg tcttgtactt cgctttcatc ccaagaaatg aatctgaagc cttgttgggt 840

agaacccaac aatctaaatc tttcgctaag ccacaaggta ttttctggac tcatagaact 900

ccaaccatga acgttaattc tccaacctct aagttctgta ctacttgtac tccatctaag 960

acctacaaga gaggtacatc tccaaagatt gaagttactg gtactttcgg cactttgaaa 1020

acttctacct ctgttttcaa ggccaagtcc gattatgtta acgaacctat ttctaaggct 1080

ggtttggaag gtttgtggca aactttgata gaagttaagg cctacctgat cttgacatta 1140

tacggtggta agatctccga gatttccaac tctgaaattc atttcccaca caggtctggt 1200

aacttgttca aaattcagta catggttacc tgggacgact acagagaaaa cgaaattggt 1260

gaatccctga tgagaaagtt gtacgattat atggctccct acgtttctaa atctccaaga 1320

gctgcttatc tgaactacaa ggatttggac ttaggtagaa acaacgatgt tcatacttct 1380

tacgctcaag ctagtatttg gggcttgaag tactttaaga acaacttcag aagattggtc 1440

cacgttaaga ctttggttga tccaggtaat ttcttcaggg acgaacaatc tattccatcc 1500

gttagatctt cccgtaagaa g 1521

<210> 31
<211> 1545
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS35-M5X864-strep Tag

<220>
<221> CDS
<222> (1)..(1545)

<400> 31

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atg cag atc att atc acc aag aga tcc tct gct tac ttc tct gct gtt         48
Met Gln Ile Ile Ile Thr Lys Arg Ser Ser Ala Tyr Phe Ser Ala Val
1               5                   10                  15

caa tcc tct atc caa aac ttg atc ttc gtt acc aga ggt act tct aga         96
Gln Ser Ser Ile Gln Asn Leu Ile Phe Val Thr Arg Gly Thr Ser Arg
            20                  25                  30

cca gaa gct att att acc ttg ttg cat gat tct cac ggt gtc ttg att        144
Pro Glu Ala Ile Ile Thr Leu Leu His Asp Ser His Gly Val Leu Ile
        35                  40                  45

aga atc aga tct aga ggt cat gac tac gaa ggt caa tct tat gtt gct        192
Arg Ile Arg Ser Arg Gly His Asp Tyr Glu Gly Gln Ser Tyr Val Ala
    50                  55                  60

aga gcc cca ttc gtt atc atc gat ttg ttt aac ttg agg tcc atc gac        240
Arg Ala Pro Phe Val Ile Ile Asp Leu Phe Asn Leu Arg Ser Ile Asp
65                  70                  75                  80

gtt gac att gaa aat ggt tct gct tgg gtt gaa tct ggt gct act ttg        288
Val Asp Ile Glu Asn Gly Ser Ala Trp Val Glu Ser Gly Ala Thr Leu
                85                  90                  95

ggt gag ttg tat tac aga att gcc gaa aag tct aag gct tac ggt ttt        336
Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Ala Tyr Gly Phe
            100                 105                 110

cca gct ggt tct tgt cca act att ggt gtt ggt ggt cat att tct ggt        384
Pro Ala Gly Ser Cys Pro Thr Ile Gly Val Gly Gly His Ile Ser Gly
        115                 120                 125

ggt ggt ttt ggt act ttg ttc aga aag tat ggt ttg gct gct gat aac        432
Gly Gly Phe Gly Thr Leu Phe Arg Lys Tyr Gly Leu Ala Ala Asp Asn
    130                 135                 140

gtt ttg gat gct aaa atc gtt gat gtc aac ggt aga gtt ttg gac aga        480
Val Leu Asp Ala Lys Ile Val Asp Val Asn Gly Arg Val Leu Asp Arg
145                 150                 155                 160

aaa cct atg ggt gaa gaa tta ttc tgg gct att aga ggt ggt ggt gga        528
Lys Pro Met Gly Glu Glu Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly
                165                 170                 175

tct tct ttt ggt gtt att ttg gct tgg aag ttg aag ttg gtt cca gtt        576
Ser Ser Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu Val Pro Val
            180                 185                 190

cca cca tct gtt act aga cat gaa gat ttg ttc ttg cac tcc gtt ata        624
Pro Pro Ser Val Thr Arg His Glu Asp Leu Phe Leu His Ser Val Ile
        195                 200                 205

ggt gtt ggt aac aaa gct ggt act aat ggt gat aag acc att att atc        672
Gly Val Gly Asn Lys Ala Gly Thr Asn Gly Asp Lys Thr Ile Ile Ile
```

```
    210                 215                 220

gag ttc agc tcc ttg ttt ttg ggt cca gtt gaa aag ttg ttg cca tcc        720
Glu Phe Ser Ser Leu Phe Leu Gly Pro Val Glu Lys Leu Leu Pro Ser
225                 230                 235                 240

atg caa gat aac ttc tcc gaa ttg tct gtt gat aga tcc gat tgc act        768
Met Gln Asp Asn Phe Ser Glu Leu Ser Val Asp Arg Ser Asp Cys Thr
                245                 250                 255

gaa atg tcc tgg att gaa tct gtc ttg tac ttc gct ttc atc cca aga        816
Glu Met Ser Trp Ile Glu Ser Val Leu Tyr Phe Ala Phe Ile Pro Arg
            260                 265                 270

aat gaa tct gaa gcc ttg ttg ggt aga acc caa caa tct aaa tct ttc        864
Asn Glu Ser Glu Ala Leu Leu Gly Arg Thr Gln Gln Ser Lys Ser Phe
        275                 280                 285

gct aag cca caa ggt att ttc tgg act cat aga act cca acc atg aac        912
Ala Lys Pro Gln Gly Ile Phe Trp Thr His Arg Thr Pro Thr Met Asn
    290                 295                 300

gtt aat tct cca acc tct aag ttc tgt act act tgt act cca tct aag        960
Val Asn Ser Pro Thr Ser Lys Phe Cys Thr Thr Cys Thr Pro Ser Lys
305                 310                 315                 320

acc tac aag aga ggt aca tct cca aag att gaa gtt act ggt act ttc       1008
Thr Tyr Lys Arg Gly Thr Ser Pro Lys Ile Glu Val Thr Gly Thr Phe
                325                 330                 335

ggc act ttg aaa act tct acc tct gtt ttc aag gcc aag tcc gat tat       1056
Gly Thr Leu Lys Thr Ser Thr Ser Val Phe Lys Ala Lys Ser Asp Tyr
            340                 345                 350

gtt aac gaa cct att tct aag gct ggt ttg gaa ggt ttg tgg caa act       1104
Val Asn Glu Pro Ile Ser Lys Ala Gly Leu Glu Gly Leu Trp Gln Thr
        355                 360                 365

ttg ata gaa gtt aag gcc tac ctg atc ttg aca tta tac ggt ggt aag       1152
Leu Ile Glu Val Lys Ala Tyr Leu Ile Leu Thr Leu Tyr Gly Gly Lys
    370                 375                 380

atc tcc gag att tcc aac tct gaa att cat ttc cca cac agg tct ggt       1200
Ile Ser Glu Ile Ser Asn Ser Glu Ile His Phe Pro His Arg Ser Gly
385                 390                 395                 400

aac ttg ttc aaa att cag tac atg gtt acc tgg gac gac tac aga gaa       1248
Asn Leu Phe Lys Ile Gln Tyr Met Val Thr Trp Asp Asp Tyr Arg Glu
                405                 410                 415

aac gaa att ggt gaa tcc ctg atg aga aag ttg tac gat tat atg gct       1296
Asn Glu Ile Gly Glu Ser Leu Met Arg Lys Leu Tyr Asp Tyr Met Ala
            420                 425                 430
```

```
ccc tac gtt tct aaa tct cca aga gct gct tat ctg aac tac aag gat       1344
Pro Tyr Val Ser Lys Ser Pro Arg Ala Ala Tyr Leu Asn Tyr Lys Asp
        435                 440                 445

ttg gac tta ggt aga aac aac gat gtt cat act tct tac gct caa gct       1392
Leu Asp Leu Gly Arg Asn Asn Asp Val His Thr Ser Tyr Ala Gln Ala
    450                 455                 460

agt att tgg ggc ttg aag tac ttt aag aac aac ttc aga aga ttg gtc       1440
Ser Ile Trp Gly Leu Lys Tyr Phe Lys Asn Asn Phe Arg Arg Leu Val
465                 470                 475                 480

cac gtt aag act ttg gtt gat cca ggt aat ttc ttc agg gac gaa caa       1488
His Val Lys Thr Leu Val Asp Pro Gly Asn Phe Phe Arg Asp Glu Gln
                485                 490                 495

tct att cca tcc gtt aga tct tcc cgt aag aag tgg tca cat cca caa       1536
Ser Ile Pro Ser Val Arg Ser Ser Arg Lys Lys Trp Ser His Pro Gln
            500                 505                 510

ttt gaa aag                                                          1545
Phe Glu Lys
        515
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<210> 32
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32

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Met Gln Ile Ile Ile Thr Lys Arg Ser Ser Ala Tyr Phe Ser Ala Val
1               5                   10                  15


Gln Ser Ser Ile Gln Asn Leu Ile Phe Val Thr Arg Gly Thr Ser Arg
            20                  25                  30


Pro Glu Ala Ile Ile Thr Leu Leu His Asp Ser His Gly Val Leu Ile
        35                  40                  45


Arg Ile Arg Ser Arg Gly His Asp Tyr Glu Gly Gln Ser Tyr Val Ala
    50                  55                  60


Arg Ala Pro Phe Val Ile Ile Asp Leu Phe Asn Leu Arg Ser Ile Asp
65                  70                  75                  80
```

```
Val Asp Ile Glu Asn Gly Ser Ala Trp Val Glu Ser Gly Ala Thr Leu
                85                  90                  95

Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Ala Tyr Gly Phe
            100                 105                 110

Pro Ala Gly Ser Cys Pro Thr Ile Gly Val Gly Gly His Ile Ser Gly
        115                 120                 125

Gly Gly Phe Gly Thr Leu Phe Arg Lys Tyr Gly Leu Ala Ala Asp Asn
    130                 135                 140

Val Leu Asp Ala Lys Ile Val Asp Val Asn Gly Arg Val Leu Asp Arg
145                 150                 155                 160

Lys Pro Met Gly Glu Glu Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly
                165                 170                 175

Ser Ser Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu Val Pro Val
            180                 185                 190

Pro Pro Ser Val Thr Arg His Glu Asp Leu Phe Leu His Ser Val Ile
        195                 200                 205

Gly Val Gly Asn Lys Ala Gly Thr Asn Gly Asp Lys Thr Ile Ile Ile
    210                 215                 220

Glu Phe Ser Ser Leu Phe Leu Gly Pro Val Glu Lys Leu Leu Pro Ser
225                 230                 235                 240

Met Gln Asp Asn Phe Ser Glu Leu Ser Val Asp Arg Ser Asp Cys Thr
                245                 250                 255

Glu Met Ser Trp Ile Glu Ser Val Leu Tyr Phe Ala Phe Ile Pro Arg
            260                 265                 270

Asn Glu Ser Glu Ala Leu Leu Gly Arg Thr Gln Gln Ser Lys Ser Phe
        275                 280                 285

Ala Lys Pro Gln Gly Ile Phe Trp Thr His Arg Thr Pro Thr Met Asn
```

```
    290                 295                 300

Val Asn Ser Pro Thr Ser Lys Phe Cys Thr Thr Cys Thr Pro Ser Lys
305                 310                 315                 320

Thr Tyr Lys Arg Gly Thr Ser Pro Lys Ile Glu Val Thr Gly Thr Phe
                325                 330                 335

Gly Thr Leu Lys Thr Ser Thr Ser Val Phe Lys Ala Lys Ser Asp Tyr
            340                 345                 350

Val Asn Glu Pro Ile Ser Lys Ala Gly Leu Glu Gly Leu Trp Gln Thr
        355                 360                 365

Leu Ile Glu Val Lys Ala Tyr Leu Ile Leu Thr Leu Tyr Gly Gly Lys
    370                 375                 380

Ile Ser Glu Ile Ser Asn Ser Glu Ile His Phe Pro His Arg Ser Gly
385                 390                 395                 400

Asn Leu Phe Lys Ile Gln Tyr Met Val Thr Trp Asp Asp Tyr Arg Glu
                405                 410                 415

Asn Glu Ile Gly Glu Ser Leu Met Arg Lys Leu Tyr Asp Tyr Met Ala
            420                 425                 430

Pro Tyr Val Ser Lys Ser Pro Arg Ala Ala Tyr Leu Asn Tyr Lys Asp
        435                 440                 445

Leu Asp Leu Gly Arg Asn Asn Asp Val His Thr Ser Tyr Ala Gln Ala
    450                 455                 460

Ser Ile Trp Gly Leu Lys Tyr Phe Lys Asn Asn Phe Arg Arg Leu Val
465                 470                 475                 480

His Val Lys Thr Leu Val Asp Pro Gly Asn Phe Phe Arg Asp Glu Gln
                485                 490                 495

Ser Ile Pro Ser Val Arg Ser Ser Arg Lys Lys Trp Ser His Pro Gln
            500                 505                 510
```

Phe Glu Lys
515

<210> 33
<211> 1602
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS35-M5X864- truncated alpha factor - strep Tag

<220>
<221> CDS
<222> (1)..(1602)

<400> 33
atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc 48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1 5 10 15

gca ctt gca atg cag atc att atc acc aag aga tcc tct gct tac ttc 96
Ala Leu Ala Met Gln Ile Ile Ile Thr Lys Arg Ser Ser Ala Tyr Phe
20 25 30

tct gct gtt caa tcc tct atc caa aac ttg atc ttc gtt acc aga ggt 144
Ser Ala Val Gln Ser Ser Ile Gln Asn Leu Ile Phe Val Thr Arg Gly
35 40 45

act tct aga cca gaa gct att att acc ttg ttg cat gat tct cac ggt 192
Thr Ser Arg Pro Glu Ala Ile Ile Thr Leu Leu His Asp Ser His Gly
50 55 60

gtc ttg att aga atc aga tct aga ggt cat gac tac gaa ggt caa tct 240
Val Leu Ile Arg Ile Arg Ser Arg Gly His Asp Tyr Glu Gly Gln Ser
65 70 75 80

tat gtt gct aga gcc cca ttc gtt atc atc gat ttg ttt aac ttg agg 288
Tyr Val Ala Arg Ala Pro Phe Val Ile Ile Asp Leu Phe Asn Leu Arg
85 90 95

tcc atc gac gtt gac att gaa aat ggt tct gct tgg gtt gaa tct ggt 336
Ser Ile Asp Val Asp Ile Glu Asn Gly Ser Ala Trp Val Glu Ser Gly
100 105 110

gct act ttg ggt gag ttg tat tac aga att gcc gaa aag tct aag gct 384
Ala Thr Leu Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Ala
115 120 125

tac ggt ttt cca gct ggt tct tgt cca act att ggt gtt ggt ggt cat 432
Tyr Gly Phe Pro Ala Gly Ser Cys Pro Thr Ile Gly Val Gly Gly His
130 135 140

```
att tct ggt ggt ggt ttt ggt act ttg ttc aga aag tat ggt ttg gct        480
Ile Ser Gly Gly Gly Phe Gly Thr Leu Phe Arg Lys Tyr Gly Leu Ala
145                 150                 155                 160

gct gat aac gtt ttg gat gct aaa atc gtt gat gtc aac ggt aga gtt        528
Ala Asp Asn Val Leu Asp Ala Lys Ile Val Asp Val Asn Gly Arg Val
                165                 170                 175

ttg gac aga aaa cct atg ggt gaa gaa tta ttc tgg gct att aga ggt        576
Leu Asp Arg Lys Pro Met Gly Glu Glu Leu Phe Trp Ala Ile Arg Gly
            180                 185                 190

ggt ggt gga tct tct ttt ggt gtt att ttg gct tgg aag ttg aag ttg        624
Gly Gly Gly Ser Ser Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu
        195                 200                 205

gtt cca gtt cca cca tct gtt act aga cat gaa gat ttg ttc ttg cac        672
Val Pro Val Pro Pro Ser Val Thr Arg His Glu Asp Leu Phe Leu His
    210                 215                 220

tcc gtt ata ggt gtt ggt aac aaa gct ggt act aat ggt gat aag acc        720
Ser Val Ile Gly Val Gly Asn Lys Ala Gly Thr Asn Gly Asp Lys Thr
225                 230                 235                 240

att att atc gag ttc agc tcc ttg ttt ttg ggt cca gtt gaa aag ttg        768
Ile Ile Ile Glu Phe Ser Ser Leu Phe Leu Gly Pro Val Glu Lys Leu
                245                 250                 255

ttg cca tcc atg caa gat aac ttc tcc gaa ttg tct gtt gat aga tcc        816
Leu Pro Ser Met Gln Asp Asn Phe Ser Glu Leu Ser Val Asp Arg Ser
            260                 265                 270

gat tgc act gaa atg tcc tgg att gaa tct gtc ttg tac ttc gct ttc        864
Asp Cys Thr Glu Met Ser Trp Ile Glu Ser Val Leu Tyr Phe Ala Phe
        275                 280                 285

atc cca aga aat gaa tct gaa gcc ttg ttg ggt aga acc caa caa tct        912
Ile Pro Arg Asn Glu Ser Glu Ala Leu Leu Gly Arg Thr Gln Gln Ser
    290                 295                 300

aaa tct ttc gct aag cca caa ggt att ttc tgg act cat aga act cca        960
Lys Ser Phe Ala Lys Pro Gln Gly Ile Phe Trp Thr His Arg Thr Pro
305                 310                 315                 320

acc atg aac gtt aat tct cca acc tct aag ttc tgt act act tgt act       1008
Thr Met Asn Val Asn Ser Pro Thr Ser Lys Phe Cys Thr Thr Cys Thr
                325                 330                 335

cca tct aag acc tac aag aga ggt aca tct cca aag att gaa gtt act       1056
Pro Ser Lys Thr Tyr Lys Arg Gly Thr Ser Pro Lys Ile Glu Val Thr
            340                 345                 350

ggt act ttc ggc act ttg aaa act tct acc tct gtt ttc aag gcc aag       1104
```

```
Gly Thr Phe Gly Thr Leu Lys Thr Ser Thr Ser Val Phe Lys Ala Lys
        355                 360                 365

tcc gat tat gtt aac gaa cct att tct aag gct ggt ttg gaa ggt ttg       1152
Ser Asp Tyr Val Asn Glu Pro Ile Ser Lys Ala Gly Leu Glu Gly Leu
    370                 375                 380

tgg caa act ttg ata gaa gtt aag gcc tac ctg atc ttg aca tta tac       1200
Trp Gln Thr Leu Ile Glu Val Lys Ala Tyr Leu Ile Leu Thr Leu Tyr
385                 390                 395                 400

ggt ggt aag atc tcc gag att tcc aac tct gaa att cat ttc cca cac       1248
Gly Gly Lys Ile Ser Glu Ile Ser Asn Ser Glu Ile His Phe Pro His
                405                 410                 415

agg tct ggt aac ttg ttc aaa att cag tac atg gtt acc tgg gac gac       1296
Arg Ser Gly Asn Leu Phe Lys Ile Gln Tyr Met Val Thr Trp Asp Asp
            420                 425                 430

tac aga gaa aac gaa att ggt gaa tcc ctg atg aga aag ttg tac gat       1344
Tyr Arg Glu Asn Glu Ile Gly Glu Ser Leu Met Arg Lys Leu Tyr Asp
        435                 440                 445

tat atg gct ccc tac gtt tct aaa tct cca aga gct gct tat ctg aac       1392
Tyr Met Ala Pro Tyr Val Ser Lys Ser Pro Arg Ala Ala Tyr Leu Asn
    450                 455                 460

tac aag gat ttg gac tta ggt aga aac aac gat gtt cat act tct tac       1440
Tyr Lys Asp Leu Asp Leu Gly Arg Asn Asn Asp Val His Thr Ser Tyr
465                 470                 475                 480

gct caa gct agt att tgg ggc ttg aag tac ttt aag aac aac ttc aga       1488
Ala Gln Ala Ser Ile Trp Gly Leu Lys Tyr Phe Lys Asn Asn Phe Arg
                485                 490                 495

aga ttg gtc cac gtt aag act ttg gtt gat cca ggt aat ttc ttc agg       1536
Arg Leu Val His Val Lys Thr Leu Val Asp Pro Gly Asn Phe Phe Arg
            500                 505                 510

gac gaa caa tct att cca tcc gtt aga tct tcc cgt aag aag tgg tca       1584
Asp Glu Gln Ser Ile Pro Ser Val Arg Ser Ser Arg Lys Lys Trp Ser
        515                 520                 525

cat cca caa ttt gaa aag                                              1602
His Pro Gln Phe Glu Lys
    530
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<210>  34
<211>  534
<212>  PRT
<213>  Artificial Sequence

<220>

<223> Synthetic Construct

<400> 34

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

Ala Leu Ala Met Gln Ile Ile Ile Thr Lys Arg Ser Ser Ala Tyr Phe
            20                  25                  30

Ser Ala Val Gln Ser Ser Ile Gln Asn Leu Ile Phe Val Thr Arg Gly
        35                  40                  45

Thr Ser Arg Pro Glu Ala Ile Ile Thr Leu Leu His Asp Ser His Gly
    50                  55                  60

Val Leu Ile Arg Ile Arg Ser Arg Gly His Asp Tyr Glu Gly Gln Ser
65                  70                  75                  80

Tyr Val Ala Arg Ala Pro Phe Val Ile Ile Asp Leu Phe Asn Leu Arg
                85                  90                  95

Ser Ile Asp Val Asp Ile Glu Asn Gly Ser Ala Trp Val Glu Ser Gly
            100                 105                 110

Ala Thr Leu Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Ala
        115                 120                 125

Tyr Gly Phe Pro Ala Gly Ser Cys Pro Thr Ile Gly Val Gly Gly His
    130                 135                 140

Ile Ser Gly Gly Gly Phe Gly Thr Leu Phe Arg Lys Tyr Gly Leu Ala
145                 150                 155                 160

Ala Asp Asn Val Leu Asp Ala Lys Ile Val Asp Val Asn Gly Arg Val
                165                 170                 175

Leu Asp Arg Lys Pro Met Gly Glu Glu Leu Phe Trp Ala Ile Arg Gly
            180                 185                 190

Gly Gly Gly Ser Ser Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu
        195                 200                 205
```

```
Val Pro Val Pro Pro Ser Val Thr Arg His Glu Asp Leu Phe Leu His
    210                 215                 220

Ser Val Ile Gly Val Gly Asn Lys Ala Gly Thr Asn Gly Asp Lys Thr
225                 230                 235                 240

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

Leu Pro Ser Met Gln Asp Asn Phe Ser Glu Leu Ser Val Asp Arg Ser
            260                 265                 270

Asp Cys Thr Glu Met Ser Trp Ile Glu Ser Val Leu Tyr Phe Ala Phe
        275                 280                 285

Ile Pro Arg Asn Glu Ser Glu Ala Leu Leu Gly Arg Thr Gln Gln Ser
    290                 295                 300

Lys Ser Phe Ala Lys Pro Gln Gly Ile Phe Trp Thr His Arg Thr Pro
305                 310                 315                 320

Thr Met Asn Val Asn Ser Pro Thr Ser Lys Phe Cys Thr Thr Cys Thr
                325                 330                 335

Pro Ser Lys Thr Tyr Lys Arg Gly Thr Ser Pro Lys Ile Glu Val Thr
            340                 345                 350

Gly Thr Phe Gly Thr Leu Lys Thr Ser Thr Ser Val Phe Lys Ala Lys
        355                 360                 365

Ser Asp Tyr Val Asn Glu Pro Ile Ser Lys Ala Gly Leu Glu Gly Leu
    370                 375                 380

Trp Gln Thr Leu Ile Glu Val Lys Ala Tyr Leu Ile Leu Thr Leu Tyr
385                 390                 395                 400

Gly Gly Lys Ile Ser Glu Ile Ser Asn Ser Glu Ile His Phe Pro His
                405                 410                 415
```

```
Arg Ser Gly Asn Leu Phe Lys Ile Gln Tyr Met Val Thr Trp Asp Asp
            420                 425                 430

Tyr Arg Glu Asn Glu Ile Gly Glu Ser Leu Met Arg Lys Leu Tyr Asp
        435                 440                 445

Tyr Met Ala Pro Tyr Val Ser Lys Ser Pro Arg Ala Ala Tyr Leu Asn
    450                 455                 460

Tyr Lys Asp Leu Asp Leu Gly Arg Asn Asn Asp Val His Thr Ser Tyr
465                 470                 475                 480

Ala Gln Ala Ser Ile Trp Gly Leu Lys Tyr Phe Lys Asn Asn Phe Arg
                485                 490                 495

Arg Leu Val His Val Lys Thr Leu Val Asp Pro Gly Asn Phe Phe Arg
            500                 505                 510

Asp Glu Gln Ser Ile Pro Ser Val Arg Ser Ser Arg Lys Lys Trp Ser
        515                 520                 525

His Pro Gln Phe Glu Lys
    530
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<210> 35
<211> 1812
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS35-M5X864- full alpha factor - strep Tag

<400> 35

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ccagtcaaca ctacaacaga agatgaaacg gcacaaattc cggctgaagc tgtcatcggt      120

tactcagatt tagaagggga tttcgatgtt gctgttttgc cattttccaa cagcacaaat      180

aacgggttat tgtttataaa tactactatt gccagcattg ctgctaaaga agaaggggta      240

tctctcgaga aaagagaggc tgaagctatg cagatcatta tcaccaagag atcctctgct      300

tacttctctg ctgttcaatc ctctatccaa aacttgatct tcgttaccag aggtacttct      360

agaccagaag ctattattac cttgttgcat gattctcacg gtgtcttgat tagaatcaga      420
```

tctagaggtc atgactacga aggtcaatct tatgttgcta gagccccatt cgttatcatc 480

gatttgttta acttgaggtc catcgacgtt gacattgaaa atggttctgc ttgggttgaa 540

tctggtgcta ctttgggtga gttgtattac agaattgccg aaaagtctaa ggcttacggt 600

tttccagctg gttcttgtcc aactattggt gttggtggtc atatttctgg tggtggtttt 660

ggtactttgt tcagaaagta tggtttggct gctgataacg ttttggatgc taaaatcgtt 720

gatgtcaacg gtagagtttt ggacagaaaa cctatgggtg aagaattatt ctgggctatt 780

agaggtggtg gtggatcttc ttttggtgtt attttggctt ggaagttgaa gttggttcca 840

gttccaccat ctgttactag acatgaagat ttgttcttgc actccgttat aggtgttggt 900

aacaaagctg gtactaatgg tgataagacc attattatcg agttcagctc cttgtttttg 960

ggtccagttg aaaagttgtt gccatccatg caagataact tctccgaatt gtctgttgat 1020

agatccgatt gcactgaaat gtcctggatt gaatctgtct tgtacttcgc tttcatccca 1080

agaaatgaat ctgaagcctt gttgggtaga acccaacaat ctaaatcttt cgctaagcca 1140

caaggtattt tctggactca tagaactcca accatgaacg ttaattctcc aacctctaag 1200

ttctgtacta cttgtactcc atctaagacc tacaagagag gtacatctcc aaagattgaa 1260

gttactggta ctttcggcac tttgaaaact tctacctctg ttttcaaggc caagtccgat 1320

tatgttaacg aacctatttc taaggctggt ttggaaggtt tgtggcaaac tttgatagaa 1380

gttaaggcct acctgatctt gacattatac ggtggtaaga tctccgagat ttccaactct 1440

gaaattcatt tcccacacag gtctggtaac ttgttcaaaa ttcagtacat ggttacctgg 1500

gacgactaca gagaaaacga aattggtgaa tccctgatga gaaagttgta cgattatatg 1560

gctccctacg tttctaaatc tccaagagct gcttatctga actacaagga tttggactta 1620

ggtagaaaca acgatgttca tacttcttac gctcaagcta gtatttgggg cttgaagtac 1680

tttaagaaca acttcagaag attggtccac gttaagactt tggttgatcc aggtaatttc 1740

ttcagggacg aacaatctat tccatccgtt agatcttccc gtaagaagtg gtcacatcca 1800

caatttgaaa ag 1812

<210> 36
<211> 1620
<212> DNA
<213> Artificial Sequence

<220>
<223>  CBS59-O64745


<220>
<221>  CDS
<222>  (1)..(1620)

<400>  36
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atg aag ttc tgg tca aga cct ttg acc ttc ttg atc atc atc atc tac         48
Met Lys Phe Trp Ser Arg Pro Leu Thr Phe Leu Ile Ile Ile Ile Tyr
1               5                   10                  15

ctg atc atc caa cag gtt aat tct tct cca cca tcc ttg tct att cca         96
Leu Ile Ile Gln Gln Val Asn Ser Ser Pro Pro Ser Leu Ser Ile Pro
            20                  25                  30

gaa cat ttc ttg aga tgc ttg gat acc caa cca tct gat cat ggt tct        144
Glu His Phe Leu Arg Cys Leu Asp Thr Gln Pro Ser Asp His Gly Ser
        35                  40                  45

cca aat tct aga act gcc gtt att cca acg aac tct tct ttt tct acc        192
Pro Asn Ser Arg Thr Ala Val Ile Pro Thr Asn Ser Ser Phe Ser Thr
    50                  55                  60

aac ttg atg aac ggc gtc aga aat ttg aga ttc gct tct gtt tct act        240
Asn Leu Met Asn Gly Val Arg Asn Leu Arg Phe Ala Ser Val Ser Thr
65                  70                  75                  80

agg aag cca gaa gtt ata gtt gct gct gtt act gaa acc cat att aga        288
Arg Lys Pro Glu Val Ile Val Ala Ala Val Thr Glu Thr His Ile Arg
                85                  90                  95

gct acc att tct tgc tgc aag ttg ttg aac ttg gaa ttg aga att aga        336
Ala Thr Ile Ser Cys Cys Lys Leu Leu Asn Leu Glu Leu Arg Ile Arg
            100                 105                 110

tcc ggt ggt cat gat tac gaa ggt ttc tct tat act tct cca gtt cca        384
Ser Gly Gly His Asp Tyr Glu Gly Phe Ser Tyr Thr Ser Pro Val Pro
        115                 120                 125

ttc gtt atc ctg gac atg tac aac ttc aac aag atc gac att aac atg        432
Phe Val Ile Leu Asp Met Tyr Asn Phe Asn Lys Ile Asp Ile Asn Met
    130                 135                 140

aag gac gaa acc gtc tgg att caa tct ggt gct tct ttg ggt cag ttg        480
Lys Asp Glu Thr Val Trp Ile Gln Ser Gly Ala Ser Leu Gly Gln Leu
145                 150                 155                 160

tac tac aat att gcc tcc aag tct aag gtt cat gct ttt cca gct ggt        528
Tyr Tyr Asn Ile Ala Ser Lys Ser Lys Val His Ala Phe Pro Ala Gly
                165                 170                 175
```

```
gtt tgt cca aaa gtt ggt gct ggt ggt cat ttt tct ggt ggt ggt ttt        576
Val Cys Pro Lys Val Gly Ala Gly Gly His Phe Ser Gly Gly Gly Phe
            180                 185                 190

ggt aat ttg atg agg aaa tac ggt ttg tcc atc gat cat atc att gac        624
Gly Asn Leu Met Arg Lys Tyr Gly Leu Ser Ile Asp His Ile Ile Asp
        195                 200                 205

gcc caa att atg gat gct aac ggt aag gtt tac aga aac aga caa gct        672
Ala Gln Ile Met Asp Ala Asn Gly Lys Val Tyr Arg Asn Arg Gln Ala
    210                 215                 220

atg ggt gaa gat gtt ttc tgg gct att aga ggt ggt ggt ggc ggt tct        720
Met Gly Glu Asp Val Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser
225                 230                 235                 240

tat ggt gtt att ttg gct tgg aag att aag ttg gtt agg gtt cca gaa        768
Tyr Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Arg Val Pro Glu
                245                 250                 255

aag gtc acc gtt ttt aag ttg gaa aga acc gtt aga gaa ggt gcc gtt        816
Lys Val Thr Val Phe Lys Leu Glu Arg Thr Val Arg Glu Gly Ala Val
            260                 265                 270

gat ttg gtt cat aag tgg caa caa gtt gcc cca gtt att gat aga gat        864
Asp Leu Val His Lys Trp Gln Gln Val Ala Pro Val Ile Asp Arg Asp
        275                 280                 285

ttg ttc atc aga ttg gag atc aag ccc atc aac aga aag att tct aag        912
Leu Phe Ile Arg Leu Glu Ile Lys Pro Ile Asn Arg Lys Ile Ser Lys
    290                 295                 300

ggt aag acc atc aag gtg tcc ttc att ggt atg ttt ttg ggt ttg cca        960
Gly Lys Thr Ile Lys Val Ser Phe Ile Gly Met Phe Leu Gly Leu Pro
305                 310                 315                 320

gaa cgt ttg ttg aac atc act aag caa tct ttc cca gaa ctg cac ttg       1008
Glu Arg Leu Leu Asn Ile Thr Lys Gln Ser Phe Pro Glu Leu His Leu
                325                 330                 335

aca aaa gaa gat tgc atg gtt aag aag tgg atc gag tca tct gtt ttt       1056
Thr Lys Glu Asp Cys Met Val Lys Lys Trp Ile Glu Ser Ser Val Phe
            340                 345                 350

tgg gca aat tac cca gaa aaa gcc cca att gag ttg ttg ttg aaa aga       1104
Trp Ala Asn Tyr Pro Glu Lys Ala Pro Ile Glu Leu Leu Leu Lys Arg
        355                 360                 365

gtc tct acc aac gag tac tac tgg aag aga act tct gat ttt gtt cag       1152
Val Ser Thr Asn Glu Tyr Tyr Trp Lys Arg Thr Ser Asp Phe Val Gln
    370                 375                 380

gcc cca att tct aaa caa ggt ttg gct aag att ttc cag acc atg att       1200
Ala Pro Ile Ser Lys Gln Gly Leu Ala Lys Ile Phe Gln Thr Met Ile
```

```
385                 390                 395                 400

gat cat tct cca ttg cct aga aga gtt tgg atg caa tgg aat cct tgg       1248
Asp His Ser Pro Leu Pro Arg Arg Val Trp Met Gln Trp Asn Pro Trp
                405                 410                 415

ggt ggt aaa atg gct gaa att gct tct gat gct act gcc ttt gtt cac       1296
Gly Gly Lys Met Ala Glu Ile Ala Ser Asp Ala Thr Ala Phe Val His
            420                 425                 430

aga ggt ggt aat gtt ttc atg atc gaa cat ttc atg aac tgg tac aga       1344
Arg Gly Gly Asn Val Phe Met Ile Glu His Phe Met Asn Trp Tyr Arg
        435                 440                 445

cca ggt gat gaa ttg gaa gaa aag ttc ttg gct att gcc agg tct ttc       1392
Pro Gly Asp Glu Leu Glu Glu Lys Phe Leu Ala Ile Ala Arg Ser Phe
    450                 455                 460

aaa gaa gct atg gct cca ttt gtt tct aag aat cca aga gaa gcc ttc       1440
Lys Glu Ala Met Ala Pro Phe Val Ser Lys Asn Pro Arg Glu Ala Phe
465                 470                 475                 480

ttc aac tac aga gat gtt gat att ggt atc act acc cca ggt tac aat       1488
Phe Asn Tyr Arg Asp Val Asp Ile Gly Ile Thr Thr Pro Gly Tyr Asn
                485                 490                 495

gct act tat gaa ggt gct aaa gtt tac ggc gat tct tac ttt aag ggt       1536
Ala Thr Tyr Glu Gly Ala Lys Val Tyr Gly Asp Ser Tyr Phe Lys Gly
            500                 505                 510

aac tac ttg agg ttg gtt aag atc aag gct aga ttc gac aga acg aac       1584
Asn Tyr Leu Arg Leu Val Lys Ile Lys Ala Arg Phe Asp Arg Thr Asn
        515                 520                 525

ttc ttc aga tct caa caa ggt att cca gtt ttg gcc                      1620
Phe Phe Arg Ser Gln Gln Gly Ile Pro Val Leu Ala
    530                 535                 540


<210>  37
<211>  540
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  37

Met Lys Phe Trp Ser Arg Pro Leu Thr Phe Leu Ile Ile Ile Ile Tyr
1               5                   10                  15


Leu Ile Ile Gln Gln Val Asn Ser Ser Pro Pro Ser Leu Ser Ile Pro
```

```
            20                  25                  30

Glu His Phe Leu Arg Cys Leu Asp Thr Gln Pro Ser Asp His Gly Ser
        35                  40                  45

Pro Asn Ser Arg Thr Ala Val Ile Pro Thr Asn Ser Ser Phe Ser Thr
    50                  55                  60

Asn Leu Met Asn Gly Val Arg Asn Leu Arg Phe Ala Ser Val Ser Thr
65                  70                  75                  80

Arg Lys Pro Glu Val Ile Val Ala Ala Val Thr Glu Thr His Ile Arg
                85                  90                  95

Ala Thr Ile Ser Cys Cys Lys Leu Leu Asn Leu Glu Leu Arg Ile Arg
            100                 105                 110

Ser Gly Gly His Asp Tyr Glu Gly Phe Ser Tyr Thr Ser Pro Val Pro
        115                 120                 125

Phe Val Ile Leu Asp Met Tyr Asn Phe Asn Lys Ile Asp Ile Asn Met
    130                 135                 140

Lys Asp Glu Thr Val Trp Ile Gln Ser Gly Ala Ser Leu Gly Gln Leu
145                 150                 155                 160

Tyr Tyr Asn Ile Ala Ser Lys Ser Lys Val His Ala Phe Pro Ala Gly
                165                 170                 175

Val Cys Pro Lys Val Gly Ala Gly Gly His Phe Ser Gly Gly Gly Phe
            180                 185                 190

Gly Asn Leu Met Arg Lys Tyr Gly Leu Ser Ile Asp His Ile Ile Asp
        195                 200                 205

Ala Gln Ile Met Asp Ala Asn Gly Lys Val Tyr Arg Asn Arg Gln Ala
    210                 215                 220

Met Gly Glu Asp Val Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser
225                 230                 235                 240
```

```
Tyr Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Arg Val Pro Glu
                245                 250                 255

Lys Val Thr Val Phe Lys Leu Glu Arg Thr Val Arg Glu Gly Ala Val
            260                 265                 270

Asp Leu Val His Lys Trp Gln Gln Val Ala Pro Val Ile Asp Arg Asp
        275                 280                 285

Leu Phe Ile Arg Leu Glu Ile Lys Pro Ile Asn Arg Lys Ile Ser Lys
    290                 295                 300

Gly Lys Thr Ile Lys Val Ser Phe Ile Gly Met Phe Leu Gly Leu Pro
305                 310                 315                 320

Glu Arg Leu Leu Asn Ile Thr Lys Gln Ser Phe Pro Glu Leu His Leu
                325                 330                 335

Thr Lys Glu Asp Cys Met Val Lys Lys Trp Ile Glu Ser Ser Val Phe
            340                 345                 350

Trp Ala Asn Tyr Pro Glu Lys Ala Pro Ile Glu Leu Leu Leu Lys Arg
        355                 360                 365

Val Ser Thr Asn Glu Tyr Tyr Trp Lys Arg Thr Ser Asp Phe Val Gln
    370                 375                 380

Ala Pro Ile Ser Lys Gln Gly Leu Ala Lys Ile Phe Gln Thr Met Ile
385                 390                 395                 400

Asp His Ser Pro Leu Pro Arg Arg Val Trp Met Gln Trp Asn Pro Trp
                405                 410                 415

Gly Gly Lys Met Ala Glu Ile Ala Ser Asp Ala Thr Ala Phe Val His
            420                 425                 430

Arg Gly Gly Asn Val Phe Met Ile Glu His Phe Met Asn Trp Tyr Arg
        435                 440                 445

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

```
    450                 455                 460

Lys Glu Ala Met Ala Pro Phe Val Ser Lys Asn Pro Arg Glu Ala Phe
465                 470                 475                 480

Phe Asn Tyr Arg Asp Val Asp Ile Gly Ile Thr Thr Pro Gly Tyr Asn
                485                 490                 495

Ala Thr Tyr Glu Gly Ala Lys Val Tyr Gly Asp Ser Tyr Phe Lys Gly
            500                 505                 510

Asn Tyr Leu Arg Leu Val Lys Ile Lys Ala Arg Phe Asp Arg Thr Asn
        515                 520                 525

Phe Phe Arg Ser Gln Gln Gly Ile Pro Val Leu Ala
    530                 535                 540


<210>  38
<211>  1551
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS59-O64745-no signal peptide


<220>
<221>  CDS
<222>  (1)..(1551)

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atg tct cca cca tcc ttg tct att cca gaa cat ttc ttg aga tgc ttg         48
Met Ser Pro Pro Ser Leu Ser Ile Pro Glu His Phe Leu Arg Cys Leu
1               5                   10                  15

gat acc caa cca tct gat cat ggt tct cca aat tct aga act gcc gtt         96
Asp Thr Gln Pro Ser Asp His Gly Ser Pro Asn Ser Arg Thr Ala Val
            20                  25                  30

att cca acg aac tct tct ttt tct acc aac ttg atg aac ggc gtc aga        144
Ile Pro Thr Asn Ser Ser Phe Ser Thr Asn Leu Met Asn Gly Val Arg
        35                  40                  45

aat ttg aga ttc gct tct gtt tct act agg aag cca gaa gtt ata gtt        192
Asn Leu Arg Phe Ala Ser Val Ser Thr Arg Lys Pro Glu Val Ile Val
    50                  55                  60

gct gct gtt act gaa acc cat att aga gct acc att tct tgc tgc aag        240
```

```
Ala Ala Val Thr Glu Thr His Ile Arg Ala Thr Ile Ser Cys Cys Lys
65                  70                  75                  80

ttg ttg aac ttg gaa ttg aga att aga tcc ggt ggt cat gat tac gaa        288
Leu Leu Asn Leu Glu Leu Arg Ile Arg Ser Gly Gly His Asp Tyr Glu
                85                  90                  95

ggt ttc tct tat act tct cca gtt cca ttc gtt atc ctg gac atg tac        336
Gly Phe Ser Tyr Thr Ser Pro Val Pro Phe Val Ile Leu Asp Met Tyr
            100                 105                 110

aac ttc aac aag atc gac att aac atg aag gac gaa acc gtc tgg att        384
Asn Phe Asn Lys Ile Asp Ile Asn Met Lys Asp Glu Thr Val Trp Ile
        115                 120                 125

caa tct ggt gct tct ttg ggt cag ttg tac tac aat att gcc tcc aag        432
Gln Ser Gly Ala Ser Leu Gly Gln Leu Tyr Tyr Asn Ile Ala Ser Lys
    130                 135                 140

tct aag gtt cat gct ttt cca gct ggt gtt tgt cca aaa gtt ggt gct        480
Ser Lys Val His Ala Phe Pro Ala Gly Val Cys Pro Lys Val Gly Ala
145                 150                 155                 160

ggt ggt cat ttt tct ggt ggt ggt ttt ggt aat ttg atg agg aaa tac        528
Gly Gly His Phe Ser Gly Gly Gly Phe Gly Asn Leu Met Arg Lys Tyr
                165                 170                 175

ggt ttg tcc atc gat cat atc att gac gcc caa att atg gat gct aac        576
Gly Leu Ser Ile Asp His Ile Ile Asp Ala Gln Ile Met Asp Ala Asn
            180                 185                 190

ggt aag gtt tac aga aac aga caa gct atg ggt gaa gat gtt ttc tgg        624
Gly Lys Val Tyr Arg Asn Arg Gln Ala Met Gly Glu Asp Val Phe Trp
        195                 200                 205

gct att aga ggt ggt ggt ggc ggt tct tat ggt gtt att ttg gct tgg        672
Ala Ile Arg Gly Gly Gly Gly Gly Ser Tyr Gly Val Ile Leu Ala Trp
    210                 215                 220

aag att aag ttg gtt agg gtt cca gaa aag gtc acc gtt ttt aag ttg        720
Lys Ile Lys Leu Val Arg Val Pro Glu Lys Val Thr Val Phe Lys Leu
225                 230                 235                 240

gaa aga acc gtt aga gaa ggt gcc gtt gat ttg gtt cat aag tgg caa        768
Glu Arg Thr Val Arg Glu Gly Ala Val Asp Leu Val His Lys Trp Gln
                245                 250                 255

caa gtt gcc cca gtt att gat aga gat ttg ttc atc aga ttg gag atc        816
Gln Val Ala Pro Val Ile Asp Arg Asp Leu Phe Ile Arg Leu Glu Ile
            260                 265                 270

aag ccc atc aac aga aag att tct aag ggt aag acc atc aag gtg tcc        864
Lys Pro Ile Asn Arg Lys Ile Ser Lys Gly Lys Thr Ile Lys Val Ser
        275                 280                 285
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ttc att ggt atg ttt ttg ggt ttg cca gaa cgt ttg ttg aac atc act        912
Phe Ile Gly Met Phe Leu Gly Leu Pro Glu Arg Leu Leu Asn Ile Thr
    290                 295                 300

aag caa tct ttc cca gaa ctg cac ttg aca aaa gaa gat tgc atg gtt        960
Lys Gln Ser Phe Pro Glu Leu His Leu Thr Lys Glu Asp Cys Met Val
305                 310                 315                 320

aag aag tgg atc gag tca tct gtt ttt tgg gca aat tac cca gaa aaa       1008
Lys Lys Trp Ile Glu Ser Ser Val Phe Trp Ala Asn Tyr Pro Glu Lys
                325                 330                 335

gcc cca att gag ttg ttg ttg aaa aga gtc tct acc aac gag tac tac       1056
Ala Pro Ile Glu Leu Leu Leu Lys Arg Val Ser Thr Asn Glu Tyr Tyr
            340                 345                 350

tgg aag aga act tct gat ttt gtt cag gcc cca att tct aaa caa ggt       1104
Trp Lys Arg Thr Ser Asp Phe Val Gln Ala Pro Ile Ser Lys Gln Gly
        355                 360                 365

ttg gct aag att ttc cag acc atg att gat cat tct cca ttg cct aga       1152
Leu Ala Lys Ile Phe Gln Thr Met Ile Asp His Ser Pro Leu Pro Arg
    370                 375                 380

aga gtt tgg atg caa tgg aat cct tgg ggt ggt aaa atg gct gaa att       1200
Arg Val Trp Met Gln Trp Asn Pro Trp Gly Gly Lys Met Ala Glu Ile
385                 390                 395                 400

gct tct gat gct act gcc ttt gtt cac aga ggt ggt aat gtt ttc atg       1248
Ala Ser Asp Ala Thr Ala Phe Val His Arg Gly Gly Asn Val Phe Met
                405                 410                 415

atc gaa cat ttc atg aac tgg tac aga cca ggt gat gaa ttg gaa gaa       1296
Ile Glu His Phe Met Asn Trp Tyr Arg Pro Gly Asp Glu Leu Glu Glu
            420                 425                 430

aag ttc ttg gct att gcc agg tct ttc aaa gaa gct atg gct cca ttt       1344
Lys Phe Leu Ala Ile Ala Arg Ser Phe Lys Glu Ala Met Ala Pro Phe
        435                 440                 445

gtt tct aag aat cca aga gaa gcc ttc ttc aac tac aga gat gtt gat       1392
Val Ser Lys Asn Pro Arg Glu Ala Phe Phe Asn Tyr Arg Asp Val Asp
    450                 455                 460

att ggt atc act acc cca ggt tac aat gct act tat gaa ggt gct aaa       1440
Ile Gly Ile Thr Thr Pro Gly Tyr Asn Ala Thr Tyr Glu Gly Ala Lys
465                 470                 475                 480

gtt tac ggc gat tct tac ttt aag ggt aac tac ttg agg ttg gtt aag       1488
Val Tyr Gly Asp Ser Tyr Phe Lys Gly Asn Tyr Leu Arg Leu Val Lys
                485                 490                 495

atc aag gct aga ttc gac aga acg aac ttc ttc aga tct caa caa ggt       1536
```

```
Ile Lys Ala Arg Phe Asp Arg Thr Asn Phe Phe Arg Ser Gln Gln Gly
            500                 505                 510

att cca gtt ttg gcc                                                 1551
Ile Pro Val Leu Ala
        515
```

<210> 39
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 39

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Met Ser Pro Pro Ser Leu Ser Ile Pro Glu His Phe Leu Arg Cys Leu
1               5                   10                  15

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

Ile Pro Thr Asn Ser Ser Phe Ser Thr Asn Leu Met Asn Gly Val Arg
        35                  40                  45

Asn Leu Arg Phe Ala Ser Val Ser Thr Arg Lys Pro Glu Val Ile Val
    50                  55                  60

Ala Ala Val Thr Glu Thr His Ile Arg Ala Thr Ile Ser Cys Cys Lys
65                  70                  75                  80

Leu Leu Asn Leu Glu Leu Arg Ile Arg Ser Gly Gly His Asp Tyr Glu
                85                  90                  95

Gly Phe Ser Tyr Thr Ser Pro Val Pro Phe Val Ile Leu Asp Met Tyr
            100                 105                 110

Asn Phe Asn Lys Ile Asp Ile Asn Met Lys Asp Glu Thr Val Trp Ile
        115                 120                 125

Gln Ser Gly Ala Ser Leu Gly Gln Leu Tyr Tyr Asn Ile Ala Ser Lys
    130                 135                 140
```

```
Ser Lys Val His Ala Phe Pro Ala Gly Val Cys Pro Lys Val Gly Ala
145                 150                 155                 160


Gly Gly His Phe Ser Gly Gly Gly Phe Gly Asn Leu Met Arg Lys Tyr
                165                 170                 175


Gly Leu Ser Ile Asp His Ile Ile Asp Ala Gln Ile Met Asp Ala Asn
            180                 185                 190


Gly Lys Val Tyr Arg Asn Arg Gln Ala Met Gly Glu Asp Val Phe Trp
        195                 200                 205


Ala Ile Arg Gly Gly Gly Gly Gly Ser Tyr Gly Val Ile Leu Ala Trp
    210                 215                 220


Lys Ile Lys Leu Val Arg Val Pro Glu Lys Val Thr Val Phe Lys Leu
225                 230                 235                 240


Glu Arg Thr Val Arg Glu Gly Ala Val Asp Leu Val His Lys Trp Gln
                245                 250                 255


Gln Val Ala Pro Val Ile Asp Arg Asp Leu Phe Ile Arg Leu Glu Ile
            260                 265                 270


Lys Pro Ile Asn Arg Lys Ile Ser Lys Gly Lys Thr Ile Lys Val Ser
        275                 280                 285


Phe Ile Gly Met Phe Leu Gly Leu Pro Glu Arg Leu Leu Asn Ile Thr
    290                 295                 300


Lys Gln Ser Phe Pro Glu Leu His Leu Thr Lys Glu Asp Cys Met Val
305                 310                 315                 320


Lys Lys Trp Ile Glu Ser Ser Val Phe Trp Ala Asn Tyr Pro Glu Lys
                325                 330                 335


Ala Pro Ile Glu Leu Leu Leu Lys Arg Val Ser Thr Asn Glu Tyr Tyr
            340                 345                 350


Trp Lys Arg Thr Ser Asp Phe Val Gln Ala Pro Ile Ser Lys Gln Gly
        355                 360                 365
```

```
Leu Ala Lys Ile Phe Gln Thr Met Ile Asp His Ser Pro Leu Pro Arg
    370                 375                 380

Arg Val Trp Met Gln Trp Asn Pro Trp Gly Gly Lys Met Ala Glu Ile
385                 390                 395                 400

Ala Ser Asp Ala Thr Ala Phe Val His Arg Gly Gly Asn Val Phe Met
                405                 410                 415

Ile Glu His Phe Met Asn Trp Tyr Arg Pro Gly Asp Glu Leu Glu Glu
            420                 425                 430

Lys Phe Leu Ala Ile Ala Arg Ser Phe Lys Glu Ala Met Ala Pro Phe
        435                 440                 445

Val Ser Lys Asn Pro Arg Glu Ala Phe Phe Asn Tyr Arg Asp Val Asp
    450                 455                 460

Ile Gly Ile Thr Thr Pro Gly Tyr Asn Ala Thr Tyr Glu Gly Ala Lys
465                 470                 475                 480

Val Tyr Gly Asp Ser Tyr Phe Lys Gly Asn Tyr Leu Arg Leu Val Lys
                485                 490                 495

Ile Lys Ala Arg Phe Asp Arg Thr Asn Phe Phe Arg Ser Gln Gln Gly
            500                 505                 510

Ile Pro Val Leu Ala
        515
```

<210>  40
<211>  1575
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS59-O64745-no signal peptide-strep Tag

<220>
<221>  CDS
<222>  (1)..(1575)

<400> 40

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atg tct cca cca tcc ttg tct att cca gaa cat ttc ttg aga tgc ttg         48
Met Ser Pro Pro Ser Leu Ser Ile Pro Glu His Phe Leu Arg Cys Leu
1               5                   10                  15

gat acc caa cca tct gat cat ggt tct cca aat tct aga act gcc gtt         96
Asp Thr Gln Pro Ser Asp His Gly Ser Pro Asn Ser Arg Thr Ala Val
            20                  25                  30

att cca acg aac tct tct ttt tct acc aac ttg atg aac ggc gtc aga        144
Ile Pro Thr Asn Ser Ser Phe Ser Thr Asn Leu Met Asn Gly Val Arg
        35                  40                  45

aat ttg aga ttc gct tct gtt tct act agg aag cca gaa gtt ata gtt        192
Asn Leu Arg Phe Ala Ser Val Ser Thr Arg Lys Pro Glu Val Ile Val
    50                  55                  60

gct gct gtt act gaa acc cat att aga gct acc att tct tgc tgc aag        240
Ala Ala Val Thr Glu Thr His Ile Arg Ala Thr Ile Ser Cys Cys Lys
65                  70                  75                  80

ttg ttg aac ttg gaa ttg aga att aga tcc ggt ggt cat gat tac gaa        288
Leu Leu Asn Leu Glu Leu Arg Ile Arg Ser Gly Gly His Asp Tyr Glu
                85                  90                  95

ggt ttc tct tat act tct cca gtt cca ttc gtt atc ctg gac atg tac        336
Gly Phe Ser Tyr Thr Ser Pro Val Pro Phe Val Ile Leu Asp Met Tyr
            100                 105                 110

aac ttc aac aag atc gac att aac atg aag gac gaa acc gtc tgg att        384
Asn Phe Asn Lys Ile Asp Ile Asn Met Lys Asp Glu Thr Val Trp Ile
        115                 120                 125

caa tct ggt gct tct ttg ggt cag ttg tac tac aat att gcc tcc aag        432
Gln Ser Gly Ala Ser Leu Gly Gln Leu Tyr Tyr Asn Ile Ala Ser Lys
    130                 135                 140

tct aag gtt cat gct ttt cca gct ggt gtt tgt cca aaa gtt ggt gct        480
Ser Lys Val His Ala Phe Pro Ala Gly Val Cys Pro Lys Val Gly Ala
145                 150                 155                 160

ggt ggt cat ttt tct ggt ggt ggt ttt ggt aat ttg atg agg aaa tac        528
Gly Gly His Phe Ser Gly Gly Gly Phe Gly Asn Leu Met Arg Lys Tyr
                165                 170                 175

ggt ttg tcc atc gat cat atc att gac gcc caa att atg gat gct aac        576
Gly Leu Ser Ile Asp His Ile Ile Asp Ala Gln Ile Met Asp Ala Asn
            180                 185                 190

ggt aag gtt tac aga aac aga caa gct atg ggt gaa gat gtt ttc tgg        624
Gly Lys Val Tyr Arg Asn Arg Gln Ala Met Gly Glu Asp Val Phe Trp
        195                 200                 205
```

```
gct att aga ggt ggt ggt ggc ggt tct tat ggt gtt att ttg gct tgg        672
Ala Ile Arg Gly Gly Gly Gly Gly Ser Tyr Gly Val Ile Leu Ala Trp
    210                 215                 220

aag att aag ttg gtt agg gtt cca gaa aag gtc acc gtt ttt aag ttg        720
Lys Ile Lys Leu Val Arg Val Pro Glu Lys Val Thr Val Phe Lys Leu
225                 230                 235                 240

gaa aga acc gtt aga gaa ggt gcc gtt gat ttg gtt cat aag tgg caa        768
Glu Arg Thr Val Arg Glu Gly Ala Val Asp Leu Val His Lys Trp Gln
                245                 250                 255

caa gtt gcc cca gtt att gat aga gat ttg ttc atc aga ttg gag atc        816
Gln Val Ala Pro Val Ile Asp Arg Asp Leu Phe Ile Arg Leu Glu Ile
            260                 265                 270

aag ccc atc aac aga aag att tct aag ggt aag acc atc aag gtg tcc        864
Lys Pro Ile Asn Arg Lys Ile Ser Lys Gly Lys Thr Ile Lys Val Ser
        275                 280                 285

ttc att ggt atg ttt ttg ggt ttg cca gaa cgt ttg ttg aac atc act        912
Phe Ile Gly Met Phe Leu Gly Leu Pro Glu Arg Leu Leu Asn Ile Thr
    290                 295                 300

aag caa tct ttc cca gaa ctg cac ttg aca aaa gaa gat tgc atg gtt        960
Lys Gln Ser Phe Pro Glu Leu His Leu Thr Lys Glu Asp Cys Met Val
305                 310                 315                 320

aag aag tgg atc gag tca tct gtt ttt tgg gca aat tac cca gaa aaa       1008
Lys Lys Trp Ile Glu Ser Ser Val Phe Trp Ala Asn Tyr Pro Glu Lys
                325                 330                 335

gcc cca att gag ttg ttg ttg aaa aga gtc tct acc aac gag tac tac       1056
Ala Pro Ile Glu Leu Leu Leu Lys Arg Val Ser Thr Asn Glu Tyr Tyr
            340                 345                 350

tgg aag aga act tct gat ttt gtt cag gcc cca att tct aaa caa ggt       1104
Trp Lys Arg Thr Ser Asp Phe Val Gln Ala Pro Ile Ser Lys Gln Gly
        355                 360                 365

ttg gct aag att ttc cag acc atg att gat cat tct cca ttg cct aga       1152
Leu Ala Lys Ile Phe Gln Thr Met Ile Asp His Ser Pro Leu Pro Arg
    370                 375                 380

aga gtt tgg atg caa tgg aat cct tgg ggt ggt aaa atg gct gaa att       1200
Arg Val Trp Met Gln Trp Asn Pro Trp Gly Gly Lys Met Ala Glu Ile
385                 390                 395                 400

gct tct gat gct act gcc ttt gtt cac aga ggt ggt aat gtt ttc atg       1248
Ala Ser Asp Ala Thr Ala Phe Val His Arg Gly Gly Asn Val Phe Met
                405                 410                 415

atc gaa cat ttc atg aac tgg tac aga cca ggt gat gaa ttg gaa gaa       1296
Ile Glu His Phe Met Asn Trp Tyr Arg Pro Gly Asp Glu Leu Glu Glu
```

```
            420                 425                 430

aag ttc ttg gct att gcc agg tct ttc aaa gaa gct atg gct cca ttt       1344
Lys Phe Leu Ala Ile Ala Arg Ser Phe Lys Glu Ala Met Ala Pro Phe
        435                 440                 445

gtt tct aag aat cca aga gaa gcc ttc ttc aac tac aga gat gtt gat       1392
Val Ser Lys Asn Pro Arg Glu Ala Phe Phe Asn Tyr Arg Asp Val Asp
    450                 455                 460

att ggt atc act acc cca ggt tac aat gct act tat gaa ggt gct aaa       1440
Ile Gly Ile Thr Thr Pro Gly Tyr Asn Ala Thr Tyr Glu Gly Ala Lys
465                 470                 475                 480

gtt tac ggc gat tct tac ttt aag ggt aac tac ttg agg ttg gtt aag       1488
Val Tyr Gly Asp Ser Tyr Phe Lys Gly Asn Tyr Leu Arg Leu Val Lys
                485                 490                 495

atc aag gct aga ttc gac aga acg aac ttc ttc aga tct caa caa ggt       1536
Ile Lys Ala Arg Phe Asp Arg Thr Asn Phe Phe Arg Ser Gln Gln Gly
            500                 505                 510

att cca gtt ttg gcc tgg tca cat cca caa ttt gaa aag                  1575
Ile Pro Val Leu Ala Trp Ser His Pro Gln Phe Glu Lys
        515                 520                 525
```

<210> 41
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41

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Met Ser Pro Pro Ser Leu Ser Ile Pro Glu His Phe Leu Arg Cys Leu
1               5                   10                  15


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


Ile Pro Thr Asn Ser Ser Phe Ser Thr Asn Leu Met Asn Gly Val Arg
        35                  40                  45


Asn Leu Arg Phe Ala Ser Val Ser Thr Arg Lys Pro Glu Val Ile Val
    50                  55                  60


Ala Ala Val Thr Glu Thr His Ile Arg Ala Thr Ile Ser Cys Cys Lys
```

```
65                  70                  75                  80

Leu Leu Asn Leu Glu Leu Arg Ile Arg Ser Gly Gly His Asp Tyr Glu
                85                  90                  95

Gly Phe Ser Tyr Thr Ser Pro Val Pro Phe Val Ile Leu Asp Met Tyr
            100                 105                 110

Asn Phe Asn Lys Ile Asp Ile Asn Met Lys Asp Glu Thr Val Trp Ile
        115                 120                 125

Gln Ser Gly Ala Ser Leu Gly Gln Leu Tyr Tyr Asn Ile Ala Ser Lys
    130                 135                 140

Ser Lys Val His Ala Phe Pro Ala Gly Val Cys Pro Lys Val Gly Ala
145                 150                 155                 160

Gly Gly His Phe Ser Gly Gly Gly Phe Gly Asn Leu Met Arg Lys Tyr
                165                 170                 175

Gly Leu Ser Ile Asp His Ile Ile Asp Ala Gln Ile Met Asp Ala Asn
            180                 185                 190

Gly Lys Val Tyr Arg Asn Arg Gln Ala Met Gly Glu Asp Val Phe Trp
        195                 200                 205

Ala Ile Arg Gly Gly Gly Gly Gly Ser Tyr Gly Val Ile Leu Ala Trp
    210                 215                 220

Lys Ile Lys Leu Val Arg Val Pro Glu Lys Val Thr Val Phe Lys Leu
225                 230                 235                 240

Glu Arg Thr Val Arg Glu Gly Ala Val Asp Leu Val His Lys Trp Gln
                245                 250                 255

Gln Val Ala Pro Val Ile Asp Arg Asp Leu Phe Ile Arg Leu Glu Ile
            260                 265                 270

Lys Pro Ile Asn Arg Lys Ile Ser Lys Gly Lys Thr Ile Lys Val Ser
        275                 280                 285
```

```
Phe Ile Gly Met Phe Leu Gly Leu Pro Glu Arg Leu Leu Asn Ile Thr
    290                 295                 300

Lys Gln Ser Phe Pro Glu Leu His Leu Thr Lys Glu Asp Cys Met Val
305                 310                 315                 320

Lys Lys Trp Ile Glu Ser Ser Val Phe Trp Ala Asn Tyr Pro Glu Lys
                325                 330                 335

Ala Pro Ile Glu Leu Leu Leu Lys Arg Val Ser Thr Asn Glu Tyr Tyr
            340                 345                 350

Trp Lys Arg Thr Ser Asp Phe Val Gln Ala Pro Ile Ser Lys Gln Gly
        355                 360                 365

Leu Ala Lys Ile Phe Gln Thr Met Ile Asp His Ser Pro Leu Pro Arg
    370                 375                 380

Arg Val Trp Met Gln Trp Asn Pro Trp Gly Gly Lys Met Ala Glu Ile
385                 390                 395                 400

Ala Ser Asp Ala Thr Ala Phe Val His Arg Gly Gly Asn Val Phe Met
                405                 410                 415

Ile Glu His Phe Met Asn Trp Tyr Arg Pro Gly Asp Glu Leu Glu Glu
            420                 425                 430

Lys Phe Leu Ala Ile Ala Arg Ser Phe Lys Glu Ala Met Ala Pro Phe
        435                 440                 445

Val Ser Lys Asn Pro Arg Glu Ala Phe Phe Asn Tyr Arg Asp Val Asp
    450                 455                 460

Ile Gly Ile Thr Thr Pro Gly Tyr Asn Ala Thr Tyr Glu Gly Ala Lys
465                 470                 475                 480

Val Tyr Gly Asp Ser Tyr Phe Lys Gly Asn Tyr Leu Arg Leu Val Lys
                485                 490                 495

Ile Lys Ala Arg Phe Asp Arg Thr Asn Phe Phe Arg Ser Gln Gln Gly
```

```
            500                 505                 510

Ile Pro Val Leu Ala Trp Ser His Pro Gln Phe Glu Lys
        515                 520                 525


<210>  42
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS59-O64745- truncated alpha factor -no signal peptide-strep Tag


<220>
<221>  CDS
<222>  (1)..(1632)

<400>  42
atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca ctt gca atg tct cca cca tcc ttg tct att cca gaa cat ttc ttg         96
Ala Leu Ala Met Ser Pro Pro Ser Leu Ser Ile Pro Glu His Phe Leu
            20                  25                  30

aga tgc ttg gat acc caa cca tct gat cat ggt tct cca aat tct aga        144
Arg Cys Leu Asp Thr Gln Pro Ser Asp His Gly Ser Pro Asn Ser Arg
        35                  40                  45

act gcc gtt att cca acg aac tct tct ttt tct acc aac ttg atg aac        192
Thr Ala Val Ile Pro Thr Asn Ser Ser Phe Ser Thr Asn Leu Met Asn
    50                  55                  60

ggc gtc aga aat ttg aga ttc gct tct gtt tct act agg aag cca gaa        240
Gly Val Arg Asn Leu Arg Phe Ala Ser Val Ser Thr Arg Lys Pro Glu
65                  70                  75                  80

gtt ata gtt gct gct gtt act gaa acc cat att aga gct acc att tct        288
Val Ile Val Ala Ala Val Thr Glu Thr His Ile Arg Ala Thr Ile Ser
                85                  90                  95

tgc tgc aag ttg ttg aac ttg gaa ttg aga att aga tcc ggt ggt cat        336
Cys Cys Lys Leu Leu Asn Leu Glu Leu Arg Ile Arg Ser Gly Gly His
            100                 105                 110

gat tac gaa ggt ttc tct tat act tct cca gtt cca ttc gtt atc ctg        384
Asp Tyr Glu Gly Phe Ser Tyr Thr Ser Pro Val Pro Phe Val Ile Leu
        115                 120                 125

gac atg tac aac ttc aac aag atc gac att aac atg aag gac gaa acc        432
```

```
Asp Met Tyr Asn Phe Asn Lys Ile Asp Ile Asn Met Lys Asp Glu Thr
    130                 135                 140

gtc tgg att caa tct ggt gct tct ttg ggt cag ttg tac tac aat att        480
Val Trp Ile Gln Ser Gly Ala Ser Leu Gly Gln Leu Tyr Tyr Asn Ile
145                 150                 155                 160

gcc tcc aag tct aag gtt cat gct ttt cca gct ggt gtt tgt cca aaa        528
Ala Ser Lys Ser Lys Val His Ala Phe Pro Ala Gly Val Cys Pro Lys
                165                 170                 175

gtt ggt gct ggt ggt cat ttt tct ggt ggt ggt ttt ggt aat ttg atg        576
Val Gly Ala Gly Gly His Phe Ser Gly Gly Gly Phe Gly Asn Leu Met
            180                 185                 190

agg aaa tac ggt ttg tcc atc gat cat atc att gac gcc caa att atg        624
Arg Lys Tyr Gly Leu Ser Ile Asp His Ile Ile Asp Ala Gln Ile Met
        195                 200                 205

gat gct aac ggt aag gtt tac aga aac aga caa gct atg ggt gaa gat        672
Asp Ala Asn Gly Lys Val Tyr Arg Asn Arg Gln Ala Met Gly Glu Asp
    210                 215                 220

gtt ttc tgg gct att aga ggt ggt ggt ggc ggt tct tat ggt gtt att        720
Val Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Tyr Gly Val Ile
225                 230                 235                 240

ttg gct tgg aag att aag ttg gtt agg gtt cca gaa aag gtc acc gtt        768
Leu Ala Trp Lys Ile Lys Leu Val Arg Val Pro Glu Lys Val Thr Val
                245                 250                 255

ttt aag ttg gaa aga acc gtt aga gaa ggt gcc gtt gat ttg gtt cat        816
Phe Lys Leu Glu Arg Thr Val Arg Glu Gly Ala Val Asp Leu Val His
            260                 265                 270

aag tgg caa caa gtt gcc cca gtt att gat aga gat ttg ttc atc aga        864
Lys Trp Gln Gln Val Ala Pro Val Ile Asp Arg Asp Leu Phe Ile Arg
        275                 280                 285

ttg gag atc aag ccc atc aac aga aag att tct aag ggt aag acc atc        912
Leu Glu Ile Lys Pro Ile Asn Arg Lys Ile Ser Lys Gly Lys Thr Ile
    290                 295                 300

aag gtg tcc ttc att ggt atg ttt ttg ggt ttg cca gaa cgt ttg ttg        960
Lys Val Ser Phe Ile Gly Met Phe Leu Gly Leu Pro Glu Arg Leu Leu
305                 310                 315                 320

aac atc act aag caa tct ttc cca gaa ctg cac ttg aca aaa gaa gat       1008
Asn Ile Thr Lys Gln Ser Phe Pro Glu Leu His Leu Thr Lys Glu Asp
                325                 330                 335

tgc atg gtt aag aag tgg atc gag tca tct gtt ttt tgg gca aat tac       1056
Cys Met Val Lys Lys Trp Ile Glu Ser Ser Val Phe Trp Ala Asn Tyr
            340                 345                 350
```

```
cca gaa aaa gcc cca att gag ttg ttg ttg aaa aga gtc tct acc aac       1104
Pro Glu Lys Ala Pro Ile Glu Leu Leu Leu Lys Arg Val Ser Thr Asn
        355                 360                 365

gag tac tac tgg aag aga act tct gat ttt gtt cag gcc cca att tct       1152
Glu Tyr Tyr Trp Lys Arg Thr Ser Asp Phe Val Gln Ala Pro Ile Ser
    370                 375                 380

aaa caa ggt ttg gct aag att ttc cag acc atg att gat cat tct cca       1200
Lys Gln Gly Leu Ala Lys Ile Phe Gln Thr Met Ile Asp His Ser Pro
385                 390                 395                 400

ttg cct aga aga gtt tgg atg caa tgg aat cct tgg ggt ggt aaa atg       1248
Leu Pro Arg Arg Val Trp Met Gln Trp Asn Pro Trp Gly Gly Lys Met
                405                 410                 415

gct gaa att gct tct gat gct act gcc ttt gtt cac aga ggt ggt aat       1296
Ala Glu Ile Ala Ser Asp Ala Thr Ala Phe Val His Arg Gly Gly Asn
            420                 425                 430

gtt ttc atg atc gaa cat ttc atg aac tgg tac aga cca ggt gat gaa       1344
Val Phe Met Ile Glu His Phe Met Asn Trp Tyr Arg Pro Gly Asp Glu
        435                 440                 445

ttg gaa gaa aag ttc ttg gct att gcc agg tct ttc aaa gaa gct atg       1392
Leu Glu Glu Lys Phe Leu Ala Ile Ala Arg Ser Phe Lys Glu Ala Met
    450                 455                 460

gct cca ttt gtt tct aag aat cca aga gaa gcc ttc ttc aac tac aga       1440
Ala Pro Phe Val Ser Lys Asn Pro Arg Glu Ala Phe Phe Asn Tyr Arg
465                 470                 475                 480

gat gtt gat att ggt atc act acc cca ggt tac aat gct act tat gaa       1488
Asp Val Asp Ile Gly Ile Thr Thr Pro Gly Tyr Asn Ala Thr Tyr Glu
                485                 490                 495

ggt gct aaa gtt tac ggc gat tct tac ttt aag ggt aac tac ttg agg       1536
Gly Ala Lys Val Tyr Gly Asp Ser Tyr Phe Lys Gly Asn Tyr Leu Arg
            500                 505                 510

ttg gtt aag atc aag gct aga ttc gac aga acg aac ttc ttc aga tct       1584
Leu Val Lys Ile Lys Ala Arg Phe Asp Arg Thr Asn Phe Phe Arg Ser
        515                 520                 525

caa caa ggt att cca gtt ttg gcc tgg tca cat cca caa ttt gaa aag       1632
Gln Gln Gly Ile Pro Val Leu Ala Trp Ser His Pro Gln Phe Glu Lys
    530                 535                 540
```

<210> 43
<211> 544
<212> PRT
<213> Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  43

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


Ala Leu Ala Met Ser Pro Pro Ser Leu Ser Ile Pro Glu His Phe Leu
            20                  25                  30


Arg Cys Leu Asp Thr Gln Pro Ser Asp His Gly Ser Pro Asn Ser Arg
        35                  40                  45


Thr Ala Val Ile Pro Thr Asn Ser Ser Phe Ser Thr Asn Leu Met Asn
    50                  55                  60


Gly Val Arg Asn Leu Arg Phe Ala Ser Val Ser Thr Arg Lys Pro Glu
65                  70                  75                  80


Val Ile Val Ala Ala Val Thr Glu Thr His Ile Arg Ala Thr Ile Ser
                85                  90                  95


Cys Cys Lys Leu Leu Asn Leu Glu Leu Arg Ile Arg Ser Gly Gly His
            100                 105                 110


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


Asp Met Tyr Asn Phe Asn Lys Ile Asp Ile Asn Met Lys Asp Glu Thr
    130                 135                 140


Val Trp Ile Gln Ser Gly Ala Ser Leu Gly Gln Leu Tyr Tyr Asn Ile
145                 150                 155                 160


Ala Ser Lys Ser Lys Val His Ala Phe Pro Ala Gly Val Cys Pro Lys
                165                 170                 175


Val Gly Ala Gly Gly His Phe Ser Gly Gly Gly Phe Gly Asn Leu Met
            180                 185                 190
```

```
Arg Lys Tyr Gly Leu Ser Ile Asp His Ile Ile Asp Ala Gln Ile Met
        195                 200                 205

Asp Ala Asn Gly Lys Val Tyr Arg Asn Arg Gln Ala Met Gly Glu Asp
    210                 215                 220

Val Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Tyr Gly Val Ile
225                 230                 235                 240

Leu Ala Trp Lys Ile Lys Leu Val Arg Val Pro Glu Lys Val Thr Val
                245                 250                 255

Phe Lys Leu Glu Arg Thr Val Arg Glu Gly Ala Val Asp Leu Val His
            260                 265                 270

Lys Trp Gln Gln Val Ala Pro Val Ile Asp Arg Asp Leu Phe Ile Arg
        275                 280                 285

Leu Glu Ile Lys Pro Ile Asn Arg Lys Ile Ser Lys Gly Lys Thr Ile
    290                 295                 300

Lys Val Ser Phe Ile Gly Met Phe Leu Gly Leu Pro Glu Arg Leu Leu
305                 310                 315                 320

Asn Ile Thr Lys Gln Ser Phe Pro Glu Leu His Leu Thr Lys Glu Asp
                325                 330                 335

Cys Met Val Lys Lys Trp Ile Glu Ser Ser Val Phe Trp Ala Asn Tyr
            340                 345                 350

Pro Glu Lys Ala Pro Ile Glu Leu Leu Leu Lys Arg Val Ser Thr Asn
        355                 360                 365

Glu Tyr Tyr Trp Lys Arg Thr Ser Asp Phe Val Gln Ala Pro Ile Ser
    370                 375                 380

Lys Gln Gly Leu Ala Lys Ile Phe Gln Thr Met Ile Asp His Ser Pro
385                 390                 395                 400

Leu Pro Arg Arg Val Trp Met Gln Trp Asn Pro Trp Gly Gly Lys Met
                405                 410                 415
```

```
Ala Glu Ile Ala Ser Asp Ala Thr Ala Phe Val His Arg Gly Gly Asn
            420                 425                 430

Val Phe Met Ile Glu His Phe Met Asn Trp Tyr Arg Pro Gly Asp Glu
        435                 440                 445

Leu Glu Glu Lys Phe Leu Ala Ile Ala Arg Ser Phe Lys Glu Ala Met
    450                 455                 460

Ala Pro Phe Val Ser Lys Asn Pro Arg Glu Ala Phe Phe Asn Tyr Arg
465                 470                 475                 480

Asp Val Asp Ile Gly Ile Thr Thr Pro Gly Tyr Asn Ala Thr Tyr Glu
                485                 490                 495

Gly Ala Lys Val Tyr Gly Asp Ser Tyr Phe Lys Gly Asn Tyr Leu Arg
            500                 505                 510

Leu Val Lys Ile Lys Ala Arg Phe Asp Arg Thr Asn Phe Phe Arg Ser
        515                 520                 525

Gln Gln Gly Ile Pro Val Leu Ala Trp Ser His Pro Gln Phe Glu Lys
    530                 535                 540
```

<210> 44
<211> 1842
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS59-O64745-full alpha factor-no signal peptide-strep Tag

<220>
<221> CDS
<222> (1)..(1842)

<400> 44

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atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
```

```
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg tct cca cca tcc ttg tct        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ser Pro Pro Ser Leu Ser
                85                  90                  95

att cca gaa cat ttc ttg aga tgc ttg gat acc caa cca tct gat cat        336
Ile Pro Glu His Phe Leu Arg Cys Leu Asp Thr Gln Pro Ser Asp His
            100                 105                 110

ggt tct cca aat tct aga act gcc gtt att cca acg aac tct tct ttt        384
Gly Ser Pro Asn Ser Arg Thr Ala Val Ile Pro Thr Asn Ser Ser Phe
        115                 120                 125

tct acc aac ttg atg aac ggc gtc aga aat ttg aga ttc gct tct gtt        432
Ser Thr Asn Leu Met Asn Gly Val Arg Asn Leu Arg Phe Ala Ser Val
    130                 135                 140

tct act agg aag cca gaa gtt ata gtt gct gct gtt act gaa acc cat        480
Ser Thr Arg Lys Pro Glu Val Ile Val Ala Ala Val Thr Glu Thr His
145                 150                 155                 160

att aga gct acc att tct tgc tgc aag ttg ttg aac ttg gaa ttg aga        528
Ile Arg Ala Thr Ile Ser Cys Cys Lys Leu Leu Asn Leu Glu Leu Arg
                165                 170                 175

att aga tcc ggt ggt cat gat tac gaa ggt ttc tct tat act tct cca        576
Ile Arg Ser Gly Gly His Asp Tyr Glu Gly Phe Ser Tyr Thr Ser Pro
            180                 185                 190

gtt cca ttc gtt atc ctg gac atg tac aac ttc aac aag atc gac att        624
Val Pro Phe Val Ile Leu Asp Met Tyr Asn Phe Asn Lys Ile Asp Ile
        195                 200                 205

aac atg aag gac gaa acc gtc tgg att caa tct ggt gct tct ttg ggt        672
Asn Met Lys Asp Glu Thr Val Trp Ile Gln Ser Gly Ala Ser Leu Gly
    210                 215                 220

cag ttg tac tac aat att gcc tcc aag tct aag gtt cat gct ttt cca        720
Gln Leu Tyr Tyr Asn Ile Ala Ser Lys Ser Lys Val His Ala Phe Pro
225                 230                 235                 240
```

```
gct ggt gtt tgt cca aaa gtt ggt gct ggt ggt cat ttt tct ggt ggt        768
Ala Gly Val Cys Pro Lys Val Gly Ala Gly Gly His Phe Ser Gly Gly
                245                 250                 255

ggt ttt ggt aat ttg atg agg aaa tac ggt ttg tcc atc gat cat atc        816
Gly Phe Gly Asn Leu Met Arg Lys Tyr Gly Leu Ser Ile Asp His Ile
            260                 265                 270

att gac gcc caa att atg gat gct aac ggt aag gtt tac aga aac aga        864
Ile Asp Ala Gln Ile Met Asp Ala Asn Gly Lys Val Tyr Arg Asn Arg
        275                 280                 285

caa gct atg ggt gaa gat gtt ttc tgg gct att aga ggt ggt ggt ggc        912
Gln Ala Met Gly Glu Asp Val Phe Trp Ala Ile Arg Gly Gly Gly Gly
    290                 295                 300

ggt tct tat ggt gtt att ttg gct tgg aag att aag ttg gtt agg gtt        960
Gly Ser Tyr Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Arg Val
305                 310                 315                 320

cca gaa aag gtc acc gtt ttt aag ttg gaa aga acc gtt aga gaa ggt       1008
Pro Glu Lys Val Thr Val Phe Lys Leu Glu Arg Thr Val Arg Glu Gly
                325                 330                 335

gcc gtt gat ttg gtt cat aag tgg caa caa gtt gcc cca gtt att gat       1056
Ala Val Asp Leu Val His Lys Trp Gln Gln Val Ala Pro Val Ile Asp
            340                 345                 350

aga gat ttg ttc atc aga ttg gag atc aag ccc atc aac aga aag att       1104
Arg Asp Leu Phe Ile Arg Leu Glu Ile Lys Pro Ile Asn Arg Lys Ile
        355                 360                 365

tct aag ggt aag acc atc aag gtg tcc ttc att ggt atg ttt ttg ggt       1152
Ser Lys Gly Lys Thr Ile Lys Val Ser Phe Ile Gly Met Phe Leu Gly
    370                 375                 380

ttg cca gaa cgt ttg ttg aac atc act aag caa tct ttc cca gaa ctg       1200
Leu Pro Glu Arg Leu Leu Asn Ile Thr Lys Gln Ser Phe Pro Glu Leu
385                 390                 395                 400

cac ttg aca aaa gaa gat tgc atg gtt aag aag tgg atc gag tca tct       1248
His Leu Thr Lys Glu Asp Cys Met Val Lys Lys Trp Ile Glu Ser Ser
                405                 410                 415

gtt ttt tgg gca aat tac cca gaa aaa gcc cca att gag ttg ttg ttg       1296
Val Phe Trp Ala Asn Tyr Pro Glu Lys Ala Pro Ile Glu Leu Leu Leu
            420                 425                 430

aaa aga gtc tct acc aac gag tac tac tgg aag aga act tct gat ttt       1344
Lys Arg Val Ser Thr Asn Glu Tyr Tyr Trp Lys Arg Thr Ser Asp Phe
        435                 440                 445

gtt cag gcc cca att tct aaa caa ggt ttg gct aag att ttc cag acc       1392
Val Gln Ala Pro Ile Ser Lys Gln Gly Leu Ala Lys Ile Phe Gln Thr
```

```
    450                 455                 460

atg att gat cat tct cca ttg cct aga aga gtt tgg atg caa tgg aat       1440
Met Ile Asp His Ser Pro Leu Pro Arg Arg Val Trp Met Gln Trp Asn
465                 470                 475                 480

cct tgg ggt ggt aaa atg gct gaa att gct tct gat gct act gcc ttt       1488
Pro Trp Gly Gly Lys Met Ala Glu Ile Ala Ser Asp Ala Thr Ala Phe
                485                 490                 495

gtt cac aga ggt ggt aat gtt ttc atg atc gaa cat ttc atg aac tgg       1536
Val His Arg Gly Gly Asn Val Phe Met Ile Glu His Phe Met Asn Trp
            500                 505                 510

tac aga cca ggt gat gaa ttg gaa gaa aag ttc ttg gct att gcc agg       1584
Tyr Arg Pro Gly Asp Glu Leu Glu Glu Lys Phe Leu Ala Ile Ala Arg
        515                 520                 525

tct ttc aaa gaa gct atg gct cca ttt gtt tct aag aat cca aga gaa       1632
Ser Phe Lys Glu Ala Met Ala Pro Phe Val Ser Lys Asn Pro Arg Glu
    530                 535                 540

gcc ttc ttc aac tac aga gat gtt gat att ggt atc act acc cca ggt       1680
Ala Phe Phe Asn Tyr Arg Asp Val Asp Ile Gly Ile Thr Thr Pro Gly
545                 550                 555                 560

tac aat gct act tat gaa ggt gct aaa gtt tac ggc gat tct tac ttt       1728
Tyr Asn Ala Thr Tyr Glu Gly Ala Lys Val Tyr Gly Asp Ser Tyr Phe
                565                 570                 575

aag ggt aac tac ttg agg ttg gtt aag atc aag gct aga ttc gac aga       1776
Lys Gly Asn Tyr Leu Arg Leu Val Lys Ile Lys Ala Arg Phe Asp Arg
            580                 585                 590

acg aac ttc ttc aga tct caa caa ggt att cca gtt ttg gcc tgg tca       1824
Thr Asn Phe Phe Arg Ser Gln Gln Gly Ile Pro Val Leu Ala Trp Ser
        595                 600                 605

cat cca caa ttt gaa aag                                               1842
His Pro Gln Phe Glu Lys
    610
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<210>  45
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<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  45

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

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

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

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ser Pro Pro Ser Leu Ser
                85                  90                  95

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

Gly Ser Pro Asn Ser Arg Thr Ala Val Ile Pro Thr Asn Ser Ser Phe
        115                 120                 125

Ser Thr Asn Leu Met Asn Gly Val Arg Asn Leu Arg Phe Ala Ser Val
    130                 135                 140

Ser Thr Arg Lys Pro Glu Val Ile Val Ala Ala Val Thr Glu Thr His
145                 150                 155                 160

Ile Arg Ala Thr Ile Ser Cys Cys Lys Leu Leu Asn Leu Glu Leu Arg
                165                 170                 175

Ile Arg Ser Gly Gly His Asp Tyr Glu Gly Phe Ser Tyr Thr Ser Pro
            180                 185                 190

Val Pro Phe Val Ile Leu Asp Met Tyr Asn Phe Asn Lys Ile Asp Ile
        195                 200                 205

Asn Met Lys Asp Glu Thr Val Trp Ile Gln Ser Gly Ala Ser Leu Gly
    210                 215                 220
```

```
Gln Leu Tyr Tyr Asn Ile Ala Ser Lys Ser Lys Val His Ala Phe Pro
225                 230                 235                 240

Ala Gly Val Cys Pro Lys Val Gly Ala Gly Gly His Phe Ser Gly Gly
                245                 250                 255

Gly Phe Gly Asn Leu Met Arg Lys Tyr Gly Leu Ser Ile Asp His Ile
            260                 265                 270

Ile Asp Ala Gln Ile Met Asp Ala Asn Gly Lys Val Tyr Arg Asn Arg
        275                 280                 285

Gln Ala Met Gly Glu Asp Val Phe Trp Ala Ile Arg Gly Gly Gly Gly
    290                 295                 300

Gly Ser Tyr Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Arg Val
305                 310                 315                 320

Pro Glu Lys Val Thr Val Phe Lys Leu Glu Arg Thr Val Arg Glu Gly
                325                 330                 335

Ala Val Asp Leu Val His Lys Trp Gln Gln Val Ala Pro Val Ile Asp
            340                 345                 350

Arg Asp Leu Phe Ile Arg Leu Glu Ile Lys Pro Ile Asn Arg Lys Ile
        355                 360                 365

Ser Lys Gly Lys Thr Ile Lys Val Ser Phe Ile Gly Met Phe Leu Gly
    370                 375                 380

Leu Pro Glu Arg Leu Leu Asn Ile Thr Lys Gln Ser Phe Pro Glu Leu
385                 390                 395                 400

His Leu Thr Lys Glu Asp Cys Met Val Lys Lys Trp Ile Glu Ser Ser
                405                 410                 415

Val Phe Trp Ala Asn Tyr Pro Glu Lys Ala Pro Ile Glu Leu Leu Leu
            420                 425                 430

Lys Arg Val Ser Thr Asn Glu Tyr Tyr Trp Lys Arg Thr Ser Asp Phe
```

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        435                 440                 445

Val Gln Ala Pro Ile Ser Lys Gln Gly Leu Ala Lys Ile Phe Gln Thr
    450                 455                 460

Met Ile Asp His Ser Pro Leu Pro Arg Arg Val Trp Met Gln Trp Asn
465                 470                 475                 480

Pro Trp Gly Gly Lys Met Ala Glu Ile Ala Ser Asp Ala Thr Ala Phe
                485                 490                 495

Val His Arg Gly Gly Asn Val Phe Met Ile Glu His Phe Met Asn Trp
            500                 505                 510

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

Ser Phe Lys Glu Ala Met Ala Pro Phe Val Ser Lys Asn Pro Arg Glu
    530                 535                 540

Ala Phe Phe Asn Tyr Arg Asp Val Asp Ile Gly Ile Thr Thr Pro Gly
545                 550                 555                 560

Tyr Asn Ala Thr Tyr Glu Gly Ala Lys Val Tyr Gly Asp Ser Tyr Phe
                565                 570                 575

Lys Gly Asn Tyr Leu Arg Leu Val Lys Ile Lys Ala Arg Phe Asp Arg
            580                 585                 590

Thr Asn Phe Phe Arg Ser Gln Gln Gly Ile Pro Val Leu Ala Trp Ser
        595                 600                 605

His Pro Gln Phe Glu Lys
    610
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<210>  46
<211>  1605
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS69-P93479

<220>
<221> CDS
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atg atg tgc aga tct ttg acc ttg agg ttc ttc ttg ttc atc gtt ttg 48
Met Met Cys Arg Ser Leu Thr Leu Arg Phe Phe Leu Phe Ile Val Leu
1 5 10 15

ttg caa acc tgt gtt aga ggt ggt gat gtt aac gat aac ttg ttg tcc 96
Leu Gln Thr Cys Val Arg Gly Gly Asp Val Asn Asp Asn Leu Leu Ser
20 25 30

tct tgc ttg aac tct cat ggt gtt cat aac ttc act act ttg tct acc 144
Ser Cys Leu Asn Ser His Gly Val His Asn Phe Thr Thr Leu Ser Thr
35 40 45

gat acc aac tcc gat tac ttc aag ttg ttg cat gct tct atg caa aac 192
Asp Thr Asn Ser Asp Tyr Phe Lys Leu Leu His Ala Ser Met Gln Asn
50 55 60

cct ttg ttt gct aag cca acc gtt tct aag cca tct ttt atc gtt atg 240
Pro Leu Phe Ala Lys Pro Thr Val Ser Lys Pro Ser Phe Ile Val Met
65 70 75 80

cca ggc tcc aaa gaa gaa ttg tca tct act gtt cat tgc tgc act aga 288
Pro Gly Ser Lys Glu Glu Leu Ser Ser Thr Val His Cys Cys Thr Arg
85 90 95

gaa tct tgg acc att aga ttg aga tct ggt ggt cat tct tac gag ggt 336
Glu Ser Trp Thr Ile Arg Leu Arg Ser Gly Gly His Ser Tyr Glu Gly
100 105 110

ttg tct tat act gct gat act cca ttc gtt atc gtc gac atg atg aac 384
Leu Ser Tyr Thr Ala Asp Thr Pro Phe Val Ile Val Asp Met Met Asn
115 120 125

ttg aac aga atc tcc atc gat gtc ttg tct gaa act gct tgg gtt gaa 432
Leu Asn Arg Ile Ser Ile Asp Val Leu Ser Glu Thr Ala Trp Val Glu
130 135 140

tct ggt gct act ttg ggt gaa ctg tat tat gct att gct caa tcc act 480
Ser Gly Ala Thr Leu Gly Glu Leu Tyr Tyr Ala Ile Ala Gln Ser Thr
145 150 155 160

gat acc ttg ggt ttt act gct ggt tgg tgt cca act gtt ggt tca ggt 528
Asp Thr Leu Gly Phe Thr Ala Gly Trp Cys Pro Thr Val Gly Ser Gly
165 170 175

ggt cat att tct ggt ggt ggt ttt ggt atg atg tct aga aag tat ggt 576
Gly His Ile Ser Gly Gly Gly Phe Gly Met Met Ser Arg Lys Tyr Gly
180 185 190

```
ttg gct gct gat aac gtt gtt gat gcc att ttg att gat tcc aac ggt        624
Leu Ala Ala Asp Asn Val Val Asp Ala Ile Leu Ile Asp Ser Asn Gly
        195                 200                 205

gct atc ttg gac aga gaa aaa atg ggt gat gat gtt ttc tgg gct att        672
Ala Ile Leu Asp Arg Glu Lys Met Gly Asp Asp Val Phe Trp Ala Ile
    210                 215                 220

aga ggc ggt ggt ggt ggc gtt tgg ggt gca atc tat gct tgg aaa atc        720
Arg Gly Gly Gly Gly Gly Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile
225                 230                 235                 240

aag tta ttg cca gtg cca gaa aag ttg acc gtt ttc aga gtt act aag        768
Lys Leu Leu Pro Val Pro Glu Lys Leu Thr Val Phe Arg Val Thr Lys
                245                 250                 255

aac gtc ggt att gaa gat gcc tct tct ttg ttg cac aaa tgg caa tat        816
Asn Val Gly Ile Glu Asp Ala Ser Ser Leu Leu His Lys Trp Gln Tyr
            260                 265                 270

gtt gcc gat gaa ttg gat gag gat ttc acc gtt tct gtt tta ggt ggt        864
Val Ala Asp Glu Leu Asp Glu Asp Phe Thr Val Ser Val Leu Gly Gly
        275                 280                 285

gtt aat ggt aat gat gcc tgg ttg atg ttc ttg ggt tta cat ttg ggt        912
Val Asn Gly Asn Asp Ala Trp Leu Met Phe Leu Gly Leu His Leu Gly
    290                 295                 300

aga aag gat gct gcc aag acc att att gac gaa aag ttt cca gaa ttg        960
Arg Lys Asp Ala Ala Lys Thr Ile Ile Asp Glu Lys Phe Pro Glu Leu
305                 310                 315                 320

ggc cta gtc gac aaa gaa ttt caa gaa atg tct tgg ggt gaa tcg atg       1008
Gly Leu Val Asp Lys Glu Phe Gln Glu Met Ser Trp Gly Glu Ser Met
                325                 330                 335

gct ttt ttg tct ggt ttg gat acc atc tct gaa ctg aac aac aga ttc       1056
Ala Phe Leu Ser Gly Leu Asp Thr Ile Ser Glu Leu Asn Asn Arg Phe
            340                 345                 350

ttg aag ttc gac gaa aga gct ttc aag acc aag gtt gat ttc acc aaa       1104
Leu Lys Phe Asp Glu Arg Ala Phe Lys Thr Lys Val Asp Phe Thr Lys
        355                 360                 365

gtt tcc gtt cca ttg aac gtt ttt aga cac gct ttg gaa atg ttg tct       1152
Val Ser Val Pro Leu Asn Val Phe Arg His Ala Leu Glu Met Leu Ser
    370                 375                 380

gaa caa cca ggt ggt ttc att gct ttg aat ggt ttc ggt ggt aag atg       1200
Glu Gln Pro Gly Gly Phe Ile Ala Leu Asn Gly Phe Gly Gly Lys Met
385                 390                 395                 400

tcc gaa att tct act gac ttt acc cca ttt cca cac aga aaa ggt acg       1248
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Ser Glu Ile Ser Thr Asp Phe Thr Pro Phe Pro His Arg Lys Gly Thr
                405                 410                 415

aag ttg atg ttt gag tac att att gcc tgg aac cag gac gaa gaa tct       1296
Lys Leu Met Phe Glu Tyr Ile Ile Ala Trp Asn Gln Asp Glu Glu Ser
            420                 425                 430

aag att ggt gaa ttt tct gaa tgg ctg gcc aag ttc tat gat tac ttg       1344
Lys Ile Gly Glu Phe Ser Glu Trp Leu Ala Lys Phe Tyr Asp Tyr Leu
        435                 440                 445

gaa cca ttc gtt tcc aaa gaa cct aga gtt ggt tac gtt aac cac atc       1392
Glu Pro Phe Val Ser Lys Glu Pro Arg Val Gly Tyr Val Asn His Ile
    450                 455                 460

gat ttg gat att ggt ggt atc gat tgg agg aac aaa tct tct act acc       1440
Asp Leu Asp Ile Gly Gly Ile Asp Trp Arg Asn Lys Ser Ser Thr Thr
465                 470                 475                 480

aac gct gtt gaa att gct aga aac tgg ggt gaa aga tac ttc agc tct       1488
Asn Ala Val Glu Ile Ala Arg Asn Trp Gly Glu Arg Tyr Phe Ser Ser
                485                 490                 495

aac tac gaa aga ttg gtt aag gcc aag act ttg atc gat cca aac aac       1536
Asn Tyr Glu Arg Leu Val Lys Ala Lys Thr Leu Ile Asp Pro Asn Asn
            500                 505                 510

gtt ttc aac cat cca caa tct att cca cca atg atg aag ttt gaa gag       1584
Val Phe Asn His Pro Gln Ser Ile Pro Pro Met Met Lys Phe Glu Glu
        515                 520                 525

atc tac atg ctg aaa gaa ttg                                          1605
Ile Tyr Met Leu Lys Glu Leu
    530                 535


<210>  47
<211>  535
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  47

Met Met Cys Arg Ser Leu Thr Leu Arg Phe Phe Leu Phe Ile Val Leu
1               5                   10                  15


Leu Gln Thr Cys Val Arg Gly Gly Asp Val Asn Asp Asn Leu Leu Ser
            20                  25                  30
```

```
Ser Cys Leu Asn Ser His Gly Val His Asn Phe Thr Thr Leu Ser Thr
        35                  40                  45

Asp Thr Asn Ser Asp Tyr Phe Lys Leu Leu His Ala Ser Met Gln Asn
    50                  55                  60

Pro Leu Phe Ala Lys Pro Thr Val Ser Lys Pro Ser Phe Ile Val Met
65                  70                  75                  80

Pro Gly Ser Lys Glu Glu Leu Ser Ser Thr Val His Cys Cys Thr Arg
                85                  90                  95

Glu Ser Trp Thr Ile Arg Leu Arg Ser Gly Gly His Ser Tyr Glu Gly
            100                 105                 110

Leu Ser Tyr Thr Ala Asp Thr Pro Phe Val Ile Val Asp Met Met Asn
        115                 120                 125

Leu Asn Arg Ile Ser Ile Asp Val Leu Ser Glu Thr Ala Trp Val Glu
    130                 135                 140

Ser Gly Ala Thr Leu Gly Glu Leu Tyr Tyr Ala Ile Ala Gln Ser Thr
145                 150                 155                 160

Asp Thr Leu Gly Phe Thr Ala Gly Trp Cys Pro Thr Val Gly Ser Gly
                165                 170                 175

Gly His Ile Ser Gly Gly Gly Phe Gly Met Met Ser Arg Lys Tyr Gly
            180                 185                 190

Leu Ala Ala Asp Asn Val Val Asp Ala Ile Leu Ile Asp Ser Asn Gly
        195                 200                 205

Ala Ile Leu Asp Arg Glu Lys Met Gly Asp Asp Val Phe Trp Ala Ile
    210                 215                 220

Arg Gly Gly Gly Gly Gly Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile
225                 230                 235                 240

Lys Leu Leu Pro Val Pro Glu Lys Leu Thr Val Phe Arg Val Thr Lys
                245                 250                 255
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Asn Val Gly Ile Glu Asp Ala Ser Ser Leu Leu His Lys Trp Gln Tyr
            260                 265                 270

Val Ala Asp Glu Leu Asp Glu Asp Phe Thr Val Ser Val Leu Gly Gly
        275                 280                 285

Val Asn Gly Asn Asp Ala Trp Leu Met Phe Leu Gly Leu His Leu Gly
    290                 295                 300

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

Gly Leu Val Asp Lys Glu Phe Gln Glu Met Ser Trp Gly Glu Ser Met
                325                 330                 335

Ala Phe Leu Ser Gly Leu Asp Thr Ile Ser Glu Leu Asn Asn Arg Phe
            340                 345                 350

Leu Lys Phe Asp Glu Arg Ala Phe Lys Thr Lys Val Asp Phe Thr Lys
        355                 360                 365

Val Ser Val Pro Leu Asn Val Phe Arg His Ala Leu Glu Met Leu Ser
    370                 375                 380

Glu Gln Pro Gly Gly Phe Ile Ala Leu Asn Gly Phe Gly Gly Lys Met
385                 390                 395                 400

Ser Glu Ile Ser Thr Asp Phe Thr Pro Phe Pro His Arg Lys Gly Thr
                405                 410                 415

Lys Leu Met Phe Glu Tyr Ile Ile Ala Trp Asn Gln Asp Glu Glu Ser
            420                 425                 430

Lys Ile Gly Glu Phe Ser Glu Trp Leu Ala Lys Phe Tyr Asp Tyr Leu
        435                 440                 445

Glu Pro Phe Val Ser Lys Glu Pro Arg Val Gly Tyr Val Asn His Ile
    450                 455                 460
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```
Asp Leu Asp Ile Gly Gly Ile Asp Trp Arg Asn Lys Ser Ser Thr Thr
465                 470                 475                 480


Asn Ala Val Glu Ile Ala Arg Asn Trp Gly Glu Arg Tyr Phe Ser Ser
                485                 490                 495


Asn Tyr Glu Arg Leu Val Lys Ala Lys Thr Leu Ile Asp Pro Asn Asn
            500                 505                 510


Val Phe Asn His Pro Gln Ser Ile Pro Pro Met Met Lys Phe Glu Glu
        515                 520                 525


Ile Tyr Met Leu Lys Glu Leu
    530                 535


<210>  48
<211>  1539
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS69-P93479-no signal peptide


<220>
<221>  CDS
<222>  (1)..(1539)

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atg ggt gat gtt aac gat aac ttg ttg tcc tct tgc ttg aac tct cat         48
Met Gly Asp Val Asn Asp Asn Leu Leu Ser Ser Cys Leu Asn Ser His
1               5                   10                  15

ggt gtt cat aac ttc act act ttg tct acc gat acc aac tcc gat tac         96
Gly Val His Asn Phe Thr Thr Leu Ser Thr Asp Thr Asn Ser Asp Tyr
            20                  25                  30

ttc aag ttg ttg cat gct tct atg caa aac cct ttg ttt gct aag cca        144
Phe Lys Leu Leu His Ala Ser Met Gln Asn Pro Leu Phe Ala Lys Pro
        35                  40                  45

acc gtt tct aag cca tct ttt atc gtt atg cca ggc tcc aaa gaa gaa        192
Thr Val Ser Lys Pro Ser Phe Ile Val Met Pro Gly Ser Lys Glu Glu
    50                  55                  60

ttg tca tct act gtt cat tgc tgc act aga gaa tct tgg acc att aga        240
Leu Ser Ser Thr Val His Cys Cys Thr Arg Glu Ser Trp Thr Ile Arg
65                  70                  75                  80
```

```
ttg aga tct ggt ggt cat tct tac gag ggt ttg tct tat act gct gat        288
Leu Arg Ser Gly Gly His Ser Tyr Glu Gly Leu Ser Tyr Thr Ala Asp
                85                  90                  95

act cca ttc gtt atc gtc gac atg atg aac ttg aac aga atc tcc atc        336
Thr Pro Phe Val Ile Val Asp Met Met Asn Leu Asn Arg Ile Ser Ile
            100                 105                 110

gat gtc ttg tct gaa act gct tgg gtt gaa tct ggt gct act ttg ggt        384
Asp Val Leu Ser Glu Thr Ala Trp Val Glu Ser Gly Ala Thr Leu Gly
        115                 120                 125

gaa ctg tat tat gct att gct caa tcc act gat acc ttg ggt ttt act        432
Glu Leu Tyr Tyr Ala Ile Ala Gln Ser Thr Asp Thr Leu Gly Phe Thr
    130                 135                 140

gct ggt tgg tgt cca act gtt ggt tca ggt ggt cat att tct ggt ggt        480
Ala Gly Trp Cys Pro Thr Val Gly Ser Gly Gly His Ile Ser Gly Gly
145                 150                 155                 160

ggt ttt ggt atg atg tct aga aag tat ggt ttg gct gct gat aac gtt        528
Gly Phe Gly Met Met Ser Arg Lys Tyr Gly Leu Ala Ala Asp Asn Val
                165                 170                 175

gtt gat gcc att ttg att gat tcc aac ggt gct atc ttg gac aga gaa        576
Val Asp Ala Ile Leu Ile Asp Ser Asn Gly Ala Ile Leu Asp Arg Glu
            180                 185                 190

aaa atg ggt gat gat gtt ttc tgg gct att aga ggc ggt ggt ggt ggc        624
Lys Met Gly Asp Asp Val Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly
        195                 200                 205

gtt tgg ggt gca atc tat gct tgg aaa atc aag tta ttg cca gtg cca        672
Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile Lys Leu Leu Pro Val Pro
    210                 215                 220

gaa aag ttg acc gtt ttc aga gtt act aag aac gtc ggt att gaa gat        720
Glu Lys Leu Thr Val Phe Arg Val Thr Lys Asn Val Gly Ile Glu Asp
225                 230                 235                 240

gcc tct tct ttg ttg cac aaa tgg caa tat gtt gcc gat gaa ttg gat        768
Ala Ser Ser Leu Leu His Lys Trp Gln Tyr Val Ala Asp Glu Leu Asp
                245                 250                 255

gag gat ttc acc gtt tct gtt tta ggt ggt gtt aat ggt aat gat gcc        816
Glu Asp Phe Thr Val Ser Val Leu Gly Gly Val Asn Gly Asn Asp Ala
            260                 265                 270

tgg ttg atg ttc ttg ggt tta cat ttg ggt aga aag gat gct gcc aag        864
Trp Leu Met Phe Leu Gly Leu His Leu Gly Arg Lys Asp Ala Ala Lys
        275                 280                 285

acc att att gac gaa aag ttt cca gaa ttg ggc cta gtc gac aaa gaa        912
Thr Ile Ile Asp Glu Lys Phe Pro Glu Leu Gly Leu Val Asp Lys Glu
```

```
    290                 295                 300

ttt caa gaa atg tct tgg ggt gaa tcg atg gct ttt ttg tct ggt ttg        960
Phe Gln Glu Met Ser Trp Gly Glu Ser Met Ala Phe Leu Ser Gly Leu
305                 310                 315                 320

gat acc atc tct gaa ctg aac aac aga ttc ttg aag ttc gac gaa aga       1008
Asp Thr Ile Ser Glu Leu Asn Asn Arg Phe Leu Lys Phe Asp Glu Arg
                325                 330                 335

gct ttc aag acc aag gtt gat ttc acc aaa gtt tcc gtt cca ttg aac       1056
Ala Phe Lys Thr Lys Val Asp Phe Thr Lys Val Ser Val Pro Leu Asn
            340                 345                 350

gtt ttt aga cac gct ttg gaa atg ttg tct gaa caa cca ggt ggt ttc       1104
Val Phe Arg His Ala Leu Glu Met Leu Ser Glu Gln Pro Gly Gly Phe
        355                 360                 365

att gct ttg aat ggt ttc ggt ggt aag atg tcc gaa att tct act gac       1152
Ile Ala Leu Asn Gly Phe Gly Gly Lys Met Ser Glu Ile Ser Thr Asp
    370                 375                 380

ttt acc cca ttt cca cac aga aaa ggt acg aag ttg atg ttt gag tac       1200
Phe Thr Pro Phe Pro His Arg Lys Gly Thr Lys Leu Met Phe Glu Tyr
385                 390                 395                 400

att att gcc tgg aac cag gac gaa gaa tct aag att ggt gaa ttt tct       1248
Ile Ile Ala Trp Asn Gln Asp Glu Glu Ser Lys Ile Gly Glu Phe Ser
                405                 410                 415

gaa tgg ctg gcc aag ttc tat gat tac ttg gaa cca ttc gtt tcc aaa       1296
Glu Trp Leu Ala Lys Phe Tyr Asp Tyr Leu Glu Pro Phe Val Ser Lys
            420                 425                 430

gaa cct aga gtt ggt tac gtt aac cac atc gat ttg gat att ggt ggt       1344
Glu Pro Arg Val Gly Tyr Val Asn His Ile Asp Leu Asp Ile Gly Gly
        435                 440                 445

atc gat tgg agg aac aaa tct tct act acc aac gct gtt gaa att gct       1392
Ile Asp Trp Arg Asn Lys Ser Ser Thr Thr Asn Ala Val Glu Ile Ala
    450                 455                 460

aga aac tgg ggt gaa aga tac ttc agc tct aac tac gaa aga ttg gtt       1440
Arg Asn Trp Gly Glu Arg Tyr Phe Ser Ser Asn Tyr Glu Arg Leu Val
465                 470                 475                 480

aag gcc aag act ttg atc gat cca aac aac gtt ttc aac cat cca caa       1488
Lys Ala Lys Thr Leu Ile Asp Pro Asn Asn Val Phe Asn His Pro Gln
                485                 490                 495

tct att cca cca atg atg aag ttt gaa gag atc tac atg ctg aaa gaa       1536
Ser Ile Pro Pro Met Met Lys Phe Glu Glu Ile Tyr Met Leu Lys Glu
            500                 505                 510
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ttg 1539
Leu

<210> 49
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 49

Met Gly Asp Val Asn Asp Asn Leu Leu Ser Ser Cys Leu Asn Ser His
1 5 10 15

Gly Val His Asn Phe Thr Thr Leu Ser Thr Asp Thr Asn Ser Asp Tyr
20 25 30

Phe Lys Leu Leu His Ala Ser Met Gln Asn Pro Leu Phe Ala Lys Pro
35 40 45

Thr Val Ser Lys Pro Ser Phe Ile Val Met Pro Gly Ser Lys Glu Glu
50 55 60

Leu Ser Ser Thr Val His Cys Cys Thr Arg Glu Ser Trp Thr Ile Arg
65 70 75 80

Leu Arg Ser Gly Gly His Ser Tyr Glu Gly Leu Ser Tyr Thr Ala Asp
85 90 95

Thr Pro Phe Val Ile Val Asp Met Met Asn Leu Asn Arg Ile Ser Ile
100 105 110

Asp Val Leu Ser Glu Thr Ala Trp Val Glu Ser Gly Ala Thr Leu Gly
115 120 125

Glu Leu Tyr Tyr Ala Ile Ala Gln Ser Thr Asp Thr Leu Gly Phe Thr
130 135 140

Ala Gly Trp Cys Pro Thr Val Gly Ser Gly Gly His Ile Ser Gly Gly
145 150 155 160

```
Gly Phe Gly Met Met Ser Arg Lys Tyr Gly Leu Ala Ala Asp Asn Val
                165                 170                 175

Val Asp Ala Ile Leu Ile Asp Ser Asn Gly Ala Ile Leu Asp Arg Glu
            180                 185                 190

Lys Met Gly Asp Asp Val Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly
        195                 200                 205

Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile Lys Leu Leu Pro Val Pro
    210                 215                 220

Glu Lys Leu Thr Val Phe Arg Val Thr Lys Asn Val Gly Ile Glu Asp
225                 230                 235                 240

Ala Ser Ser Leu Leu His Lys Trp Gln Tyr Val Ala Asp Glu Leu Asp
                245                 250                 255

Glu Asp Phe Thr Val Ser Val Leu Gly Gly Val Asn Gly Asn Asp Ala
            260                 265                 270

Trp Leu Met Phe Leu Gly Leu His Leu Gly Arg Lys Asp Ala Ala Lys
        275                 280                 285

Thr Ile Ile Asp Glu Lys Phe Pro Glu Leu Gly Leu Val Asp Lys Glu
    290                 295                 300

Phe Gln Glu Met Ser Trp Gly Glu Ser Met Ala Phe Leu Ser Gly Leu
305                 310                 315                 320

Asp Thr Ile Ser Glu Leu Asn Asn Arg Phe Leu Lys Phe Asp Glu Arg
                325                 330                 335

Ala Phe Lys Thr Lys Val Asp Phe Thr Lys Val Ser Val Pro Leu Asn
            340                 345                 350

Val Phe Arg His Ala Leu Glu Met Leu Ser Glu Gln Pro Gly Gly Phe
        355                 360                 365

Ile Ala Leu Asn Gly Phe Gly Gly Lys Met Ser Glu Ile Ser Thr Asp
```

```
    370                 375                 380

Phe Thr Pro Phe Pro His Arg Lys Gly Thr Lys Leu Met Phe Glu Tyr
385                 390                 395                 400

Ile Ile Ala Trp Asn Gln Asp Glu Glu Ser Lys Ile Gly Glu Phe Ser
                405                 410                 415

Glu Trp Leu Ala Lys Phe Tyr Asp Tyr Leu Glu Pro Phe Val Ser Lys
            420                 425                 430

Glu Pro Arg Val Gly Tyr Val Asn His Ile Asp Leu Asp Ile Gly Gly
        435                 440                 445

Ile Asp Trp Arg Asn Lys Ser Ser Thr Thr Asn Ala Val Glu Ile Ala
    450                 455                 460

Arg Asn Trp Gly Glu Arg Tyr Phe Ser Ser Asn Tyr Glu Arg Leu Val
465                 470                 475                 480

Lys Ala Lys Thr Leu Ile Asp Pro Asn Asn Val Phe Asn His Pro Gln
                485                 490                 495

Ser Ile Pro Pro Met Met Lys Phe Glu Glu Ile Tyr Met Leu Lys Glu
            500                 505                 510

Leu
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<210>  50
<211>  1563
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS69-P93479-no signal peptide-strep Tag

<220>
<221>  CDS
<222>  (1)..(1563)

<400>  50
atg ggt gat gtt aac gat aac ttg ttg tcc tct tgc ttg aac tct cat  48

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Met Gly Asp Val Asn Asp Asn Leu Leu Ser Ser Cys Leu Asn Ser His
1               5                  10                  15

ggt gtt cat aac ttc act act ttg tct acc gat acc aac tcc gat tac         96
Gly Val His Asn Phe Thr Thr Leu Ser Thr Asp Thr Asn Ser Asp Tyr
            20                  25                  30

ttc aag ttg ttg cat gct tct atg caa aac cct ttg ttt gct aag cca        144
Phe Lys Leu Leu His Ala Ser Met Gln Asn Pro Leu Phe Ala Lys Pro
        35                  40                  45

acc gtt tct aag cca tct ttt atc gtt atg cca ggc tcc aaa gaa gaa        192
Thr Val Ser Lys Pro Ser Phe Ile Val Met Pro Gly Ser Lys Glu Glu
    50                  55                  60

ttg tca tct act gtt cat tgc tgc act aga gaa tct tgg acc att aga        240
Leu Ser Ser Thr Val His Cys Cys Thr Arg Glu Ser Trp Thr Ile Arg
65                  70                  75                  80

ttg aga tct ggt ggt cat tct tac gag ggt ttg tct tat act gct gat        288
Leu Arg Ser Gly Gly His Ser Tyr Glu Gly Leu Ser Tyr Thr Ala Asp
                85                  90                  95

act cca ttc gtt atc gtc gac atg atg aac ttg aac aga atc tcc atc        336
Thr Pro Phe Val Ile Val Asp Met Met Asn Leu Asn Arg Ile Ser Ile
            100                 105                 110

gat gtc ttg tct gaa act gct tgg gtt gaa tct ggt gct act ttg ggt        384
Asp Val Leu Ser Glu Thr Ala Trp Val Glu Ser Gly Ala Thr Leu Gly
        115                 120                 125

gaa ctg tat tat gct att gct caa tcc act gat acc ttg ggt ttt act        432
Glu Leu Tyr Tyr Ala Ile Ala Gln Ser Thr Asp Thr Leu Gly Phe Thr
    130                 135                 140

gct ggt tgg tgt cca act gtt ggt tca ggt ggt cat att tct ggt ggt        480
Ala Gly Trp Cys Pro Thr Val Gly Ser Gly Gly His Ile Ser Gly Gly
145                 150                 155                 160

ggt ttt ggt atg atg tct aga aag tat ggt ttg gct gct gat aac gtt        528
Gly Phe Gly Met Met Ser Arg Lys Tyr Gly Leu Ala Ala Asp Asn Val
                165                 170                 175

gtt gat gcc att ttg att gat tcc aac ggt gct atc ttg gac aga gaa        576
Val Asp Ala Ile Leu Ile Asp Ser Asn Gly Ala Ile Leu Asp Arg Glu
            180                 185                 190

aaa atg ggt gat gat gtt ttc tgg gct att aga ggc ggt ggt ggt ggc        624
Lys Met Gly Asp Asp Val Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly
        195                 200                 205

gtt tgg ggt gca atc tat gct tgg aaa atc aag tta ttg cca gtg cca        672
Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile Lys Leu Leu Pro Val Pro
    210                 215                 220
```

```
gaa aag ttg acc gtt ttc aga gtt act aag aac gtc ggt att gaa gat        720
Glu Lys Leu Thr Val Phe Arg Val Thr Lys Asn Val Gly Ile Glu Asp
225                 230                 235                 240

gcc tct tct ttg ttg cac aaa tgg caa tat gtt gcc gat gaa ttg gat        768
Ala Ser Ser Leu Leu His Lys Trp Gln Tyr Val Ala Asp Glu Leu Asp
                245                 250                 255

gag gat ttc acc gtt tct gtt tta ggt ggt gtt aat ggt aat gat gcc        816
Glu Asp Phe Thr Val Ser Val Leu Gly Gly Val Asn Gly Asn Asp Ala
            260                 265                 270

tgg ttg atg ttc ttg ggt tta cat ttg ggt aga aag gat gct gcc aag        864
Trp Leu Met Phe Leu Gly Leu His Leu Gly Arg Lys Asp Ala Ala Lys
        275                 280                 285

acc att att gac gaa aag ttt cca gaa ttg ggc cta gtc gac aaa gaa        912
Thr Ile Ile Asp Glu Lys Phe Pro Glu Leu Gly Leu Val Asp Lys Glu
    290                 295                 300

ttt caa gaa atg tct tgg ggt gaa tcg atg gct ttt ttg tct ggt ttg        960
Phe Gln Glu Met Ser Trp Gly Glu Ser Met Ala Phe Leu Ser Gly Leu
305                 310                 315                 320

gat acc atc tct gaa ctg aac aac aga ttc ttg aag ttc gac gaa aga       1008
Asp Thr Ile Ser Glu Leu Asn Asn Arg Phe Leu Lys Phe Asp Glu Arg
                325                 330                 335

gct ttc aag acc aag gtt gat ttc acc aaa gtt tcc gtt cca ttg aac       1056
Ala Phe Lys Thr Lys Val Asp Phe Thr Lys Val Ser Val Pro Leu Asn
            340                 345                 350

gtt ttt aga cac gct ttg gaa atg ttg tct gaa caa cca ggt ggt ttc       1104
Val Phe Arg His Ala Leu Glu Met Leu Ser Glu Gln Pro Gly Gly Phe
        355                 360                 365

att gct ttg aat ggt ttc ggt ggt aag atg tcc gaa att tct act gac       1152
Ile Ala Leu Asn Gly Phe Gly Gly Lys Met Ser Glu Ile Ser Thr Asp
    370                 375                 380

ttt acc cca ttt cca cac aga aaa ggt acg aag ttg atg ttt gag tac       1200
Phe Thr Pro Phe Pro His Arg Lys Gly Thr Lys Leu Met Phe Glu Tyr
385                 390                 395                 400

att att gcc tgg aac cag gac gaa gaa tct aag att ggt gaa ttt tct       1248
Ile Ile Ala Trp Asn Gln Asp Glu Glu Ser Lys Ile Gly Glu Phe Ser
                405                 410                 415

gaa tgg ctg gcc aag ttc tat gat tac ttg gaa cca ttc gtt tcc aaa       1296
Glu Trp Leu Ala Lys Phe Tyr Asp Tyr Leu Glu Pro Phe Val Ser Lys
            420                 425                 430

gaa cct aga gtt ggt tac gtt aac cac atc gat ttg gat att ggt ggt       1344
```

```
Glu Pro Arg Val Gly Tyr Val Asn His Ile Asp Leu Asp Ile Gly Gly
        435                 440                 445

atc gat tgg agg aac aaa tct tct act acc aac gct gtt gaa att gct       1392
Ile Asp Trp Arg Asn Lys Ser Ser Thr Thr Asn Ala Val Glu Ile Ala
    450                 455                 460

aga aac tgg ggt gaa aga tac ttc agc tct aac tac gaa aga ttg gtt       1440
Arg Asn Trp Gly Glu Arg Tyr Phe Ser Ser Asn Tyr Glu Arg Leu Val
465                 470                 475                 480

aag gcc aag act ttg atc gat cca aac aac gtt ttc aac cat cca caa       1488
Lys Ala Lys Thr Leu Ile Asp Pro Asn Asn Val Phe Asn His Pro Gln
                485                 490                 495

tct att cca cca atg atg aag ttt gaa gag atc tac atg ctg aaa gaa       1536
Ser Ile Pro Pro Met Met Lys Phe Glu Glu Ile Tyr Met Leu Lys Glu
            500                 505                 510

ttg tgg tca cat cca caa ttt gaa aag                                  1563
Leu Trp Ser His Pro Gln Phe Glu Lys
        515                 520
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<210> 51
<211> 521
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 51

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Met Gly Asp Val Asn Asp Asn Leu Leu Ser Ser Cys Leu Asn Ser His
1               5                   10                  15

Gly Val His Asn Phe Thr Thr Leu Ser Thr Asp Thr Asn Ser Asp Tyr
            20                  25                  30

Phe Lys Leu Leu His Ala Ser Met Gln Asn Pro Leu Phe Ala Lys Pro
        35                  40                  45

Thr Val Ser Lys Pro Ser Phe Ile Val Met Pro Gly Ser Lys Glu Glu
    50                  55                  60

Leu Ser Ser Thr Val His Cys Cys Thr Arg Glu Ser Trp Thr Ile Arg
65                  70                  75                  80
```

```
Leu Arg Ser Gly Gly His Ser Tyr Glu Gly Leu Ser Tyr Thr Ala Asp
                85                  90                  95

Thr Pro Phe Val Ile Val Asp Met Met Asn Leu Asn Arg Ile Ser Ile
            100                 105                 110

Asp Val Leu Ser Glu Thr Ala Trp Val Glu Ser Gly Ala Thr Leu Gly
        115                 120                 125

Glu Leu Tyr Tyr Ala Ile Ala Gln Ser Thr Asp Thr Leu Gly Phe Thr
    130                 135                 140

Ala Gly Trp Cys Pro Thr Val Gly Ser Gly Gly His Ile Ser Gly Gly
145                 150                 155                 160

Gly Phe Gly Met Met Ser Arg Lys Tyr Gly Leu Ala Ala Asp Asn Val
                165                 170                 175

Val Asp Ala Ile Leu Ile Asp Ser Asn Gly Ala Ile Leu Asp Arg Glu
            180                 185                 190

Lys Met Gly Asp Asp Val Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly
        195                 200                 205

Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile Lys Leu Leu Pro Val Pro
    210                 215                 220

Glu Lys Leu Thr Val Phe Arg Val Thr Lys Asn Val Gly Ile Glu Asp
225                 230                 235                 240

Ala Ser Ser Leu Leu His Lys Trp Gln Tyr Val Ala Asp Glu Leu Asp
                245                 250                 255

Glu Asp Phe Thr Val Ser Val Leu Gly Gly Val Asn Gly Asn Asp Ala
            260                 265                 270

Trp Leu Met Phe Leu Gly Leu His Leu Gly Arg Lys Asp Ala Ala Lys
        275                 280                 285

Thr Ile Ile Asp Glu Lys Phe Pro Glu Leu Gly Leu Val Asp Lys Glu
    290                 295                 300
```

```
Phe Gln Glu Met Ser Trp Gly Glu Ser Met Ala Phe Leu Ser Gly Leu
305                 310                 315                 320

Asp Thr Ile Ser Glu Leu Asn Asn Arg Phe Leu Lys Phe Asp Glu Arg
                325                 330                 335

Ala Phe Lys Thr Lys Val Asp Phe Thr Lys Val Ser Val Pro Leu Asn
            340                 345                 350

Val Phe Arg His Ala Leu Glu Met Leu Ser Glu Gln Pro Gly Gly Phe
        355                 360                 365

Ile Ala Leu Asn Gly Phe Gly Gly Lys Met Ser Glu Ile Ser Thr Asp
    370                 375                 380

Phe Thr Pro Phe Pro His Arg Lys Gly Thr Lys Leu Met Phe Glu Tyr
385                 390                 395                 400

Ile Ile Ala Trp Asn Gln Asp Glu Glu Ser Lys Ile Gly Glu Phe Ser
                405                 410                 415

Glu Trp Leu Ala Lys Phe Tyr Asp Tyr Leu Glu Pro Phe Val Ser Lys
            420                 425                 430

Glu Pro Arg Val Gly Tyr Val Asn His Ile Asp Leu Asp Ile Gly Gly
        435                 440                 445

Ile Asp Trp Arg Asn Lys Ser Ser Thr Thr Asn Ala Val Glu Ile Ala
    450                 455                 460

Arg Asn Trp Gly Glu Arg Tyr Phe Ser Ser Asn Tyr Glu Arg Leu Val
465                 470                 475                 480

Lys Ala Lys Thr Leu Ile Asp Pro Asn Asn Val Phe Asn His Pro Gln
                485                 490                 495

Ser Ile Pro Pro Met Met Lys Phe Glu Glu Ile Tyr Met Leu Lys Glu
            500                 505                 510
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Leu Trp Ser His Pro Gln Phe Glu Lys
        515                 520


<210>  52
<211>  1620
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS69-P93479- truncated alpha factor -no signal peptide-strep Tag


<220>
<221>  CDS
<222>  (1)..(1620)

<400>  52
atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca ctt gca atg ggt gat gtt aac gat aac ttg ttg tcc tct tgc ttg         96
Ala Leu Ala Met Gly Asp Val Asn Asp Asn Leu Leu Ser Ser Cys Leu
            20                  25                  30

aac tct cat ggt gtt cat aac ttc act act ttg tct acc gat acc aac        144
Asn Ser His Gly Val His Asn Phe Thr Thr Leu Ser Thr Asp Thr Asn
        35                  40                  45

tcc gat tac ttc aag ttg ttg cat gct tct atg caa aac cct ttg ttt        192
Ser Asp Tyr Phe Lys Leu Leu His Ala Ser Met Gln Asn Pro Leu Phe
    50                  55                  60

gct aag cca acc gtt tct aag cca tct ttt atc gtt atg cca ggc tcc        240
Ala Lys Pro Thr Val Ser Lys Pro Ser Phe Ile Val Met Pro Gly Ser
65                  70                  75                  80

aaa gaa gaa ttg tca tct act gtt cat tgc tgc act aga gaa tct tgg        288
Lys Glu Glu Leu Ser Ser Thr Val His Cys Cys Thr Arg Glu Ser Trp
                85                  90                  95

acc att aga ttg aga tct ggt ggt cat tct tac gag ggt ttg tct tat        336
Thr Ile Arg Leu Arg Ser Gly Gly His Ser Tyr Glu Gly Leu Ser Tyr
            100                 105                 110

act gct gat act cca ttc gtt atc gtc gac atg atg aac ttg aac aga        384
Thr Ala Asp Thr Pro Phe Val Ile Val Asp Met Met Asn Leu Asn Arg
        115                 120                 125

atc tcc atc gat gtc ttg tct gaa act gct tgg gtt gaa tct ggt gct        432
Ile Ser Ile Asp Val Leu Ser Glu Thr Ala Trp Val Glu Ser Gly Ala
    130                 135                 140
```

```
act ttg ggt gaa ctg tat tat gct att gct caa tcc act gat acc ttg        480
Thr Leu Gly Glu Leu Tyr Tyr Ala Ile Ala Gln Ser Thr Asp Thr Leu
145                 150                 155                 160

ggt ttt act gct ggt tgg tgt cca act gtt ggt tca ggt ggt cat att        528
Gly Phe Thr Ala Gly Trp Cys Pro Thr Val Gly Ser Gly Gly His Ile
                165                 170                 175

tct ggt ggt ggt ttt ggt atg atg tct aga aag tat ggt ttg gct gct        576
Ser Gly Gly Gly Phe Gly Met Met Ser Arg Lys Tyr Gly Leu Ala Ala
            180                 185                 190

gat aac gtt gtt gat gcc att ttg att gat tcc aac ggt gct atc ttg        624
Asp Asn Val Val Asp Ala Ile Leu Ile Asp Ser Asn Gly Ala Ile Leu
        195                 200                 205

gac aga gaa aaa atg ggt gat gat gtt ttc tgg gct att aga ggc ggt        672
Asp Arg Glu Lys Met Gly Asp Asp Val Phe Trp Ala Ile Arg Gly Gly
    210                 215                 220

ggt ggt ggc gtt tgg ggt gca atc tat gct tgg aaa atc aag tta ttg        720
Gly Gly Gly Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile Lys Leu Leu
225                 230                 235                 240

cca gtg cca gaa aag ttg acc gtt ttc aga gtt act aag aac gtc ggt        768
Pro Val Pro Glu Lys Leu Thr Val Phe Arg Val Thr Lys Asn Val Gly
                245                 250                 255

att gaa gat gcc tct tct ttg ttg cac aaa tgg caa tat gtt gcc gat        816
Ile Glu Asp Ala Ser Ser Leu Leu His Lys Trp Gln Tyr Val Ala Asp
            260                 265                 270

gaa ttg gat gag gat ttc acc gtt tct gtt tta ggt ggt gtt aat ggt        864
Glu Leu Asp Glu Asp Phe Thr Val Ser Val Leu Gly Gly Val Asn Gly
        275                 280                 285

aat gat gcc tgg ttg atg ttc ttg ggt tta cat ttg ggt aga aag gat        912
Asn Asp Ala Trp Leu Met Phe Leu Gly Leu His Leu Gly Arg Lys Asp
    290                 295                 300

gct gcc aag acc att att gac gaa aag ttt cca gaa ttg ggc cta gtc        960
Ala Ala Lys Thr Ile Ile Asp Glu Lys Phe Pro Glu Leu Gly Leu Val
305                 310                 315                 320

gac aaa gaa ttt caa gaa atg tct tgg ggt gaa tcg atg gct ttt ttg       1008
Asp Lys Glu Phe Gln Glu Met Ser Trp Gly Glu Ser Met Ala Phe Leu
                325                 330                 335

tct ggt ttg gat acc atc tct gaa ctg aac aac aga ttc ttg aag ttc       1056
Ser Gly Leu Asp Thr Ile Ser Glu Leu Asn Asn Arg Phe Leu Lys Phe
            340                 345                 350

gac gaa aga gct ttc aag acc aag gtt gat ttc acc aaa gtt tcc gtt       1104
Asp Glu Arg Ala Phe Lys Thr Lys Val Asp Phe Thr Lys Val Ser Val
```

```
        355                 360                 365

cca ttg aac gtt ttt aga cac gct ttg gaa atg ttg tct gaa caa cca       1152
Pro Leu Asn Val Phe Arg His Ala Leu Glu Met Leu Ser Glu Gln Pro
    370                 375                 380

ggt ggt ttc att gct ttg aat ggt ttc ggt ggt aag atg tcc gaa att       1200
Gly Gly Phe Ile Ala Leu Asn Gly Phe Gly Gly Lys Met Ser Glu Ile
385                 390                 395                 400

tct act gac ttt acc cca ttt cca cac aga aaa ggt acg aag ttg atg       1248
Ser Thr Asp Phe Thr Pro Phe Pro His Arg Lys Gly Thr Lys Leu Met
                405                 410                 415

ttt gag tac att att gcc tgg aac cag gac gaa gaa tct aag att ggt       1296
Phe Glu Tyr Ile Ile Ala Trp Asn Gln Asp Glu Glu Ser Lys Ile Gly
            420                 425                 430

gaa ttt tct gaa tgg ctg gcc aag ttc tat gat tac ttg gaa cca ttc       1344
Glu Phe Ser Glu Trp Leu Ala Lys Phe Tyr Asp Tyr Leu Glu Pro Phe
        435                 440                 445

gtt tcc aaa gaa cct aga gtt ggt tac gtt aac cac atc gat ttg gat       1392
Val Ser Lys Glu Pro Arg Val Gly Tyr Val Asn His Ile Asp Leu Asp
    450                 455                 460

att ggt ggt atc gat tgg agg aac aaa tct tct act acc aac gct gtt       1440
Ile Gly Gly Ile Asp Trp Arg Asn Lys Ser Ser Thr Thr Asn Ala Val
465                 470                 475                 480

gaa att gct aga aac tgg ggt gaa aga tac ttc agc tct aac tac gaa       1488
Glu Ile Ala Arg Asn Trp Gly Glu Arg Tyr Phe Ser Ser Asn Tyr Glu
                485                 490                 495

aga ttg gtt aag gcc aag act ttg atc gat cca aac aac gtt ttc aac       1536
Arg Leu Val Lys Ala Lys Thr Leu Ile Asp Pro Asn Asn Val Phe Asn
            500                 505                 510

cat cca caa tct att cca cca atg atg aag ttt gaa gag atc tac atg       1584
His Pro Gln Ser Ile Pro Pro Met Met Lys Phe Glu Glu Ile Tyr Met
        515                 520                 525

ctg aaa gaa ttg tgg tca cat cca caa ttt gaa aag                       1620
Leu Lys Glu Leu Trp Ser His Pro Gln Phe Glu Lys
    530                 535                 540
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<210> 53
<211> 540
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 53

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

Ala Leu Ala Met Gly Asp Val Asn Asp Asn Leu Leu Ser Ser Cys Leu
            20                  25                  30

Asn Ser His Gly Val His Asn Phe Thr Thr Leu Ser Thr Asp Thr Asn
        35                  40                  45

Ser Asp Tyr Phe Lys Leu Leu His Ala Ser Met Gln Asn Pro Leu Phe
    50                  55                  60

Ala Lys Pro Thr Val Ser Lys Pro Ser Phe Ile Val Met Pro Gly Ser
65                  70                  75                  80

Lys Glu Glu Leu Ser Ser Thr Val His Cys Cys Thr Arg Glu Ser Trp
                85                  90                  95

Thr Ile Arg Leu Arg Ser Gly Gly His Ser Tyr Glu Gly Leu Ser Tyr
            100                 105                 110

Thr Ala Asp Thr Pro Phe Val Ile Val Asp Met Met Asn Leu Asn Arg
        115                 120                 125

Ile Ser Ile Asp Val Leu Ser Glu Thr Ala Trp Val Glu Ser Gly Ala
    130                 135                 140

Thr Leu Gly Glu Leu Tyr Tyr Ala Ile Ala Gln Ser Thr Asp Thr Leu
145                 150                 155                 160

Gly Phe Thr Ala Gly Trp Cys Pro Thr Val Gly Ser Gly Gly His Ile
                165                 170                 175

Ser Gly Gly Gly Phe Gly Met Met Ser Arg Lys Tyr Gly Leu Ala Ala
            180                 185                 190

Asp Asn Val Val Asp Ala Ile Leu Ile Asp Ser Asn Gly Ala Ile Leu
        195                 200                 205
```

```
Asp Arg Glu Lys Met Gly Asp Asp Val Phe Trp Ala Ile Arg Gly Gly
    210                 215                 220

Gly Gly Gly Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile Lys Leu Leu
225                 230                 235                 240

Pro Val Pro Glu Lys Leu Thr Val Phe Arg Val Thr Lys Asn Val Gly
                245                 250                 255

Ile Glu Asp Ala Ser Ser Leu Leu His Lys Trp Gln Tyr Val Ala Asp
            260                 265                 270

Glu Leu Asp Glu Asp Phe Thr Val Ser Val Leu Gly Gly Val Asn Gly
        275                 280                 285

Asn Asp Ala Trp Leu Met Phe Leu Gly Leu His Leu Gly Arg Lys Asp
    290                 295                 300

Ala Ala Lys Thr Ile Ile Asp Glu Lys Phe Pro Glu Leu Gly Leu Val
305                 310                 315                 320

Asp Lys Glu Phe Gln Glu Met Ser Trp Gly Glu Ser Met Ala Phe Leu
                325                 330                 335

Ser Gly Leu Asp Thr Ile Ser Glu Leu Asn Asn Arg Phe Leu Lys Phe
            340                 345                 350

Asp Glu Arg Ala Phe Lys Thr Lys Val Asp Phe Thr Lys Val Ser Val
        355                 360                 365

Pro Leu Asn Val Phe Arg His Ala Leu Glu Met Leu Ser Glu Gln Pro
    370                 375                 380

Gly Gly Phe Ile Ala Leu Asn Gly Phe Gly Gly Lys Met Ser Glu Ile
385                 390                 395                 400

Ser Thr Asp Phe Thr Pro Phe Pro His Arg Lys Gly Thr Lys Leu Met
                405                 410                 415

Phe Glu Tyr Ile Ile Ala Trp Asn Gln Asp Glu Glu Ser Lys Ile Gly
```

```
            420                 425                 430

Glu Phe Ser Glu Trp Leu Ala Lys Phe Tyr Asp Tyr Leu Glu Pro Phe
        435                 440                 445

Val Ser Lys Glu Pro Arg Val Gly Tyr Val Asn His Ile Asp Leu Asp
    450                 455                 460

Ile Gly Gly Ile Asp Trp Arg Asn Lys Ser Ser Thr Thr Asn Ala Val
465                 470                 475                 480

Glu Ile Ala Arg Asn Trp Gly Glu Arg Tyr Phe Ser Ser Asn Tyr Glu
                485                 490                 495

Arg Leu Val Lys Ala Lys Thr Leu Ile Asp Pro Asn Asn Val Phe Asn
            500                 505                 510

His Pro Gln Ser Ile Pro Pro Met Met Lys Phe Glu Glu Ile Tyr Met
        515                 520                 525

Leu Lys Glu Leu Trp Ser His Pro Gln Phe Glu Lys
    530                 535                 540
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<210> 54
<211> 1830
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS69-P93479-full alpha factor -no signal peptide-strep Tag

<220>
<221> CDS
<222> (1)..(1830)

<400> 54

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atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
```

```
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg ggt gat gtt aac gat aac        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Gly Asp Val Asn Asp Asn
                85                  90                  95

ttg ttg tcc tct tgc ttg aac tct cat ggt gtt cat aac ttc act act        336
Leu Leu Ser Ser Cys Leu Asn Ser His Gly Val His Asn Phe Thr Thr
            100                 105                 110

ttg tct acc gat acc aac tcc gat tac ttc aag ttg ttg cat gct tct        384
Leu Ser Thr Asp Thr Asn Ser Asp Tyr Phe Lys Leu Leu His Ala Ser
        115                 120                 125

atg caa aac cct ttg ttt gct aag cca acc gtt tct aag cca tct ttt        432
Met Gln Asn Pro Leu Phe Ala Lys Pro Thr Val Ser Lys Pro Ser Phe
    130                 135                 140

atc gtt atg cca ggc tcc aaa gaa gaa ttg tca tct act gtt cat tgc        480
Ile Val Met Pro Gly Ser Lys Glu Glu Leu Ser Ser Thr Val His Cys
145                 150                 155                 160

tgc act aga gaa tct tgg acc att aga ttg aga tct ggt ggt cat tct        528
Cys Thr Arg Glu Ser Trp Thr Ile Arg Leu Arg Ser Gly Gly His Ser
                165                 170                 175

tac gag ggt ttg tct tat act gct gat act cca ttc gtt atc gtc gac        576
Tyr Glu Gly Leu Ser Tyr Thr Ala Asp Thr Pro Phe Val Ile Val Asp
            180                 185                 190

atg atg aac ttg aac aga atc tcc atc gat gtc ttg tct gaa act gct        624
Met Met Asn Leu Asn Arg Ile Ser Ile Asp Val Leu Ser Glu Thr Ala
        195                 200                 205

tgg gtt gaa tct ggt gct act ttg ggt gaa ctg tat tat gct att gct        672
Trp Val Glu Ser Gly Ala Thr Leu Gly Glu Leu Tyr Tyr Ala Ile Ala
    210                 215                 220

caa tcc act gat acc ttg ggt ttt act gct ggt tgg tgt cca act gtt        720
Gln Ser Thr Asp Thr Leu Gly Phe Thr Ala Gly Trp Cys Pro Thr Val
225                 230                 235                 240

ggt tca ggt ggt cat att tct ggt ggt ggt ttt ggt atg atg tct aga        768
Gly Ser Gly Gly His Ile Ser Gly Gly Gly Phe Gly Met Met Ser Arg
                245                 250                 255
```

```
aag tat ggt ttg gct gct gat aac gtt gtt gat gcc att ttg att gat        816
Lys Tyr Gly Leu Ala Ala Asp Asn Val Val Asp Ala Ile Leu Ile Asp
            260                 265                 270

tcc aac ggt gct atc ttg gac aga gaa aaa atg ggt gat gat gtt ttc        864
Ser Asn Gly Ala Ile Leu Asp Arg Glu Lys Met Gly Asp Asp Val Phe
        275                 280                 285

tgg gct att aga ggc ggt ggt ggt ggc gtt tgg ggt gca atc tat gct        912
Trp Ala Ile Arg Gly Gly Gly Gly Gly Val Trp Gly Ala Ile Tyr Ala
    290                 295                 300

tgg aaa atc aag tta ttg cca gtg cca gaa aag ttg acc gtt ttc aga        960
Trp Lys Ile Lys Leu Leu Pro Val Pro Glu Lys Leu Thr Val Phe Arg
305                 310                 315                 320

gtt act aag aac gtc ggt att gaa gat gcc tct tct ttg ttg cac aaa       1008
Val Thr Lys Asn Val Gly Ile Glu Asp Ala Ser Ser Leu Leu His Lys
                325                 330                 335

tgg caa tat gtt gcc gat gaa ttg gat gag gat ttc acc gtt tct gtt       1056
Trp Gln Tyr Val Ala Asp Glu Leu Asp Glu Asp Phe Thr Val Ser Val
            340                 345                 350

tta ggt ggt gtt aat ggt aat gat gcc tgg ttg atg ttc ttg ggt tta       1104
Leu Gly Gly Val Asn Gly Asn Asp Ala Trp Leu Met Phe Leu Gly Leu
        355                 360                 365

cat ttg ggt aga aag gat gct gcc aag acc att att gac gaa aag ttt       1152
His Leu Gly Arg Lys Asp Ala Ala Lys Thr Ile Ile Asp Glu Lys Phe
    370                 375                 380

cca gaa ttg ggc cta gtc gac aaa gaa ttt caa gaa atg tct tgg ggt       1200
Pro Glu Leu Gly Leu Val Asp Lys Glu Phe Gln Glu Met Ser Trp Gly
385                 390                 395                 400

gaa tcg atg gct ttt ttg tct ggt ttg gat acc atc tct gaa ctg aac       1248
Glu Ser Met Ala Phe Leu Ser Gly Leu Asp Thr Ile Ser Glu Leu Asn
                405                 410                 415

aac aga ttc ttg aag ttc gac gaa aga gct ttc aag acc aag gtt gat       1296
Asn Arg Phe Leu Lys Phe Asp Glu Arg Ala Phe Lys Thr Lys Val Asp
            420                 425                 430

ttc acc aaa gtt tcc gtt cca ttg aac gtt ttt aga cac gct ttg gaa       1344
Phe Thr Lys Val Ser Val Pro Leu Asn Val Phe Arg His Ala Leu Glu
        435                 440                 445

atg ttg tct gaa caa cca ggt ggt ttc att gct ttg aat ggt ttc ggt       1392
Met Leu Ser Glu Gln Pro Gly Gly Phe Ile Ala Leu Asn Gly Phe Gly
    450                 455                 460

ggt aag atg tcc gaa att tct act gac ttt acc cca ttt cca cac aga       1440
```

```
Gly Lys Met Ser Glu Ile Ser Thr Asp Phe Thr Pro Phe Pro His Arg
465                 470                 475                 480

aaa ggt acg aag ttg atg ttt gag tac att att gcc tgg aac cag gac       1488
Lys Gly Thr Lys Leu Met Phe Glu Tyr Ile Ile Ala Trp Asn Gln Asp
                485                 490                 495

gaa gaa tct aag att ggt gaa ttt tct gaa tgg ctg gcc aag ttc tat       1536
Glu Glu Ser Lys Ile Gly Glu Phe Ser Glu Trp Leu Ala Lys Phe Tyr
            500                 505                 510

gat tac ttg gaa cca ttc gtt tcc aaa gaa cct aga gtt ggt tac gtt       1584
Asp Tyr Leu Glu Pro Phe Val Ser Lys Glu Pro Arg Val Gly Tyr Val
        515                 520                 525

aac cac atc gat ttg gat att ggt ggt atc gat tgg agg aac aaa tct       1632
Asn His Ile Asp Leu Asp Ile Gly Gly Ile Asp Trp Arg Asn Lys Ser
    530                 535                 540

tct act acc aac gct gtt gaa att gct aga aac tgg ggt gaa aga tac       1680
Ser Thr Thr Asn Ala Val Glu Ile Ala Arg Asn Trp Gly Glu Arg Tyr
545                 550                 555                 560

ttc agc tct aac tac gaa aga ttg gtt aag gcc aag act ttg atc gat       1728
Phe Ser Ser Asn Tyr Glu Arg Leu Val Lys Ala Lys Thr Leu Ile Asp
                565                 570                 575

cca aac aac gtt ttc aac cat cca caa tct att cca cca atg atg aag       1776
Pro Asn Asn Val Phe Asn His Pro Gln Ser Ile Pro Pro Met Met Lys
            580                 585                 590

ttt gaa gag atc tac atg ctg aaa gaa ttg tgg tca cat cca caa ttt       1824
Phe Glu Glu Ile Tyr Met Leu Lys Glu Leu Trp Ser His Pro Gln Phe
        595                 600                 605

gaa aag                                                              1830
Glu Lys
    610
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<210>  55
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<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  55

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Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15
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Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

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

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Gly Asp Val Asn Asp Asn
                85                  90                  95

Leu Leu Ser Ser Cys Leu Asn Ser His Gly Val His Asn Phe Thr Thr
            100                 105                 110

Leu Ser Thr Asp Thr Asn Ser Asp Tyr Phe Lys Leu Leu His Ala Ser
        115                 120                 125

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

Ile Val Met Pro Gly Ser Lys Glu Glu Leu Ser Ser Thr Val His Cys
145                 150                 155                 160

Cys Thr Arg Glu Ser Trp Thr Ile Arg Leu Arg Ser Gly Gly His Ser
                165                 170                 175

Tyr Glu Gly Leu Ser Tyr Thr Ala Asp Thr Pro Phe Val Ile Val Asp
            180                 185                 190

Met Met Asn Leu Asn Arg Ile Ser Ile Asp Val Leu Ser Glu Thr Ala
        195                 200                 205

Trp Val Glu Ser Gly Ala Thr Leu Gly Glu Leu Tyr Tyr Ala Ile Ala
    210                 215                 220

Gln Ser Thr Asp Thr Leu Gly Phe Thr Ala Gly Trp Cys Pro Thr Val
225                 230                 235                 240
```

```
Gly Ser Gly Gly His Ile Ser Gly Gly Gly Phe Gly Met Met Ser Arg
                245                 250                 255

Lys Tyr Gly Leu Ala Ala Asp Asn Val Val Asp Ala Ile Leu Ile Asp
            260                 265                 270

Ser Asn Gly Ala Ile Leu Asp Arg Glu Lys Met Gly Asp Asp Val Phe
        275                 280                 285

Trp Ala Ile Arg Gly Gly Gly Gly Gly Val Trp Gly Ala Ile Tyr Ala
    290                 295                 300

Trp Lys Ile Lys Leu Leu Pro Val Pro Glu Lys Leu Thr Val Phe Arg
305                 310                 315                 320

Val Thr Lys Asn Val Gly Ile Glu Asp Ala Ser Ser Leu Leu His Lys
                325                 330                 335

Trp Gln Tyr Val Ala Asp Glu Leu Asp Glu Asp Phe Thr Val Ser Val
            340                 345                 350

Leu Gly Gly Val Asn Gly Asn Asp Ala Trp Leu Met Phe Leu Gly Leu
        355                 360                 365

His Leu Gly Arg Lys Asp Ala Ala Lys Thr Ile Ile Asp Glu Lys Phe
    370                 375                 380

Pro Glu Leu Gly Leu Val Asp Lys Glu Phe Gln Glu Met Ser Trp Gly
385                 390                 395                 400

Glu Ser Met Ala Phe Leu Ser Gly Leu Asp Thr Ile Ser Glu Leu Asn
                405                 410                 415

Asn Arg Phe Leu Lys Phe Asp Glu Arg Ala Phe Lys Thr Lys Val Asp
            420                 425                 430

Phe Thr Lys Val Ser Val Pro Leu Asn Val Phe Arg His Ala Leu Glu
        435                 440                 445
```

```
Met Leu Ser Glu Gln Pro Gly Gly Phe Ile Ala Leu Asn Gly Phe Gly
    450                 455                 460

Gly Lys Met Ser Glu Ile Ser Thr Asp Phe Thr Pro Phe Pro His Arg
465                 470                 475                 480

Lys Gly Thr Lys Leu Met Phe Glu Tyr Ile Ile Ala Trp Asn Gln Asp
                485                 490                 495

Glu Glu Ser Lys Ile Gly Glu Phe Ser Glu Trp Leu Ala Lys Phe Tyr
            500                 505                 510

Asp Tyr Leu Glu Pro Phe Val Ser Lys Glu Pro Arg Val Gly Tyr Val
        515                 520                 525

Asn His Ile Asp Leu Asp Ile Gly Gly Ile Asp Trp Arg Asn Lys Ser
    530                 535                 540

Ser Thr Thr Asn Ala Val Glu Ile Ala Arg Asn Trp Gly Glu Arg Tyr
545                 550                 555                 560

Phe Ser Ser Asn Tyr Glu Arg Leu Val Lys Ala Lys Thr Leu Ile Asp
                565                 570                 575

Pro Asn Asn Val Phe Asn His Pro Gln Ser Ile Pro Pro Met Met Lys
            580                 585                 590

Phe Glu Glu Ile Tyr Met Leu Lys Glu Leu Trp Ser His Pro Gln Phe
        595                 600                 605

Glu Lys
    610
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<210>  56
<211>  1611
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS86-A0A1U8G0D2

<220>

<221> CDS
<222> (1)..(1611)

<400> 56
atg atg ggt tcc ttg caa atc ttg ttc gtc ttg ttg ttc tcc ctg gtt 48
Met Met Gly Ser Leu Gln Ile Leu Phe Val Leu Leu Phe Ser Leu Val
1 5 10 15

ttg att aag tgc tac tct caa gag gat ttc ttg gag tgt ttg tcc aag 96
Leu Ile Lys Cys Tyr Ser Gln Glu Asp Phe Leu Glu Cys Leu Ser Lys
20 25 30

tac tct aag tcc aac gtt gaa caa aac gtt tac act cca act tct cca 144
Tyr Ser Lys Ser Asn Val Glu Gln Asn Val Tyr Thr Pro Thr Ser Pro
35 40 45

acc tac tcc tct att ttg gaa tac gct caa aag aac cca aga tgg gtt 192
Thr Tyr Ser Ser Ile Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Val
50 55 60

aat tct tct cac cca aac ttt att gcc tcg cca aga aaa gaa tct gac 240
Asn Ser Ser His Pro Asn Phe Ile Ala Ser Pro Arg Lys Glu Ser Asp
65 70 75 80

atc aag cca att atc ttg tgc gct aag aaa ttg ggc ttg cag att aag 288
Ile Lys Pro Ile Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys
85 90 95

att aag tcc ggt ggt cat gat tac gag ggt att tct tac aga tct aag 336
Ile Lys Ser Gly Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Lys
100 105 110

tcc cca ttc gtt atg ttg gac ttg tct aac ttg aac aag atc gag atc 384
Ser Pro Phe Val Met Leu Asp Leu Ser Asn Leu Asn Lys Ile Glu Ile
115 120 125

aac tgg aag aaa gaa acc gtt tgg gtt caa act ggt gct act ttg ggt 432
Asn Trp Lys Lys Glu Thr Val Trp Val Gln Thr Gly Ala Thr Leu Gly
130 135 140

caa ctg tat tat gct att gcc aac aag tct aac gtt cat ggt ttt cca 480
Gln Leu Tyr Tyr Ala Ile Ala Asn Lys Ser Asn Val His Gly Phe Pro
145 150 155 160

ggt ggt gtt tgt ttc tct att ggt act ggt ggt att att tct ggt ggt 528
Gly Gly Val Cys Phe Ser Ile Gly Thr Gly Gly Ile Ile Ser Gly Gly
165 170 175

ggt ata ggt act atg atg aga aaa ttt ggt gtt gcc gct gat aac gtt 576
Gly Ile Gly Thr Met Met Arg Lys Phe Gly Val Ala Ala Asp Asn Val
180 185 190

gtt gat gct aga gtt atg gat gtc aac ggt aag atc ttg gac aag aaa 624
Val Asp Ala Arg Val Met Asp Val Asn Gly Lys Ile Leu Asp Lys Lys

```
        195                 200                 205

aag atg aag gaa gat ttg ttc tgg gcc att aga ggt ggt ggt ggc gct        672
Lys Met Lys Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala
    210                 215                 220

tct ttt ggt gtt att ttg gct tgg aaa ttg aag ttg gtt agg gtt cca        720
Ser Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro
225                 230                 235                 240

gaa aag gtc act gtt ttt aac gtc tac aaa aag ttg gaa ggc aac cag        768
Glu Lys Val Thr Val Phe Asn Val Tyr Lys Lys Leu Glu Gly Asn Gln
                245                 250                 255

aac ttg ttg caa aag tgg gaa aac att gct cat caa ttg acc gac aag        816
Asn Leu Leu Gln Lys Trp Glu Asn Ile Ala His Gln Leu Thr Asp Lys
            260                 265                 270

ttg ttg atc aga gtc atc att caa aac gac ggt act ggt aag gat aag        864
Leu Leu Ile Arg Val Ile Ile Gln Asn Asp Gly Thr Gly Lys Asp Lys
        275                 280                 285

tac atc gaa gtt atc ttc caa gcc ttg ttc ttg ggt tta gtt gat gaa        912
Tyr Ile Glu Val Ile Phe Gln Ala Leu Phe Leu Gly Leu Val Asp Glu
    290                 295                 300

ttg atc ccc ttg ctg aaa gaa aag ttc cca gaa ttc gat ttg gaa aag        960
Leu Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys
305                 310                 315                 320

aag gac tgt ttc caa gaa cca gtt gtt gac tgt tct aac aga cca tgc       1008
Lys Asp Cys Phe Gln Glu Pro Val Val Asp Cys Ser Asn Arg Pro Cys
                325                 330                 335

att aag aaa gaa tgc aga gaa act acc tgg atc ggt tct gtt ttg ttt       1056
Ile Lys Lys Glu Cys Arg Glu Thr Thr Trp Ile Gly Ser Val Leu Phe
            340                 345                 350

ttc tac ggt aga agg acc aac gaa tcc ttg gaa gtt ttg ttg gat aag       1104
Phe Tyr Gly Arg Arg Thr Asn Glu Ser Leu Glu Val Leu Leu Asp Lys
        355                 360                 365

tcc att cca acg cag aag aac tac aac aaa ggt act tct gat ttc gtc       1152
Ser Ile Pro Thr Gln Lys Asn Tyr Asn Lys Gly Thr Ser Asp Phe Val
    370                 375                 380

aag acc cca att cca gaa tct ggt tgg aaa atg gtt caa agg ttg ttc       1200
Lys Thr Pro Ile Pro Glu Ser Gly Trp Lys Met Val Gln Arg Leu Phe
385                 390                 395                 400

tta gaa gag gaa cgt cca caa atg atc ttg gaa cca tta ggt ggt aag       1248
Leu Glu Glu Glu Arg Pro Gln Met Ile Leu Glu Pro Leu Gly Gly Lys
                405                 410                 415
```

```
ttg gac gaa atc tcc aaa tcc gaa att tca ttc cca cac aga aag ggc       1296
Leu Asp Glu Ile Ser Lys Ser Glu Ile Ser Phe Pro His Arg Lys Gly
            420                 425                 430

aac ttg tac aac att caa tac ttg gtt aac tgg ggt gac aac tcc gaa       1344
Asn Leu Tyr Asn Ile Gln Tyr Leu Val Asn Trp Gly Asp Asn Ser Glu
        435                 440                 445

aat gtt tcc tct caa aaa ttg gcc tgg atg cgt aag ttg tac aaa gat       1392
Asn Val Ser Ser Gln Lys Leu Ala Trp Met Arg Lys Leu Tyr Lys Asp
    450                 455                 460

atg gaa cca tac gtt gcc aac tct cca aga act gct tat ttg aac tac       1440
Met Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr
465                 470                 475                 480

aga gat ttg gac ttc ggt tcc aat gat gaa ggt tac tct tac tcc aaa       1488
Arg Asp Leu Asp Phe Gly Ser Asn Asp Glu Gly Tyr Ser Tyr Ser Lys
                485                 490                 495

gct aag att tgg ggt gaa aag tac ttc aac ggc aac ttt aag aga ttg       1536
Ala Lys Ile Trp Gly Glu Lys Tyr Phe Asn Gly Asn Phe Lys Arg Leu
            500                 505                 510

gcc aag gtt aag tct aag gtc gat cca aac aat ttc ttc aga aac gaa       1584
Ala Lys Val Lys Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Asn Glu
        515                 520                 525

caa tcg atc cca cca tat caa tcc cat                                  1611
Gln Ser Ile Pro Pro Tyr Gln Ser His
    530                 535
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<210> 57
<211> 537
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 57

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Met Met Gly Ser Leu Gln Ile Leu Phe Val Leu Leu Phe Ser Leu Val
1               5                   10                  15


Leu Ile Lys Cys Tyr Ser Gln Glu Asp Phe Leu Glu Cys Leu Ser Lys
            20                  25                  30


Tyr Ser Lys Ser Asn Val Glu Gln Asn Val Tyr Thr Pro Thr Ser Pro
        35                  40                  45
```

```
Thr Tyr Ser Ser Ile Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Val
    50                  55                  60

Asn Ser Ser His Pro Asn Phe Ile Ala Ser Pro Arg Lys Glu Ser Asp
65                  70                  75                  80

Ile Lys Pro Ile Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys
                85                  90                  95

Ile Lys Ser Gly Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Lys
            100                 105                 110

Ser Pro Phe Val Met Leu Asp Leu Ser Asn Leu Asn Lys Ile Glu Ile
        115                 120                 125

Asn Trp Lys Lys Glu Thr Val Trp Val Gln Thr Gly Ala Thr Leu Gly
    130                 135                 140

Gln Leu Tyr Tyr Ala Ile Ala Asn Lys Ser Asn Val His Gly Phe Pro
145                 150                 155                 160

Gly Gly Val Cys Phe Ser Ile Gly Thr Gly Gly Ile Ile Ser Gly Gly
                165                 170                 175

Gly Ile Gly Thr Met Met Arg Lys Phe Gly Val Ala Ala Asp Asn Val
            180                 185                 190

Val Asp Ala Arg Val Met Asp Val Asn Gly Lys Ile Leu Asp Lys Lys
        195                 200                 205

Lys Met Lys Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala
    210                 215                 220

Ser Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro
225                 230                 235                 240

Glu Lys Val Thr Val Phe Asn Val Tyr Lys Lys Leu Glu Gly Asn Gln
                245                 250                 255

Asn Leu Leu Gln Lys Trp Glu Asn Ile Ala His Gln Leu Thr Asp Lys
```

```
            260                 265                 270

Leu Leu Ile Arg Val Ile Ile Gln Asn Asp Gly Thr Gly Lys Asp Lys
        275                 280                 285

Tyr Ile Glu Val Ile Phe Gln Ala Leu Phe Leu Gly Leu Val Asp Glu
    290                 295                 300

Leu Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys
305                 310                 315                 320

Lys Asp Cys Phe Gln Glu Pro Val Val Asp Cys Ser Asn Arg Pro Cys
                325                 330                 335

Ile Lys Lys Glu Cys Arg Glu Thr Thr Trp Ile Gly Ser Val Leu Phe
            340                 345                 350

Phe Tyr Gly Arg Arg Thr Asn Glu Ser Leu Glu Val Leu Leu Asp Lys
        355                 360                 365

Ser Ile Pro Thr Gln Lys Asn Tyr Asn Lys Gly Thr Ser Asp Phe Val
    370                 375                 380

Lys Thr Pro Ile Pro Glu Ser Gly Trp Lys Met Val Gln Arg Leu Phe
385                 390                 395                 400

Leu Glu Glu Glu Arg Pro Gln Met Ile Leu Glu Pro Leu Gly Gly Lys
                405                 410                 415

Leu Asp Glu Ile Ser Lys Ser Glu Ile Ser Phe Pro His Arg Lys Gly
            420                 425                 430

Asn Leu Tyr Asn Ile Gln Tyr Leu Val Asn Trp Gly Asp Asn Ser Glu
        435                 440                 445

Asn Val Ser Ser Gln Lys Leu Ala Trp Met Arg Lys Leu Tyr Lys Asp
    450                 455                 460

Met Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr
465                 470                 475                 480
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```
Arg Asp Leu Asp Phe Gly Ser Asn Asp Glu Gly Tyr Ser Tyr Ser Lys
                485                 490                 495

Ala Lys Ile Trp Gly Glu Lys Tyr Phe Asn Gly Asn Phe Lys Arg Leu
            500                 505                 510

Ala Lys Val Lys Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Asn Glu
        515                 520                 525

Gln Ser Ile Pro Pro Tyr Gln Ser His
    530                 535
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<210> 58
<211> 1551
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS86-A0A1U8G0D2-no signal peptide

<220>
<221> CDS
<222> (1)..(1551)

<400> 58

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atg tct caa gag gat ttc ttg gag tgt ttg tcc aag tac tct aag tcc         48
Met Ser Gln Glu Asp Phe Leu Glu Cys Leu Ser Lys Tyr Ser Lys Ser
1               5                   10                  15

aac gtt gaa caa aac gtt tac act cca act tct cca acc tac tcc tct         96
Asn Val Glu Gln Asn Val Tyr Thr Pro Thr Ser Pro Thr Tyr Ser Ser
            20                  25                  30

att ttg gaa tac gct caa aag aac cca aga tgg gtt aat tct tct cac        144
Ile Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Val Asn Ser Ser His
        35                  40                  45

cca aac ttt att gcc tcg cca aga aaa gaa tct gac atc aag cca att        192
Pro Asn Phe Ile Ala Ser Pro Arg Lys Glu Ser Asp Ile Lys Pro Ile
    50                  55                  60

atc ttg tgc gct aag aaa ttg ggc ttg cag att aag att aag tcc ggt        240
Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile Lys Ser Gly
65                  70                  75                  80

ggt cat gat tac gag ggt att tct tac aga tct aag tcc cca ttc gtt        288
Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Lys Ser Pro Phe Val
                85                  90                  95
```

```
atg ttg gac ttg tct aac ttg aac aag atc gag atc aac tgg aag aaa        336
Met Leu Asp Leu Ser Asn Leu Asn Lys Ile Glu Ile Asn Trp Lys Lys
            100                 105                 110

gaa acc gtt tgg gtt caa act ggt gct act ttg ggt caa ctg tat tat        384
Glu Thr Val Trp Val Gln Thr Gly Ala Thr Leu Gly Gln Leu Tyr Tyr
        115                 120                 125

gct att gcc aac aag tct aac gtt cat ggt ttt cca ggt ggt gtt tgt        432
Ala Ile Ala Asn Lys Ser Asn Val His Gly Phe Pro Gly Gly Val Cys
    130                 135                 140

ttc tct att ggt act ggt ggt att att tct ggt ggt ggt ata ggt act        480
Phe Ser Ile Gly Thr Gly Gly Ile Ile Ser Gly Gly Gly Ile Gly Thr
145                 150                 155                 160

atg atg aga aaa ttt ggt gtt gcc gct gat aac gtt gtt gat gct aga        528
Met Met Arg Lys Phe Gly Val Ala Ala Asp Asn Val Val Asp Ala Arg
                165                 170                 175

gtt atg gat gtc aac ggt aag atc ttg gac aag aaa aag atg aag gaa        576
Val Met Asp Val Asn Gly Lys Ile Leu Asp Lys Lys Lys Met Lys Glu
            180                 185                 190

gat ttg ttc tgg gcc att aga ggt ggt ggt ggc gct tct ttt ggt gtt        624
Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Val
        195                 200                 205

att ttg gct tgg aaa ttg aag ttg gtt agg gtt cca gaa aag gtc act        672
Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu Lys Val Thr
    210                 215                 220

gtt ttt aac gtc tac aaa aag ttg gaa ggc aac cag aac ttg ttg caa        720
Val Phe Asn Val Tyr Lys Lys Leu Glu Gly Asn Gln Asn Leu Leu Gln
225                 230                 235                 240

aag tgg gaa aac att gct cat caa ttg acc gac aag ttg ttg atc aga        768
Lys Trp Glu Asn Ile Ala His Gln Leu Thr Asp Lys Leu Leu Ile Arg
                245                 250                 255

gtc atc att caa aac gac ggt act ggt aag gat aag tac atc gaa gtt        816
Val Ile Ile Gln Asn Asp Gly Thr Gly Lys Asp Lys Tyr Ile Glu Val
            260                 265                 270

atc ttc caa gcc ttg ttc ttg ggt tta gtt gat gaa ttg atc ccc ttg        864
Ile Phe Gln Ala Leu Phe Leu Gly Leu Val Asp Glu Leu Ile Pro Leu
        275                 280                 285

ctg aaa gaa aag ttc cca gaa ttc gat ttg gaa aag aag gac tgt ttc        912
Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys Asp Cys Phe
    290                 295                 300

caa gaa cca gtt gtt gac tgt tct aac aga cca tgc att aag aaa gaa        960
```

```
Gln Glu Pro Val Val Asp Cys Ser Asn Arg Pro Cys Ile Lys Lys Glu
305                 310                 315                 320

tgc aga gaa act acc tgg atc ggt tct gtt ttg ttt ttc tac ggt aga       1008
Cys Arg Glu Thr Thr Trp Ile Gly Ser Val Leu Phe Phe Tyr Gly Arg
                325                 330                 335

agg acc aac gaa tcc ttg gaa gtt ttg ttg gat aag tcc att cca acg       1056
Arg Thr Asn Glu Ser Leu Glu Val Leu Leu Asp Lys Ser Ile Pro Thr
            340                 345                 350

cag aag aac tac aac aaa ggt act tct gat ttc gtc aag acc cca att       1104
Gln Lys Asn Tyr Asn Lys Gly Thr Ser Asp Phe Val Lys Thr Pro Ile
        355                 360                 365

cca gaa tct ggt tgg aaa atg gtt caa agg ttg ttc tta gaa gag gaa       1152
Pro Glu Ser Gly Trp Lys Met Val Gln Arg Leu Phe Leu Glu Glu Glu
    370                 375                 380

cgt cca caa atg atc ttg gaa cca tta ggt ggt aag ttg gac gaa atc       1200
Arg Pro Gln Met Ile Leu Glu Pro Leu Gly Gly Lys Leu Asp Glu Ile
385                 390                 395                 400

tcc aaa tcc gaa att tca ttc cca cac aga aag ggc aac ttg tac aac       1248
Ser Lys Ser Glu Ile Ser Phe Pro His Arg Lys Gly Asn Leu Tyr Asn
                405                 410                 415

att caa tac ttg gtt aac tgg ggt gac aac tcc gaa aat gtt tcc tct       1296
Ile Gln Tyr Leu Val Asn Trp Gly Asp Asn Ser Glu Asn Val Ser Ser
            420                 425                 430

caa aaa ttg gcc tgg atg cgt aag ttg tac aaa gat atg gaa cca tac       1344
Gln Lys Leu Ala Trp Met Arg Lys Leu Tyr Lys Asp Met Glu Pro Tyr
        435                 440                 445

gtt gcc aac tct cca aga act gct tat ttg aac tac aga gat ttg gac       1392
Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg Asp Leu Asp
    450                 455                 460

ttc ggt tcc aat gat gaa ggt tac tct tac tcc aaa gct aag att tgg       1440
Phe Gly Ser Asn Asp Glu Gly Tyr Ser Tyr Ser Lys Ala Lys Ile Trp
465                 470                 475                 480

ggt gaa aag tac ttc aac ggc aac ttt aag aga ttg gcc aag gtt aag       1488
Gly Glu Lys Tyr Phe Asn Gly Asn Phe Lys Arg Leu Ala Lys Val Lys
                485                 490                 495

tct aag gtc gat cca aac aat ttc ttc aga aac gaa caa tcg atc cca       1536
Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro
            500                 505                 510

cca tat caa tcc cat                                                  1551
Pro Tyr Gln Ser His
        515
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<210> 59
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 59

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Met Ser Gln Glu Asp Phe Leu Glu Cys Leu Ser Lys Tyr Ser Lys Ser
1               5                  10                  15


Asn Val Glu Gln Asn Val Tyr Thr Pro Thr Ser Pro Thr Tyr Ser Ser
            20                  25                  30


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


Pro Asn Phe Ile Ala Ser Pro Arg Lys Glu Ser Asp Ile Lys Pro Ile
    50                  55                  60


Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile Lys Ser Gly
65                  70                  75                  80


Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Lys Ser Pro Phe Val
                85                  90                  95


Met Leu Asp Leu Ser Asn Leu Asn Lys Ile Glu Ile Asn Trp Lys Lys
            100                 105                 110


Glu Thr Val Trp Val Gln Thr Gly Ala Thr Leu Gly Gln Leu Tyr Tyr
        115                 120                 125


Ala Ile Ala Asn Lys Ser Asn Val His Gly Phe Pro Gly Gly Val Cys
    130                 135                 140


Phe Ser Ile Gly Thr Gly Gly Ile Ile Ser Gly Gly Gly Ile Gly Thr
145                 150                 155                 160


Met Met Arg Lys Phe Gly Val Ala Ala Asp Asn Val Val Asp Ala Arg
                165                 170                 175
```

```
Val Met Asp Val Asn Gly Lys Ile Leu Asp Lys Lys Lys Met Lys Glu
            180                 185                 190

Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Val
        195                 200                 205

Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu Lys Val Thr
    210                 215                 220

Val Phe Asn Val Tyr Lys Lys Leu Glu Gly Asn Gln Asn Leu Leu Gln
225                 230                 235                 240

Lys Trp Glu Asn Ile Ala His Gln Leu Thr Asp Lys Leu Leu Ile Arg
                245                 250                 255

Val Ile Ile Gln Asn Asp Gly Thr Gly Lys Asp Lys Tyr Ile Glu Val
            260                 265                 270

Ile Phe Gln Ala Leu Phe Leu Gly Leu Val Asp Glu Leu Ile Pro Leu
        275                 280                 285

Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys Asp Cys Phe
    290                 295                 300

Gln Glu Pro Val Val Asp Cys Ser Asn Arg Pro Cys Ile Lys Lys Glu
305                 310                 315                 320

Cys Arg Glu Thr Thr Trp Ile Gly Ser Val Leu Phe Phe Tyr Gly Arg
                325                 330                 335

Arg Thr Asn Glu Ser Leu Glu Val Leu Leu Asp Lys Ser Ile Pro Thr
            340                 345                 350

Gln Lys Asn Tyr Asn Lys Gly Thr Ser Asp Phe Val Lys Thr Pro Ile
        355                 360                 365

Pro Glu Ser Gly Trp Lys Met Val Gln Arg Leu Phe Leu Glu Glu Glu
    370                 375                 380
```

```
Arg Pro Gln Met Ile Leu Glu Pro Leu Gly Gly Lys Leu Asp Glu Ile
385                 390                 395                 400

Ser Lys Ser Glu Ile Ser Phe Pro His Arg Lys Gly Asn Leu Tyr Asn
                405                 410                 415

Ile Gln Tyr Leu Val Asn Trp Gly Asp Asn Ser Glu Asn Val Ser Ser
            420                 425                 430

Gln Lys Leu Ala Trp Met Arg Lys Leu Tyr Lys Asp Met Glu Pro Tyr
        435                 440                 445

Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg Asp Leu Asp
    450                 455                 460

Phe Gly Ser Asn Asp Glu Gly Tyr Ser Tyr Ser Lys Ala Lys Ile Trp
465                 470                 475                 480

Gly Glu Lys Tyr Phe Asn Gly Asn Phe Lys Arg Leu Ala Lys Val Lys
                485                 490                 495

Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro
            500                 505                 510

Pro Tyr Gln Ser His
        515


<210>  60
<211>  1575
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS86-A0A1U8G0D2-no signal peptide-strep Tag


<220>
<221>  CDS
<222>  (1)..(1575)

<400>  60
atg tct caa gag gat ttc ttg gag tgt ttg tcc aag tac tct aag tcc         48
Met Ser Gln Glu Asp Phe Leu Glu Cys Leu Ser Lys Tyr Ser Lys Ser
1               5                   10                  15
```

```
aac gtt gaa caa aac gtt tac act cca act tct cca acc tac tcc tct         96
Asn Val Glu Gln Asn Val Tyr Thr Pro Thr Ser Pro Thr Tyr Ser Ser
            20                  25                  30

att ttg gaa tac gct caa aag aac cca aga tgg gtt aat tct tct cac        144
Ile Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Val Asn Ser Ser His
        35                  40                  45

cca aac ttt att gcc tcg cca aga aaa gaa tct gac atc aag cca att        192
Pro Asn Phe Ile Ala Ser Pro Arg Lys Glu Ser Asp Ile Lys Pro Ile
    50                  55                  60

atc ttg tgc gct aag aaa ttg ggc ttg cag att aag att aag tcc ggt        240
Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile Lys Ser Gly
65                  70                  75                  80

ggt cat gat tac gag ggt att tct tac aga tct aag tcc cca ttc gtt        288
Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Lys Ser Pro Phe Val
                85                  90                  95

atg ttg gac ttg tct aac ttg aac aag atc gag atc aac tgg aag aaa        336
Met Leu Asp Leu Ser Asn Leu Asn Lys Ile Glu Ile Asn Trp Lys Lys
            100                 105                 110

gaa acc gtt tgg gtt caa act ggt gct act ttg ggt caa ctg tat tat        384
Glu Thr Val Trp Val Gln Thr Gly Ala Thr Leu Gly Gln Leu Tyr Tyr
        115                 120                 125

gct att gcc aac aag tct aac gtt cat ggt ttt cca ggt ggt gtt tgt        432
Ala Ile Ala Asn Lys Ser Asn Val His Gly Phe Pro Gly Gly Val Cys
    130                 135                 140

ttc tct att ggt act ggt ggt att att tct ggt ggt ggt ata ggt act        480
Phe Ser Ile Gly Thr Gly Gly Ile Ile Ser Gly Gly Gly Ile Gly Thr
145                 150                 155                 160

atg atg aga aaa ttt ggt gtt gcc gct gat aac gtt gtt gat gct aga        528
Met Met Arg Lys Phe Gly Val Ala Ala Asp Asn Val Val Asp Ala Arg
                165                 170                 175

gtt atg gat gtc aac ggt aag atc ttg gac aag aaa aag atg aag gaa        576
Val Met Asp Val Asn Gly Lys Ile Leu Asp Lys Lys Lys Met Lys Glu
            180                 185                 190

gat ttg ttc tgg gcc att aga ggt ggt ggt ggc gct tct ttt ggt gtt        624
Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Val
        195                 200                 205

att ttg gct tgg aaa ttg aag ttg gtt agg gtt cca gaa aag gtc act        672
Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu Lys Val Thr
    210                 215                 220

gtt ttt aac gtc tac aaa aag ttg gaa ggc aac cag aac ttg ttg caa        720
Val Phe Asn Val Tyr Lys Lys Leu Glu Gly Asn Gln Asn Leu Leu Gln
```

```
225                 230                 235                 240

aag tgg gaa aac att gct cat caa ttg acc gac aag ttg ttg atc aga        768
Lys Trp Glu Asn Ile Ala His Gln Leu Thr Asp Lys Leu Leu Ile Arg
                245                 250                 255

gtc atc att caa aac gac ggt act ggt aag gat aag tac atc gaa gtt        816
Val Ile Ile Gln Asn Asp Gly Thr Gly Lys Asp Lys Tyr Ile Glu Val
            260                 265                 270

atc ttc caa gcc ttg ttc ttg ggt tta gtt gat gaa ttg atc ccc ttg        864
Ile Phe Gln Ala Leu Phe Leu Gly Leu Val Asp Glu Leu Ile Pro Leu
        275                 280                 285

ctg aaa gaa aag ttc cca gaa ttc gat ttg gaa aag aag gac tgt ttc        912
Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys Asp Cys Phe
    290                 295                 300

caa gaa cca gtt gtt gac tgt tct aac aga cca tgc att aag aaa gaa        960
Gln Glu Pro Val Val Asp Cys Ser Asn Arg Pro Cys Ile Lys Lys Glu
305                 310                 315                 320

tgc aga gaa act acc tgg atc ggt tct gtt ttg ttt ttc tac ggt aga       1008
Cys Arg Glu Thr Thr Trp Ile Gly Ser Val Leu Phe Phe Tyr Gly Arg
                325                 330                 335

agg acc aac gaa tcc ttg gaa gtt ttg ttg gat aag tcc att cca acg       1056
Arg Thr Asn Glu Ser Leu Glu Val Leu Leu Asp Lys Ser Ile Pro Thr
            340                 345                 350

cag aag aac tac aac aaa ggt act tct gat ttc gtc aag acc cca att       1104
Gln Lys Asn Tyr Asn Lys Gly Thr Ser Asp Phe Val Lys Thr Pro Ile
        355                 360                 365

cca gaa tct ggt tgg aaa atg gtt caa agg ttg ttc tta gaa gag gaa       1152
Pro Glu Ser Gly Trp Lys Met Val Gln Arg Leu Phe Leu Glu Glu Glu
    370                 375                 380

cgt cca caa atg atc ttg gaa cca tta ggt ggt aag ttg gac gaa atc       1200
Arg Pro Gln Met Ile Leu Glu Pro Leu Gly Gly Lys Leu Asp Glu Ile
385                 390                 395                 400

tcc aaa tcc gaa att tca ttc cca cac aga aag ggc aac ttg tac aac       1248
Ser Lys Ser Glu Ile Ser Phe Pro His Arg Lys Gly Asn Leu Tyr Asn
                405                 410                 415

att caa tac ttg gtt aac tgg ggt gac aac tcc gaa aat gtt tcc tct       1296
Ile Gln Tyr Leu Val Asn Trp Gly Asp Asn Ser Glu Asn Val Ser Ser
            420                 425                 430

caa aaa ttg gcc tgg atg cgt aag ttg tac aaa gat atg gaa cca tac       1344
Gln Lys Leu Ala Trp Met Arg Lys Leu Tyr Lys Asp Met Glu Pro Tyr
        435                 440                 445
```

```
gtt gcc aac tct cca aga act gct tat ttg aac tac aga gat ttg gac       1392
Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg Asp Leu Asp
    450                 455                 460

ttc ggt tcc aat gat gaa ggt tac tct tac tcc aaa gct aag att tgg       1440
Phe Gly Ser Asn Asp Glu Gly Tyr Ser Tyr Ser Lys Ala Lys Ile Trp
465                 470                 475                 480

ggt gaa aag tac ttc aac ggc aac ttt aag aga ttg gcc aag gtt aag       1488
Gly Glu Lys Tyr Phe Asn Gly Asn Phe Lys Arg Leu Ala Lys Val Lys
                485                 490                 495

tct aag gtc gat cca aac aat ttc ttc aga aac gaa caa tcg atc cca       1536
Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro
            500                 505                 510

cca tat caa tcc cat tgg tca cat cca caa ttt gaa aag                  1575
Pro Tyr Gln Ser His Trp Ser His Pro Gln Phe Glu Lys
        515                 520                 525
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<210> 61
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 61

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Met Ser Gln Glu Asp Phe Leu Glu Cys Leu Ser Lys Tyr Ser Lys Ser
1               5                   10                  15


Asn Val Glu Gln Asn Val Tyr Thr Pro Thr Ser Pro Thr Tyr Ser Ser
            20                  25                  30


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


Pro Asn Phe Ile Ala Ser Pro Arg Lys Glu Ser Asp Ile Lys Pro Ile
    50                  55                  60


Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile Lys Ser Gly
65                  70                  75                  80


Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Lys Ser Pro Phe Val
                85                  90                  95
```

```
Met Leu Asp Leu Ser Asn Leu Asn Lys Ile Glu Ile Asn Trp Lys Lys
            100                 105                 110

Glu Thr Val Trp Val Gln Thr Gly Ala Thr Leu Gly Gln Leu Tyr Tyr
        115                 120                 125

Ala Ile Ala Asn Lys Ser Asn Val His Gly Phe Pro Gly Gly Val Cys
    130                 135                 140

Phe Ser Ile Gly Thr Gly Gly Ile Ile Ser Gly Gly Gly Ile Gly Thr
145                 150                 155                 160

Met Met Arg Lys Phe Gly Val Ala Ala Asp Asn Val Val Asp Ala Arg
                165                 170                 175

Val Met Asp Val Asn Gly Lys Ile Leu Asp Lys Lys Lys Met Lys Glu
            180                 185                 190

Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Val
        195                 200                 205

Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu Lys Val Thr
    210                 215                 220

Val Phe Asn Val Tyr Lys Lys Leu Glu Gly Asn Gln Asn Leu Leu Gln
225                 230                 235                 240

Lys Trp Glu Asn Ile Ala His Gln Leu Thr Asp Lys Leu Leu Ile Arg
                245                 250                 255

Val Ile Ile Gln Asn Asp Gly Thr Gly Lys Asp Lys Tyr Ile Glu Val
            260                 265                 270

Ile Phe Gln Ala Leu Phe Leu Gly Leu Val Asp Glu Leu Ile Pro Leu
        275                 280                 285

Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys Asp Cys Phe
    290                 295                 300

Gln Glu Pro Val Val Asp Cys Ser Asn Arg Pro Cys Ile Lys Lys Glu
```

```
305                 310                 315                 320

Cys Arg Glu Thr Thr Trp Ile Gly Ser Val Leu Phe Phe Tyr Gly Arg
                325                 330                 335

Arg Thr Asn Glu Ser Leu Glu Val Leu Leu Asp Lys Ser Ile Pro Thr
            340                 345                 350

Gln Lys Asn Tyr Asn Lys Gly Thr Ser Asp Phe Val Lys Thr Pro Ile
        355                 360                 365

Pro Glu Ser Gly Trp Lys Met Val Gln Arg Leu Phe Leu Glu Glu Glu
    370                 375                 380

Arg Pro Gln Met Ile Leu Glu Pro Leu Gly Gly Lys Leu Asp Glu Ile
385                 390                 395                 400

Ser Lys Ser Glu Ile Ser Phe Pro His Arg Lys Gly Asn Leu Tyr Asn
                405                 410                 415

Ile Gln Tyr Leu Val Asn Trp Gly Asp Asn Ser Glu Asn Val Ser Ser
            420                 425                 430

Gln Lys Leu Ala Trp Met Arg Lys Leu Tyr Lys Asp Met Glu Pro Tyr
        435                 440                 445

Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg Asp Leu Asp
    450                 455                 460

Phe Gly Ser Asn Asp Glu Gly Tyr Ser Tyr Ser Lys Ala Lys Ile Trp
465                 470                 475                 480

Gly Glu Lys Tyr Phe Asn Gly Asn Phe Lys Arg Leu Ala Lys Val Lys
                485                 490                 495

Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro
            500                 505                 510

Pro Tyr Gln Ser His Trp Ser His Pro Gln Phe Glu Lys
        515                 520                 525
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<210> 62
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS86-A0A1U8G0D2-truncated alpha factor -no signal peptide-strep Tag

<220>
<221> CDS
<222> (1)..(1632)

<400> 62
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atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca ctt gca atg tct caa gag gat ttc ttg gag tgt ttg tcc aag tac         96
Ala Leu Ala Met Ser Gln Glu Asp Phe Leu Glu Cys Leu Ser Lys Tyr
            20                  25                  30

tct aag tcc aac gtt gaa caa aac gtt tac act cca act tct cca acc        144
Ser Lys Ser Asn Val Glu Gln Asn Val Tyr Thr Pro Thr Ser Pro Thr
        35                  40                  45

tac tcc tct att ttg gaa tac gct caa aag aac cca aga tgg gtt aat        192
Tyr Ser Ser Ile Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Val Asn
    50                  55                  60

tct tct cac cca aac ttt att gcc tcg cca aga aaa gaa tct gac atc        240
Ser Ser His Pro Asn Phe Ile Ala Ser Pro Arg Lys Glu Ser Asp Ile
65                  70                  75                  80

aag cca att atc ttg tgc gct aag aaa ttg ggc ttg cag att aag att        288
Lys Pro Ile Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile
                85                  90                  95

aag tcc ggt ggt cat gat tac gag ggt att tct tac aga tct aag tcc        336
Lys Ser Gly Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Lys Ser
            100                 105                 110

cca ttc gtt atg ttg gac ttg tct aac ttg aac aag atc gag atc aac        384
Pro Phe Val Met Leu Asp Leu Ser Asn Leu Asn Lys Ile Glu Ile Asn
        115                 120                 125

tgg aag aaa gaa acc gtt tgg gtt caa act ggt gct act ttg ggt caa        432
Trp Lys Lys Glu Thr Val Trp Val Gln Thr Gly Ala Thr Leu Gly Gln
    130                 135                 140

ctg tat tat gct att gcc aac aag tct aac gtt cat ggt ttt cca ggt        480
Leu Tyr Tyr Ala Ile Ala Asn Lys Ser Asn Val His Gly Phe Pro Gly
```

```
145                 150                 155                 160

ggt gtt tgt ttc tct att ggt act ggt ggt att att tct ggt ggt ggt        528
Gly Val Cys Phe Ser Ile Gly Thr Gly Gly Ile Ile Ser Gly Gly Gly
                165                 170                 175

ata ggt act atg atg aga aaa ttt ggt gtt gcc gct gat aac gtt gtt        576
Ile Gly Thr Met Met Arg Lys Phe Gly Val Ala Ala Asp Asn Val Val
            180                 185                 190

gat gct aga gtt atg gat gtc aac ggt aag atc ttg gac aag aaa aag        624
Asp Ala Arg Val Met Asp Val Asn Gly Lys Ile Leu Asp Lys Lys Lys
        195                 200                 205

atg aag gaa gat ttg ttc tgg gcc att aga ggt ggt ggt ggc gct tct        672
Met Lys Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser
    210                 215                 220

ttt ggt gtt att ttg gct tgg aaa ttg aag ttg gtt agg gtt cca gaa        720
Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu
225                 230                 235                 240

aag gtc act gtt ttt aac gtc tac aaa aag ttg gaa ggc aac cag aac        768
Lys Val Thr Val Phe Asn Val Tyr Lys Lys Leu Glu Gly Asn Gln Asn
                245                 250                 255

ttg ttg caa aag tgg gaa aac att gct cat caa ttg acc gac aag ttg        816
Leu Leu Gln Lys Trp Glu Asn Ile Ala His Gln Leu Thr Asp Lys Leu
            260                 265                 270

ttg atc aga gtc atc att caa aac gac ggt act ggt aag gat aag tac        864
Leu Ile Arg Val Ile Ile Gln Asn Asp Gly Thr Gly Lys Asp Lys Tyr
        275                 280                 285

atc gaa gtt atc ttc caa gcc ttg ttc ttg ggt tta gtt gat gaa ttg        912
Ile Glu Val Ile Phe Gln Ala Leu Phe Leu Gly Leu Val Asp Glu Leu
    290                 295                 300

atc ccc ttg ctg aaa gaa aag ttc cca gaa ttc gat ttg gaa aag aag        960
Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys
305                 310                 315                 320

gac tgt ttc caa gaa cca gtt gtt gac tgt tct aac aga cca tgc att       1008
Asp Cys Phe Gln Glu Pro Val Val Asp Cys Ser Asn Arg Pro Cys Ile
                325                 330                 335

aag aaa gaa tgc aga gaa act acc tgg atc ggt tct gtt ttg ttt ttc       1056
Lys Lys Glu Cys Arg Glu Thr Thr Trp Ile Gly Ser Val Leu Phe Phe
            340                 345                 350

tac ggt aga agg acc aac gaa tcc ttg gaa gtt ttg ttg gat aag tcc       1104
Tyr Gly Arg Arg Thr Asn Glu Ser Leu Glu Val Leu Leu Asp Lys Ser
        355                 360                 365
```

```
att cca acg cag aag aac tac aac aaa ggt act tct gat ttc gtc aag       1152
Ile Pro Thr Gln Lys Asn Tyr Asn Lys Gly Thr Ser Asp Phe Val Lys
    370                 375                 380

acc cca att cca gaa tct ggt tgg aaa atg gtt caa agg ttg ttc tta       1200
Thr Pro Ile Pro Glu Ser Gly Trp Lys Met Val Gln Arg Leu Phe Leu
385                 390                 395                 400

gaa gag gaa cgt cca caa atg atc ttg gaa cca tta ggt ggt aag ttg       1248
Glu Glu Glu Arg Pro Gln Met Ile Leu Glu Pro Leu Gly Gly Lys Leu
                405                 410                 415

gac gaa atc tcc aaa tcc gaa att tca ttc cca cac aga aag ggc aac       1296
Asp Glu Ile Ser Lys Ser Glu Ile Ser Phe Pro His Arg Lys Gly Asn
            420                 425                 430

ttg tac aac att caa tac ttg gtt aac tgg ggt gac aac tcc gaa aat       1344
Leu Tyr Asn Ile Gln Tyr Leu Val Asn Trp Gly Asp Asn Ser Glu Asn
        435                 440                 445

gtt tcc tct caa aaa ttg gcc tgg atg cgt aag ttg tac aaa gat atg       1392
Val Ser Ser Gln Lys Leu Ala Trp Met Arg Lys Leu Tyr Lys Asp Met
    450                 455                 460

gaa cca tac gtt gcc aac tct cca aga act gct tat ttg aac tac aga       1440
Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg
465                 470                 475                 480

gat ttg gac ttc ggt tcc aat gat gaa ggt tac tct tac tcc aaa gct       1488
Asp Leu Asp Phe Gly Ser Asn Asp Glu Gly Tyr Ser Tyr Ser Lys Ala
                485                 490                 495

aag att tgg ggt gaa aag tac ttc aac ggc aac ttt aag aga ttg gcc       1536
Lys Ile Trp Gly Glu Lys Tyr Phe Asn Gly Asn Phe Lys Arg Leu Ala
            500                 505                 510

aag gtt aag tct aag gtc gat cca aac aat ttc ttc aga aac gaa caa       1584
Lys Val Lys Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Asn Glu Gln
        515                 520                 525

tcg atc cca cca tat caa tcc cat tgg tca cat cca caa ttt gaa aag       1632
Ser Ile Pro Pro Tyr Gln Ser His Trp Ser His Pro Gln Phe Glu Lys
    530                 535                 540
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<210>  63
<211>  544
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  63

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

Ala Leu Ala Met Ser Gln Glu Asp Phe Leu Glu Cys Leu Ser Lys Tyr
            20                  25                  30

Ser Lys Ser Asn Val Glu Gln Asn Val Tyr Thr Pro Thr Ser Pro Thr
        35                  40                  45

Tyr Ser Ser Ile Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Val Asn
    50                  55                  60

Ser Ser His Pro Asn Phe Ile Ala Ser Pro Arg Lys Glu Ser Asp Ile
65                  70                  75                  80

Lys Pro Ile Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile
                85                  90                  95

Lys Ser Gly Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Lys Ser
            100                 105                 110

Pro Phe Val Met Leu Asp Leu Ser Asn Leu Asn Lys Ile Glu Ile Asn
        115                 120                 125

Trp Lys Lys Glu Thr Val Trp Val Gln Thr Gly Ala Thr Leu Gly Gln
    130                 135                 140

Leu Tyr Tyr Ala Ile Ala Asn Lys Ser Asn Val His Gly Phe Pro Gly
145                 150                 155                 160

Gly Val Cys Phe Ser Ile Gly Thr Gly Gly Ile Ile Ser Gly Gly Gly
                165                 170                 175

Ile Gly Thr Met Met Arg Lys Phe Gly Val Ala Ala Asp Asn Val Val
            180                 185                 190

Asp Ala Arg Val Met Asp Val Asn Gly Lys Ile Leu Asp Lys Lys Lys
        195                 200                 205

Met Lys Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser
```

```
    210                 215                 220

Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu
225                 230                 235                 240

Lys Val Thr Val Phe Asn Val Tyr Lys Lys Leu Glu Gly Asn Gln Asn
                245                 250                 255

Leu Leu Gln Lys Trp Glu Asn Ile Ala His Gln Leu Thr Asp Lys Leu
            260                 265                 270

Leu Ile Arg Val Ile Ile Gln Asn Asp Gly Thr Gly Lys Asp Lys Tyr
        275                 280                 285

Ile Glu Val Ile Phe Gln Ala Leu Phe Leu Gly Leu Val Asp Glu Leu
    290                 295                 300

Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys
305                 310                 315                 320

Asp Cys Phe Gln Glu Pro Val Val Asp Cys Ser Asn Arg Pro Cys Ile
                325                 330                 335

Lys Lys Glu Cys Arg Glu Thr Thr Trp Ile Gly Ser Val Leu Phe Phe
            340                 345                 350

Tyr Gly Arg Arg Thr Asn Glu Ser Leu Glu Val Leu Leu Asp Lys Ser
        355                 360                 365

Ile Pro Thr Gln Lys Asn Tyr Asn Lys Gly Thr Ser Asp Phe Val Lys
    370                 375                 380

Thr Pro Ile Pro Glu Ser Gly Trp Lys Met Val Gln Arg Leu Phe Leu
385                 390                 395                 400

Glu Glu Glu Arg Pro Gln Met Ile Leu Glu Pro Leu Gly Gly Lys Leu
                405                 410                 415

Asp Glu Ile Ser Lys Ser Glu Ile Ser Phe Pro His Arg Lys Gly Asn
            420                 425                 430
```

```
Leu Tyr Asn Ile Gln Tyr Leu Val Asn Trp Gly Asp Asn Ser Glu Asn
        435                 440                 445

Val Ser Ser Gln Lys Leu Ala Trp Met Arg Lys Leu Tyr Lys Asp Met
    450                 455                 460

Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg
465                 470                 475                 480

Asp Leu Asp Phe Gly Ser Asn Asp Glu Gly Tyr Ser Tyr Ser Lys Ala
                485                 490                 495

Lys Ile Trp Gly Glu Lys Tyr Phe Asn Gly Asn Phe Lys Arg Leu Ala
            500                 505                 510

Lys Val Lys Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Asn Glu Gln
        515                 520                 525

Ser Ile Pro Pro Tyr Gln Ser His Trp Ser His Pro Gln Phe Glu Lys
    530                 535                 540
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<210> 64
<211> 1842
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS86-A0A1U8G0D2-full alpha factor -no signal peptide-strep Tag

<220>
<221> CDS
<222> (1)..(1842)

<400> 64

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atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45
```

```
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg tct caa gag gat ttc ttg        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ser Gln Glu Asp Phe Leu
                85                  90                  95

gag tgt ttg tcc aag tac tct aag tcc aac gtt gaa caa aac gtt tac        336
Glu Cys Leu Ser Lys Tyr Ser Lys Ser Asn Val Glu Gln Asn Val Tyr
            100                 105                 110

act cca act tct cca acc tac tcc tct att ttg gaa tac gct caa aag        384
Thr Pro Thr Ser Pro Thr Tyr Ser Ser Ile Leu Glu Tyr Ala Gln Lys
        115                 120                 125

aac cca aga tgg gtt aat tct tct cac cca aac ttt att gcc tcg cca        432
Asn Pro Arg Trp Val Asn Ser Ser His Pro Asn Phe Ile Ala Ser Pro
    130                 135                 140

aga aaa gaa tct gac atc aag cca att atc ttg tgc gct aag aaa ttg        480
Arg Lys Glu Ser Asp Ile Lys Pro Ile Ile Leu Cys Ala Lys Lys Leu
145                 150                 155                 160

ggc ttg cag att aag att aag tcc ggt ggt cat gat tac gag ggt att        528
Gly Leu Gln Ile Lys Ile Lys Ser Gly Gly His Asp Tyr Glu Gly Ile
                165                 170                 175

tct tac aga tct aag tcc cca ttc gtt atg ttg gac ttg tct aac ttg        576
Ser Tyr Arg Ser Lys Ser Pro Phe Val Met Leu Asp Leu Ser Asn Leu
            180                 185                 190

aac aag atc gag atc aac tgg aag aaa gaa acc gtt tgg gtt caa act        624
Asn Lys Ile Glu Ile Asn Trp Lys Lys Glu Thr Val Trp Val Gln Thr
        195                 200                 205

ggt gct act ttg ggt caa ctg tat tat gct att gcc aac aag tct aac        672
Gly Ala Thr Leu Gly Gln Leu Tyr Tyr Ala Ile Ala Asn Lys Ser Asn
    210                 215                 220

gtt cat ggt ttt cca ggt ggt gtt tgt ttc tct att ggt act ggt ggt        720
Val His Gly Phe Pro Gly Gly Val Cys Phe Ser Ile Gly Thr Gly Gly
225                 230                 235                 240

att att tct ggt ggt ggt ata ggt act atg atg aga aaa ttt ggt gtt        768
Ile Ile Ser Gly Gly Gly Ile Gly Thr Met Met Arg Lys Phe Gly Val
                245                 250                 255

gcc gct gat aac gtt gtt gat gct aga gtt atg gat gtc aac ggt aag        816
```

```
Ala Ala Asp Asn Val Val Asp Ala Arg Val Met Asp Val Asn Gly Lys
            260                 265                 270

atc ttg gac aag aaa aag atg aag gaa gat ttg ttc tgg gcc att aga        864
Ile Leu Asp Lys Lys Lys Met Lys Glu Asp Leu Phe Trp Ala Ile Arg
        275                 280                 285

ggt ggt ggt ggc gct tct ttt ggt gtt att ttg gct tgg aaa ttg aag        912
Gly Gly Gly Gly Ala Ser Phe Gly Val Ile Leu Ala Trp Lys Leu Lys
    290                 295                 300

ttg gtt agg gtt cca gaa aag gtc act gtt ttt aac gtc tac aaa aag        960
Leu Val Arg Val Pro Glu Lys Val Thr Val Phe Asn Val Tyr Lys Lys
305                 310                 315                 320

ttg gaa ggc aac cag aac ttg ttg caa aag tgg gaa aac att gct cat       1008
Leu Glu Gly Asn Gln Asn Leu Leu Gln Lys Trp Glu Asn Ile Ala His
                325                 330                 335

caa ttg acc gac aag ttg ttg atc aga gtc atc att caa aac gac ggt       1056
Gln Leu Thr Asp Lys Leu Leu Ile Arg Val Ile Ile Gln Asn Asp Gly
            340                 345                 350

act ggt aag gat aag tac atc gaa gtt atc ttc caa gcc ttg ttc ttg       1104
Thr Gly Lys Asp Lys Tyr Ile Glu Val Ile Phe Gln Ala Leu Phe Leu
        355                 360                 365

ggt tta gtt gat gaa ttg atc ccc ttg ctg aaa gaa aag ttc cca gaa       1152
Gly Leu Val Asp Glu Leu Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu
    370                 375                 380

ttc gat ttg gaa aag aag gac tgt ttc caa gaa cca gtt gtt gac tgt       1200
Phe Asp Leu Glu Lys Lys Asp Cys Phe Gln Glu Pro Val Val Asp Cys
385                 390                 395                 400

tct aac aga cca tgc att aag aaa gaa tgc aga gaa act acc tgg atc       1248
Ser Asn Arg Pro Cys Ile Lys Lys Glu Cys Arg Glu Thr Thr Trp Ile
                405                 410                 415

ggt tct gtt ttg ttt ttc tac ggt aga agg acc aac gaa tcc ttg gaa       1296
Gly Ser Val Leu Phe Phe Tyr Gly Arg Arg Thr Asn Glu Ser Leu Glu
            420                 425                 430

gtt ttg ttg gat aag tcc att cca acg cag aag aac tac aac aaa ggt       1344
Val Leu Leu Asp Lys Ser Ile Pro Thr Gln Lys Asn Tyr Asn Lys Gly
        435                 440                 445

act tct gat ttc gtc aag acc cca att cca gaa tct ggt tgg aaa atg       1392
Thr Ser Asp Phe Val Lys Thr Pro Ile Pro Glu Ser Gly Trp Lys Met
    450                 455                 460

gtt caa agg ttg ttc tta gaa gag gaa cgt cca caa atg atc ttg gaa       1440
Val Gln Arg Leu Phe Leu Glu Glu Glu Arg Pro Gln Met Ile Leu Glu
465                 470                 475                 480
```

```
cca tta ggt ggt aag ttg gac gaa atc tcc aaa tcc gaa att tca ttc       1488
Pro Leu Gly Gly Lys Leu Asp Glu Ile Ser Lys Ser Glu Ile Ser Phe
                485                 490                 495

cca cac aga aag ggc aac ttg tac aac att caa tac ttg gtt aac tgg       1536
Pro His Arg Lys Gly Asn Leu Tyr Asn Ile Gln Tyr Leu Val Asn Trp
            500                 505                 510

ggt gac aac tcc gaa aat gtt tcc tct caa aaa ttg gcc tgg atg cgt       1584
Gly Asp Asn Ser Glu Asn Val Ser Ser Gln Lys Leu Ala Trp Met Arg
        515                 520                 525

aag ttg tac aaa gat atg gaa cca tac gtt gcc aac tct cca aga act       1632
Lys Leu Tyr Lys Asp Met Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr
    530                 535                 540

gct tat ttg aac tac aga gat ttg gac ttc ggt tcc aat gat gaa ggt       1680
Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Phe Gly Ser Asn Asp Glu Gly
545                 550                 555                 560

tac tct tac tcc aaa gct aag att tgg ggt gaa aag tac ttc aac ggc       1728
Tyr Ser Tyr Ser Lys Ala Lys Ile Trp Gly Glu Lys Tyr Phe Asn Gly
                565                 570                 575

aac ttt aag aga ttg gcc aag gtt aag tct aag gtc gat cca aac aat       1776
Asn Phe Lys Arg Leu Ala Lys Val Lys Ser Lys Val Asp Pro Asn Asn
            580                 585                 590

ttc ttc aga aac gaa caa tcg atc cca cca tat caa tcc cat tgg tca       1824
Phe Phe Arg Asn Glu Gln Ser Ile Pro Pro Tyr Gln Ser His Trp Ser
        595                 600                 605

cat cca caa ttt gaa aag                                              1842
His Pro Gln Phe Glu Lys
    610
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<210> 65
<211> 614
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 65

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


Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30
```

```
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

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

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ser Gln Glu Asp Phe Leu
                85                  90                  95

Glu Cys Leu Ser Lys Tyr Ser Lys Ser Asn Val Glu Gln Asn Val Tyr
            100                 105                 110

Thr Pro Thr Ser Pro Thr Tyr Ser Ser Ile Leu Glu Tyr Ala Gln Lys
        115                 120                 125

Asn Pro Arg Trp Val Asn Ser Ser His Pro Asn Phe Ile Ala Ser Pro
    130                 135                 140

Arg Lys Glu Ser Asp Ile Lys Pro Ile Ile Leu Cys Ala Lys Lys Leu
145                 150                 155                 160

Gly Leu Gln Ile Lys Ile Lys Ser Gly Gly His Asp Tyr Glu Gly Ile
                165                 170                 175

Ser Tyr Arg Ser Lys Ser Pro Phe Val Met Leu Asp Leu Ser Asn Leu
            180                 185                 190

Asn Lys Ile Glu Ile Asn Trp Lys Lys Glu Thr Val Trp Val Gln Thr
        195                 200                 205

Gly Ala Thr Leu Gly Gln Leu Tyr Tyr Ala Ile Ala Asn Lys Ser Asn
    210                 215                 220

Val His Gly Phe Pro Gly Gly Val Cys Phe Ser Ile Gly Thr Gly Gly
225                 230                 235                 240
```

```
Ile Ile Ser Gly Gly Gly Ile Gly Thr Met Met Arg Lys Phe Gly Val
                245                 250                 255

Ala Ala Asp Asn Val Val Asp Ala Arg Val Met Asp Val Asn Gly Lys
            260                 265                 270

Ile Leu Asp Lys Lys Lys Met Lys Glu Asp Leu Phe Trp Ala Ile Arg
        275                 280                 285

Gly Gly Gly Gly Ala Ser Phe Gly Val Ile Leu Ala Trp Lys Leu Lys
    290                 295                 300

Leu Val Arg Val Pro Glu Lys Val Thr Val Phe Asn Val Tyr Lys Lys
305                 310                 315                 320

Leu Glu Gly Asn Gln Asn Leu Leu Gln Lys Trp Glu Asn Ile Ala His
                325                 330                 335

Gln Leu Thr Asp Lys Leu Leu Ile Arg Val Ile Ile Gln Asn Asp Gly
            340                 345                 350

Thr Gly Lys Asp Lys Tyr Ile Glu Val Ile Phe Gln Ala Leu Phe Leu
        355                 360                 365

Gly Leu Val Asp Glu Leu Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu
    370                 375                 380

Phe Asp Leu Glu Lys Lys Asp Cys Phe Gln Glu Pro Val Val Asp Cys
385                 390                 395                 400

Ser Asn Arg Pro Cys Ile Lys Lys Glu Cys Arg Glu Thr Thr Trp Ile
                405                 410                 415

Gly Ser Val Leu Phe Phe Tyr Gly Arg Arg Thr Asn Glu Ser Leu Glu
            420                 425                 430

Val Leu Leu Asp Lys Ser Ile Pro Thr Gln Lys Asn Tyr Asn Lys Gly
        435                 440                 445

Thr Ser Asp Phe Val Lys Thr Pro Ile Pro Glu Ser Gly Trp Lys Met
    450                 455                 460
```

```
Val Gln Arg Leu Phe Leu Glu Glu Glu Arg Pro Gln Met Ile Leu Glu
465                 470                 475                 480


Pro Leu Gly Gly Lys Leu Asp Glu Ile Ser Lys Ser Glu Ile Ser Phe
                485                 490                 495


Pro His Arg Lys Gly Asn Leu Tyr Asn Ile Gln Tyr Leu Val Asn Trp
            500                 505                 510


Gly Asp Asn Ser Glu Asn Val Ser Ser Gln Lys Leu Ala Trp Met Arg
        515                 520                 525


Lys Leu Tyr Lys Asp Met Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr
    530                 535                 540


Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Phe Gly Ser Asn Asp Glu Gly
545                 550                 555                 560


Tyr Ser Tyr Ser Lys Ala Lys Ile Trp Gly Glu Lys Tyr Phe Asn Gly
                565                 570                 575


Asn Phe Lys Arg Leu Ala Lys Val Lys Ser Lys Val Asp Pro Asn Asn
            580                 585                 590


Phe Phe Arg Asn Glu Gln Ser Ile Pro Pro Tyr Gln Ser His Trp Ser
        595                 600                 605


His Pro Gln Phe Glu Lys
    610


<210>  66
<211>  1629
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS94-A0A1S3XA06


<220>
<221>  CDS
<222>  (1)..(1629)
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<400> 66

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atg ggt aga ttg cag ttg ttc tct tgc ttg ttg gtt tcc ttc ttg ttg         48
Met Gly Arg Leu Gln Leu Phe Ser Cys Leu Leu Val Ser Phe Leu Leu
1               5                  10                  15

ttg att gaa gct aac gcc caa caa gag ttc ttg caa tgt atc tac tct         96
Leu Ile Glu Ala Asn Ala Gln Gln Glu Phe Leu Gln Cys Ile Tyr Ser
            20                  25                  30

cac tcc tcc gag aat att aag aag cac att cat ttc cca aac agc cca        144
His Ser Ser Glu Asn Ile Lys Lys His Ile His Phe Pro Asn Ser Pro
        35                  40                  45

act tac tct tcg ttg ttg gaa tac gct caa aag aat cca aga tgg ctg        192
Thr Tyr Ser Ser Leu Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Leu
    50                  55                  60

aat tct tct ttc gcc cat cca att ttc att atc gct cca aag aac gaa        240
Asn Ser Ser Phe Ala His Pro Ile Phe Ile Ile Ala Pro Lys Asn Glu
65                  70                  75                  80

tcc gaa atc cag cca att atc ttg tgc tct caa aag ttc ggc ttg caa        288
Ser Glu Ile Gln Pro Ile Ile Leu Cys Ser Gln Lys Phe Gly Leu Gln
                85                  90                  95

atc aga gtt aag tct ggt ggt cat gat tac gaa ggt ttg tct ttc aga        336
Ile Arg Val Lys Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Phe Arg
            100                 105                 110

tct gtc act aac acc caa ttc gtt atc ttg gac ttg atc aac ttg gac        384
Ser Val Thr Asn Thr Gln Phe Val Ile Leu Asp Leu Ile Asn Leu Asp
        115                 120                 125

gat atc aga atc gac aag aac gaa gaa act gct tgg att caa act ggt        432
Asp Ile Arg Ile Asp Lys Asn Glu Glu Thr Ala Trp Ile Gln Thr Gly
    130                 135                 140

gtt act atg ggt cag ttg tac tac gaa att gcc aag aag tct aag atc        480
Val Thr Met Gly Gln Leu Tyr Tyr Glu Ile Ala Lys Lys Ser Lys Ile
145                 150                 155                 160

ttg gct ttt cca ggt ggt cta tat cca tct gtt ggt tct ggt ggt ttg        528
Leu Ala Phe Pro Gly Gly Leu Tyr Pro Ser Val Gly Ser Gly Gly Leu
                165                 170                 175

att tca ggt ggt ggt att ggt act ttg atg aga aag ttt ggt ttg tcc        576
Ile Ser Gly Gly Gly Ile Gly Thr Leu Met Arg Lys Phe Gly Leu Ser
            180                 185                 190

gct gat aac gtc att gat gct aga gtt atg gat gtc aac ggt aga atc        624
Ala Asp Asn Val Ile Asp Ala Arg Val Met Asp Val Asn Gly Arg Ile
        195                 200                 205
```

```
ttg gac aaa aag tct atg ggc gaa gat atg ttc tgg gct att aga ggt        672
Leu Asp Lys Lys Ser Met Gly Glu Asp Met Phe Trp Ala Ile Arg Gly
    210                 215                 220

ggt ggc ggt tct tct ttt ggt gtt att ttg gct tgg aag atc aag ttg        720
Gly Gly Gly Ser Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu
225                 230                 235                 240

gtt aga atc cca cca aag gtt act gtt ttc acc gtt aga aga aag ttg        768
Val Arg Ile Pro Pro Lys Val Thr Val Phe Thr Val Arg Arg Lys Leu
                245                 250                 255

gaa ggt aac acc atc aac ttg ttg caa aga tgg caa aac gtt tcc cat        816
Glu Gly Asn Thr Ile Asn Leu Leu Gln Arg Trp Gln Asn Val Ser His
            260                 265                 270

aag ttc cca aag gat ttg ttc atg aga gtc ttg atc caa aac atg ggt        864
Lys Phe Pro Lys Asp Leu Phe Met Arg Val Leu Ile Gln Asn Met Gly
        275                 280                 285

ttc ggt aac gaa aag atc gtt caa gtt tca ttc cag ggt ttg ttt ttg        912
Phe Gly Asn Glu Lys Ile Val Gln Val Ser Phe Gln Gly Leu Phe Leu
    290                 295                 300

ggt aga gct tct gaa ttg acc cct ttg ttg aat caa act ttc cca gaa        960
Gly Arg Ala Ser Glu Leu Thr Pro Leu Leu Asn Gln Thr Phe Pro Glu
305                 310                 315                 320

ttc ggt ttg gac cca aaa aac tgt ttc caa gat cca gtt gtt aac tgc       1008
Phe Gly Leu Asp Pro Lys Asn Cys Phe Gln Asp Pro Val Val Asn Cys
                325                 330                 335

aac gaa ttg ccc ttc att aag aaa gaa tgc ttc gaa gtt cca tgg atc       1056
Asn Glu Leu Pro Phe Ile Lys Lys Glu Cys Phe Glu Val Pro Trp Ile
            340                 345                 350

aga tct acc ttg tac ttt gct tct aag agg acc aac aac tcc att gaa       1104
Arg Ser Thr Leu Tyr Phe Ala Ser Lys Arg Thr Asn Asn Ser Ile Glu
        355                 360                 365

ttc ttg gtt aac aac acc gtt tct cag acc aag aac tac caa aaa gct       1152
Phe Leu Val Asn Asn Thr Val Ser Gln Thr Lys Asn Tyr Gln Lys Ala
    370                 375                 380

act tcc gat ttc gtt aag acc cca atg caa gaa gag gtt tgg ggt atg       1200
Thr Ser Asp Phe Val Lys Thr Pro Met Gln Glu Glu Val Trp Gly Met
385                 390                 395                 400

atc aaa gac ttg ttc ttg gaa gaa gag aag ccc atg att att ttg gac       1248
Ile Lys Asp Leu Phe Leu Glu Glu Glu Lys Pro Met Ile Ile Leu Asp
                405                 410                 415

cct tta ggt ggt aag ttg gac gaa att tct gaa tcc gaa ttg cca ttt       1296
Pro Leu Gly Gly Lys Leu Asp Glu Ile Ser Glu Ser Glu Leu Pro Phe
```

```
            420                 425                 430

cca cac aga aag ggt aac ttg ttc aac atc cag tac atg gtt aat tgg       1344
Pro His Arg Lys Gly Asn Leu Phe Asn Ile Gln Tyr Met Val Asn Trp
        435                 440                 445

ggt gac aac tcc gaa tct atc tcc tcc aaa aaa atc aaa tgg ctg cgt       1392
Gly Asp Asn Ser Glu Ser Ile Ser Ser Lys Lys Ile Lys Trp Leu Arg
    450                 455                 460

gag ttg tac gag aag atg aag cca ttt ttg tct cat tgt cct aga acc       1440
Glu Leu Tyr Glu Lys Met Lys Pro Phe Leu Ser His Cys Pro Arg Thr
465                 470                 475                 480

gct tac ttg aac tac aga gat ttg gac ttc ggt act aat gat ggt gtc       1488
Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Phe Gly Thr Asn Asp Gly Val
                485                 490                 495

tac aga tac tct aaa gcc aaa gtt tgg ggt gct aag tac ttc aac gaa       1536
Tyr Arg Tyr Ser Lys Ala Lys Val Trp Gly Ala Lys Tyr Phe Asn Glu
            500                 505                 510

aac ttt gaa aga ttg gcc aag gtc aag tct aaa gtt gat cca ggt aat       1584
Asn Phe Glu Arg Leu Ala Lys Val Lys Ser Lys Val Asp Pro Gly Asn
        515                 520                 525

ttc ttc agg tac gaa caa tct att cca cca ttc tct gtt tcc acc           1629
Phe Phe Arg Tyr Glu Gln Ser Ile Pro Pro Phe Ser Val Ser Thr
    530                 535                 540


<210>  67
<211>  543
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  67

Met Gly Arg Leu Gln Leu Phe Ser Cys Leu Leu Val Ser Phe Leu Leu
1               5                   10                  15


Leu Ile Glu Ala Asn Ala Gln Gln Glu Phe Leu Gln Cys Ile Tyr Ser
            20                  25                  30


His Ser Ser Glu Asn Ile Lys Lys His Ile His Phe Pro Asn Ser Pro
        35                  40                  45


Thr Tyr Ser Ser Leu Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Leu
```

```
    50                  55                  60

Asn Ser Ser Phe Ala His Pro Ile Phe Ile Ile Ala Pro Lys Asn Glu
65                  70                  75                  80

Ser Glu Ile Gln Pro Ile Ile Leu Cys Ser Gln Lys Phe Gly Leu Gln
                85                  90                  95

Ile Arg Val Lys Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Phe Arg
            100                 105                 110

Ser Val Thr Asn Thr Gln Phe Val Ile Leu Asp Leu Ile Asn Leu Asp
        115                 120                 125

Asp Ile Arg Ile Asp Lys Asn Glu Glu Thr Ala Trp Ile Gln Thr Gly
    130                 135                 140

Val Thr Met Gly Gln Leu Tyr Tyr Glu Ile Ala Lys Lys Ser Lys Ile
145                 150                 155                 160

Leu Ala Phe Pro Gly Gly Leu Tyr Pro Ser Val Gly Ser Gly Gly Leu
                165                 170                 175

Ile Ser Gly Gly Gly Ile Gly Thr Leu Met Arg Lys Phe Gly Leu Ser
            180                 185                 190

Ala Asp Asn Val Ile Asp Ala Arg Val Met Asp Val Asn Gly Arg Ile
        195                 200                 205

Leu Asp Lys Lys Ser Met Gly Glu Asp Met Phe Trp Ala Ile Arg Gly
    210                 215                 220

Gly Gly Gly Ser Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu
225                 230                 235                 240

Val Arg Ile Pro Pro Lys Val Thr Val Phe Thr Val Arg Arg Lys Leu
                245                 250                 255

Glu Gly Asn Thr Ile Asn Leu Leu Gln Arg Trp Gln Asn Val Ser His
            260                 265                 270
```

```
Lys Phe Pro Lys Asp Leu Phe Met Arg Val Leu Ile Gln Asn Met Gly
        275                 280                 285

Phe Gly Asn Glu Lys Ile Val Gln Val Ser Phe Gln Gly Leu Phe Leu
    290                 295                 300

Gly Arg Ala Ser Glu Leu Thr Pro Leu Leu Asn Gln Thr Phe Pro Glu
305                 310                 315                 320

Phe Gly Leu Asp Pro Lys Asn Cys Phe Gln Asp Pro Val Val Asn Cys
                325                 330                 335

Asn Glu Leu Pro Phe Ile Lys Lys Glu Cys Phe Glu Val Pro Trp Ile
            340                 345                 350

Arg Ser Thr Leu Tyr Phe Ala Ser Lys Arg Thr Asn Asn Ser Ile Glu
        355                 360                 365

Phe Leu Val Asn Asn Thr Val Ser Gln Thr Lys Asn Tyr Gln Lys Ala
    370                 375                 380

Thr Ser Asp Phe Val Lys Thr Pro Met Gln Glu Glu Val Trp Gly Met
385                 390                 395                 400

Ile Lys Asp Leu Phe Leu Glu Glu Glu Lys Pro Met Ile Ile Leu Asp
                405                 410                 415

Pro Leu Gly Gly Lys Leu Asp Glu Ile Ser Glu Ser Glu Leu Pro Phe
            420                 425                 430

Pro His Arg Lys Gly Asn Leu Phe Asn Ile Gln Tyr Met Val Asn Trp
        435                 440                 445

Gly Asp Asn Ser Glu Ser Ile Ser Ser Lys Lys Ile Lys Trp Leu Arg
    450                 455                 460

Glu Leu Tyr Glu Lys Met Lys Pro Phe Leu Ser His Cys Pro Arg Thr
465                 470                 475                 480

Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Phe Gly Thr Asn Asp Gly Val
```

```
                485                 490                 495

Tyr Arg Tyr Ser Lys Ala Lys Val Trp Gly Ala Lys Tyr Phe Asn Glu
            500                 505                 510

Asn Phe Glu Arg Leu Ala Lys Val Lys Ser Lys Val Asp Pro Gly Asn
        515                 520                 525

Phe Phe Arg Tyr Glu Gln Ser Ile Pro Pro Phe Ser Val Ser Thr
    530                 535                 540
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<210> 68
<211> 1569
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS94-A0A1S3XA06-no signal peptide

<220>
<221> CDS
<222> (1)..(1569)

<400> 68

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atg gcc caa caa gag ttc ttg caa tgt atc tac tct cac tcc tcc gag         48
Met Ala Gln Gln Glu Phe Leu Gln Cys Ile Tyr Ser His Ser Ser Glu
1               5                   10                  15

aat att aag aag cac att cat ttc cca aac agc cca act tac tct tcg         96
Asn Ile Lys Lys His Ile His Phe Pro Asn Ser Pro Thr Tyr Ser Ser
            20                  25                  30

ttg ttg gaa tac gct caa aag aat cca aga tgg ctg aat tct tct ttc        144
Leu Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Leu Asn Ser Ser Phe
        35                  40                  45

gcc cat cca att ttc att atc gct cca aag aac gaa tcc gaa atc cag        192
Ala His Pro Ile Phe Ile Ile Ala Pro Lys Asn Glu Ser Glu Ile Gln
    50                  55                  60

cca att atc ttg tgc tct caa aag ttc ggc ttg caa atc aga gtt aag        240
Pro Ile Ile Leu Cys Ser Gln Lys Phe Gly Leu Gln Ile Arg Val Lys
65                  70                  75                  80

tct ggt ggt cat gat tac gaa ggt ttg tct ttc aga tct gtc act aac        288
Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Phe Arg Ser Val Thr Asn
                85                  90                  95

acc caa ttc gtt atc ttg gac ttg atc aac ttg gac gat atc aga atc        336
```

```
Thr Gln Phe Val Ile Leu Asp Leu Ile Asn Leu Asp Asp Ile Arg Ile
            100                 105                 110

gac aag aac gaa gaa act gct tgg att caa act ggt gtt act atg ggt        384
Asp Lys Asn Glu Glu Thr Ala Trp Ile Gln Thr Gly Val Thr Met Gly
        115                 120                 125

cag ttg tac tac gaa att gcc aag aag tct aag atc ttg gct ttt cca        432
Gln Leu Tyr Tyr Glu Ile Ala Lys Lys Ser Lys Ile Leu Ala Phe Pro
    130                 135                 140

ggt ggt cta tat cca tct gtt ggt tct ggt ggt ttg att tca ggt ggt        480
Gly Gly Leu Tyr Pro Ser Val Gly Ser Gly Gly Leu Ile Ser Gly Gly
145                 150                 155                 160

ggt att ggt act ttg atg aga aag ttt ggt ttg tcc gct gat aac gtc        528
Gly Ile Gly Thr Leu Met Arg Lys Phe Gly Leu Ser Ala Asp Asn Val
                165                 170                 175

att gat gct aga gtt atg gat gtc aac ggt aga atc ttg gac aaa aag        576
Ile Asp Ala Arg Val Met Asp Val Asn Gly Arg Ile Leu Asp Lys Lys
            180                 185                 190

tct atg ggc gaa gat atg ttc tgg gct att aga ggt ggt ggc ggt tct        624
Ser Met Gly Glu Asp Met Phe Trp Ala Ile Arg Gly Gly Gly Gly Ser
        195                 200                 205

tct ttt ggt gtt att ttg gct tgg aag atc aag ttg gtt aga atc cca        672
Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Arg Ile Pro
    210                 215                 220

cca aag gtt act gtt ttc acc gtt aga aga aag ttg gaa ggt aac acc        720
Pro Lys Val Thr Val Phe Thr Val Arg Arg Lys Leu Glu Gly Asn Thr
225                 230                 235                 240

atc aac ttg ttg caa aga tgg caa aac gtt tcc cat aag ttc cca aag        768
Ile Asn Leu Leu Gln Arg Trp Gln Asn Val Ser His Lys Phe Pro Lys
                245                 250                 255

gat ttg ttc atg aga gtc ttg atc caa aac atg ggt ttc ggt aac gaa        816
Asp Leu Phe Met Arg Val Leu Ile Gln Asn Met Gly Phe Gly Asn Glu
            260                 265                 270

aag atc gtt caa gtt tca ttc cag ggt ttg ttt ttg ggt aga gct tct        864
Lys Ile Val Gln Val Ser Phe Gln Gly Leu Phe Leu Gly Arg Ala Ser
        275                 280                 285

gaa ttg acc cct ttg ttg aat caa act ttc cca gaa ttc ggt ttg gac        912
Glu Leu Thr Pro Leu Leu Asn Gln Thr Phe Pro Glu Phe Gly Leu Asp
    290                 295                 300

cca aaa aac tgt ttc caa gat cca gtt gtt aac tgc aac gaa ttg ccc        960
Pro Lys Asn Cys Phe Gln Asp Pro Val Val Asn Cys Asn Glu Leu Pro
305                 310                 315                 320
```

```
ttc att aag aaa gaa tgc ttc gaa gtt cca tgg atc aga tct acc ttg       1008
Phe Ile Lys Lys Glu Cys Phe Glu Val Pro Trp Ile Arg Ser Thr Leu
               325                 330                 335

tac ttt gct tct aag agg acc aac aac tcc att gaa ttc ttg gtt aac       1056
Tyr Phe Ala Ser Lys Arg Thr Asn Asn Ser Ile Glu Phe Leu Val Asn
            340                 345                 350

aac acc gtt tct cag acc aag aac tac caa aaa gct act tcc gat ttc       1104
Asn Thr Val Ser Gln Thr Lys Asn Tyr Gln Lys Ala Thr Ser Asp Phe
        355                 360                 365

gtt aag acc cca atg caa gaa gag gtt tgg ggt atg atc aaa gac ttg       1152
Val Lys Thr Pro Met Gln Glu Glu Val Trp Gly Met Ile Lys Asp Leu
    370                 375                 380

ttc ttg gaa gaa gag aag ccc atg att att ttg gac cct tta ggt ggt       1200
Phe Leu Glu Glu Glu Lys Pro Met Ile Ile Leu Asp Pro Leu Gly Gly
385                 390                 395                 400

aag ttg gac gaa att tct gaa tcc gaa ttg cca ttt cca cac aga aag       1248
Lys Leu Asp Glu Ile Ser Glu Ser Glu Leu Pro Phe Pro His Arg Lys
               405                 410                 415

ggt aac ttg ttc aac atc cag tac atg gtt aat tgg ggt gac aac tcc       1296
Gly Asn Leu Phe Asn Ile Gln Tyr Met Val Asn Trp Gly Asp Asn Ser
            420                 425                 430

gaa tct atc tcc tcc aaa aaa atc aaa tgg ctg cgt gag ttg tac gag       1344
Glu Ser Ile Ser Ser Lys Lys Ile Lys Trp Leu Arg Glu Leu Tyr Glu
        435                 440                 445

aag atg aag cca ttt ttg tct cat tgt cct aga acc gct tac ttg aac       1392
Lys Met Lys Pro Phe Leu Ser His Cys Pro Arg Thr Ala Tyr Leu Asn
    450                 455                 460

tac aga gat ttg gac ttc ggt act aat gat ggt gtc tac aga tac tct       1440
Tyr Arg Asp Leu Asp Phe Gly Thr Asn Asp Gly Val Tyr Arg Tyr Ser
465                 470                 475                 480

aaa gcc aaa gtt tgg ggt gct aag tac ttc aac gaa aac ttt gaa aga       1488
Lys Ala Lys Val Trp Gly Ala Lys Tyr Phe Asn Glu Asn Phe Glu Arg
               485                 490                 495

ttg gcc aag gtc aag tct aaa gtt gat cca ggt aat ttc ttc agg tac       1536
Leu Ala Lys Val Lys Ser Lys Val Asp Pro Gly Asn Phe Phe Arg Tyr
            500                 505                 510

gaa caa tct att cca cca ttc tct gtt tcc acc                           1569
Glu Gln Ser Ile Pro Pro Phe Ser Val Ser Thr
        515                 520
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<210> 69
<211> 523
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 69

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Met Ala Gln Gln Glu Phe Leu Gln Cys Ile Tyr Ser His Ser Ser Glu
1               5                  10                  15


Asn Ile Lys Lys His Ile His Phe Pro Asn Ser Pro Thr Tyr Ser Ser
            20                  25                  30


Leu Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Leu Asn Ser Ser Phe
        35                  40                  45


Ala His Pro Ile Phe Ile Ile Ala Pro Lys Asn Glu Ser Glu Ile Gln
    50                  55                  60


Pro Ile Ile Leu Cys Ser Gln Lys Phe Gly Leu Gln Ile Arg Val Lys
65                  70                  75                  80


Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Phe Arg Ser Val Thr Asn
                85                  90                  95


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


Asp Lys Asn Glu Glu Thr Ala Trp Ile Gln Thr Gly Val Thr Met Gly
        115                 120                 125


Gln Leu Tyr Tyr Glu Ile Ala Lys Lys Ser Lys Ile Leu Ala Phe Pro
    130                 135                 140


Gly Gly Leu Tyr Pro Ser Val Gly Ser Gly Gly Leu Ile Ser Gly Gly
145                 150                 155                 160


Gly Ile Gly Thr Leu Met Arg Lys Phe Gly Leu Ser Ala Asp Asn Val
                165                 170                 175
```

```
Ile Asp Ala Arg Val Met Asp Val Asn Gly Arg Ile Leu Asp Lys Lys
            180                 185                 190

Ser Met Gly Glu Asp Met Phe Trp Ala Ile Arg Gly Gly Gly Gly Ser
        195                 200                 205

Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Arg Ile Pro
    210                 215                 220

Pro Lys Val Thr Val Phe Thr Val Arg Arg Lys Leu Glu Gly Asn Thr
225                 230                 235                 240

Ile Asn Leu Leu Gln Arg Trp Gln Asn Val Ser His Lys Phe Pro Lys
                245                 250                 255

Asp Leu Phe Met Arg Val Leu Ile Gln Asn Met Gly Phe Gly Asn Glu
            260                 265                 270

Lys Ile Val Gln Val Ser Phe Gln Gly Leu Phe Leu Gly Arg Ala Ser
        275                 280                 285

Glu Leu Thr Pro Leu Leu Asn Gln Thr Phe Pro Glu Phe Gly Leu Asp
    290                 295                 300

Pro Lys Asn Cys Phe Gln Asp Pro Val Val Asn Cys Asn Glu Leu Pro
305                 310                 315                 320

Phe Ile Lys Lys Glu Cys Phe Glu Val Pro Trp Ile Arg Ser Thr Leu
                325                 330                 335

Tyr Phe Ala Ser Lys Arg Thr Asn Asn Ser Ile Glu Phe Leu Val Asn
            340                 345                 350

Asn Thr Val Ser Gln Thr Lys Asn Tyr Gln Lys Ala Thr Ser Asp Phe
        355                 360                 365

Val Lys Thr Pro Met Gln Glu Glu Val Trp Gly Met Ile Lys Asp Leu
    370                 375                 380

Phe Leu Glu Glu Glu Lys Pro Met Ile Ile Leu Asp Pro Leu Gly Gly
385                 390                 395                 400
```

```
Lys Leu Asp Glu Ile Ser Glu Ser Glu Leu Pro Phe Pro His Arg Lys
                405                 410                 415


Gly Asn Leu Phe Asn Ile Gln Tyr Met Val Asn Trp Gly Asp Asn Ser
            420                 425                 430


Glu Ser Ile Ser Ser Lys Lys Ile Lys Trp Leu Arg Glu Leu Tyr Glu
        435                 440                 445


Lys Met Lys Pro Phe Leu Ser His Cys Pro Arg Thr Ala Tyr Leu Asn
    450                 455                 460


Tyr Arg Asp Leu Asp Phe Gly Thr Asn Asp Gly Val Tyr Arg Tyr Ser
465                 470                 475                 480


Lys Ala Lys Val Trp Gly Ala Lys Tyr Phe Asn Glu Asn Phe Glu Arg
                485                 490                 495


Leu Ala Lys Val Lys Ser Lys Val Asp Pro Gly Asn Phe Phe Arg Tyr
            500                 505                 510


Glu Gln Ser Ile Pro Pro Phe Ser Val Ser Thr
        515                 520


<210>  70
<211>  1593
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS94-A0A1S3XA06-no signal peptide-strep Tag


<220>
<221>  CDS
<222>  (1)..(1593)

<400>  70
atg gcc caa caa gag ttc ttg caa tgt atc tac tct cac tcc tcc gag         48
Met Ala Gln Gln Glu Phe Leu Gln Cys Ile Tyr Ser His Ser Ser Glu
1               5                   10                  15

aat att aag aag cac att cat ttc cca aac agc cca act tac tct tcg         96
Asn Ile Lys Lys His Ile His Phe Pro Asn Ser Pro Thr Tyr Ser Ser
```

```
            20                  25                  30

ttg ttg gaa tac gct caa aag aat cca aga tgg ctg aat tct tct ttc        144
Leu Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Leu Asn Ser Ser Phe
        35                  40                  45

gcc cat cca att ttc att atc gct cca aag aac gaa tcc gaa atc cag        192
Ala His Pro Ile Phe Ile Ile Ala Pro Lys Asn Glu Ser Glu Ile Gln
    50                  55                  60

cca att atc ttg tgc tct caa aag ttc ggc ttg caa atc aga gtt aag        240
Pro Ile Ile Leu Cys Ser Gln Lys Phe Gly Leu Gln Ile Arg Val Lys
65                  70                  75                  80

tct ggt ggt cat gat tac gaa ggt ttg tct ttc aga tct gtc act aac        288
Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Phe Arg Ser Val Thr Asn
                85                  90                  95

acc caa ttc gtt atc ttg gac ttg atc aac ttg gac gat atc aga atc        336
Thr Gln Phe Val Ile Leu Asp Leu Ile Asn Leu Asp Asp Ile Arg Ile
            100                 105                 110

gac aag aac gaa gaa act gct tgg att caa act ggt gtt act atg ggt        384
Asp Lys Asn Glu Glu Thr Ala Trp Ile Gln Thr Gly Val Thr Met Gly
        115                 120                 125

cag ttg tac tac gaa att gcc aag aag tct aag atc ttg gct ttt cca        432
Gln Leu Tyr Tyr Glu Ile Ala Lys Lys Ser Lys Ile Leu Ala Phe Pro
    130                 135                 140

ggt ggt cta tat cca tct gtt ggt tct ggt ggt ttg att tca ggt ggt        480
Gly Gly Leu Tyr Pro Ser Val Gly Ser Gly Gly Leu Ile Ser Gly Gly
145                 150                 155                 160

ggt att ggt act ttg atg aga aag ttt ggt ttg tcc gct gat aac gtc        528
Gly Ile Gly Thr Leu Met Arg Lys Phe Gly Leu Ser Ala Asp Asn Val
                165                 170                 175

att gat gct aga gtt atg gat gtc aac ggt aga atc ttg gac aaa aag        576
Ile Asp Ala Arg Val Met Asp Val Asn Gly Arg Ile Leu Asp Lys Lys
            180                 185                 190

tct atg ggc gaa gat atg ttc tgg gct att aga ggt ggt ggc ggt tct        624
Ser Met Gly Glu Asp Met Phe Trp Ala Ile Arg Gly Gly Gly Gly Ser
        195                 200                 205

tct ttt ggt gtt att ttg gct tgg aag atc aag ttg gtt aga atc cca        672
Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Arg Ile Pro
    210                 215                 220

cca aag gtt act gtt ttc acc gtt aga aga aag ttg gaa ggt aac acc        720
Pro Lys Val Thr Val Phe Thr Val Arg Arg Lys Leu Glu Gly Asn Thr
225                 230                 235                 240
```

```
atc aac ttg ttg caa aga tgg caa aac gtt tcc cat aag ttc cca aag        768
Ile Asn Leu Leu Gln Arg Trp Gln Asn Val Ser His Lys Phe Pro Lys
                245                 250                 255

gat ttg ttc atg aga gtc ttg atc caa aac atg ggt ttc ggt aac gaa        816
Asp Leu Phe Met Arg Val Leu Ile Gln Asn Met Gly Phe Gly Asn Glu
            260                 265                 270

aag atc gtt caa gtt tca ttc cag ggt ttg ttt ttg ggt aga gct tct        864
Lys Ile Val Gln Val Ser Phe Gln Gly Leu Phe Leu Gly Arg Ala Ser
        275                 280                 285

gaa ttg acc cct ttg ttg aat caa act ttc cca gaa ttc ggt ttg gac        912
Glu Leu Thr Pro Leu Leu Asn Gln Thr Phe Pro Glu Phe Gly Leu Asp
    290                 295                 300

cca aaa aac tgt ttc caa gat cca gtt gtt aac tgc aac gaa ttg ccc        960
Pro Lys Asn Cys Phe Gln Asp Pro Val Val Asn Cys Asn Glu Leu Pro
305                 310                 315                 320

ttc att aag aaa gaa tgc ttc gaa gtt cca tgg atc aga tct acc ttg       1008
Phe Ile Lys Lys Glu Cys Phe Glu Val Pro Trp Ile Arg Ser Thr Leu
                325                 330                 335

tac ttt gct tct aag agg acc aac aac tcc att gaa ttc ttg gtt aac       1056
Tyr Phe Ala Ser Lys Arg Thr Asn Asn Ser Ile Glu Phe Leu Val Asn
            340                 345                 350

aac acc gtt tct cag acc aag aac tac caa aaa gct act tcc gat ttc       1104
Asn Thr Val Ser Gln Thr Lys Asn Tyr Gln Lys Ala Thr Ser Asp Phe
        355                 360                 365

gtt aag acc cca atg caa gaa gag gtt tgg ggt atg atc aaa gac ttg       1152
Val Lys Thr Pro Met Gln Glu Glu Val Trp Gly Met Ile Lys Asp Leu
    370                 375                 380

ttc ttg gaa gaa gag aag ccc atg att att ttg gac cct tta ggt ggt       1200
Phe Leu Glu Glu Glu Lys Pro Met Ile Ile Leu Asp Pro Leu Gly Gly
385                 390                 395                 400

aag ttg gac gaa att tct gaa tcc gaa ttg cca ttt cca cac aga aag       1248
Lys Leu Asp Glu Ile Ser Glu Ser Glu Leu Pro Phe Pro His Arg Lys
                405                 410                 415

ggt aac ttg ttc aac atc cag tac atg gtt aat tgg ggt gac aac tcc       1296
Gly Asn Leu Phe Asn Ile Gln Tyr Met Val Asn Trp Gly Asp Asn Ser
            420                 425                 430

gaa tct atc tcc tcc aaa aaa atc aaa tgg ctg cgt gag ttg tac gag       1344
Glu Ser Ile Ser Ser Lys Lys Ile Lys Trp Leu Arg Glu Leu Tyr Glu
        435                 440                 445

aag atg aag cca ttt ttg tct cat tgt cct aga acc gct tac ttg aac       1392
Lys Met Lys Pro Phe Leu Ser His Cys Pro Arg Thr Ala Tyr Leu Asn
```

```
    450                 455                 460

tac aga gat ttg gac ttc ggt act aat gat ggt gtc tac aga tac tct       1440
Tyr Arg Asp Leu Asp Phe Gly Thr Asn Asp Gly Val Tyr Arg Tyr Ser
465                 470                 475                 480

aaa gcc aaa gtt tgg ggt gct aag tac ttc aac gaa aac ttt gaa aga       1488
Lys Ala Lys Val Trp Gly Ala Lys Tyr Phe Asn Glu Asn Phe Glu Arg
                485                 490                 495

ttg gcc aag gtc aag tct aaa gtt gat cca ggt aat ttc ttc agg tac       1536
Leu Ala Lys Val Lys Ser Lys Val Asp Pro Gly Asn Phe Phe Arg Tyr
            500                 505                 510

gaa caa tct att cca cca ttc tct gtt tcc acc tgg tca cat cca caa       1584
Glu Gln Ser Ile Pro Pro Phe Ser Val Ser Thr Trp Ser His Pro Gln
        515                 520                 525

ttt gaa aag                                                          1593
Phe Glu Lys
    530
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<210> 71
<211> 531
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 71

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Met Ala Gln Gln Glu Phe Leu Gln Cys Ile Tyr Ser His Ser Ser Glu
1               5                   10                  15


Asn Ile Lys Lys His Ile His Phe Pro Asn Ser Pro Thr Tyr Ser Ser
            20                  25                  30


Leu Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Leu Asn Ser Ser Phe
        35                  40                  45


Ala His Pro Ile Phe Ile Ile Ala Pro Lys Asn Glu Ser Glu Ile Gln
    50                  55                  60


Pro Ile Ile Leu Cys Ser Gln Lys Phe Gly Leu Gln Ile Arg Val Lys
65                  70                  75                  80


Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Phe Arg Ser Val Thr Asn
```

```
                85                  90                  95

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

Asp Lys Asn Glu Glu Thr Ala Trp Ile Gln Thr Gly Val Thr Met Gly
        115                 120                 125

Gln Leu Tyr Tyr Glu Ile Ala Lys Lys Ser Lys Ile Leu Ala Phe Pro
    130                 135                 140

Gly Gly Leu Tyr Pro Ser Val Gly Ser Gly Gly Leu Ile Ser Gly Gly
145                 150                 155                 160

Gly Ile Gly Thr Leu Met Arg Lys Phe Gly Leu Ser Ala Asp Asn Val
                165                 170                 175

Ile Asp Ala Arg Val Met Asp Val Asn Gly Arg Ile Leu Asp Lys Lys
            180                 185                 190

Ser Met Gly Glu Asp Met Phe Trp Ala Ile Arg Gly Gly Gly Gly Ser
        195                 200                 205

Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Arg Ile Pro
    210                 215                 220

Pro Lys Val Thr Val Phe Thr Val Arg Arg Lys Leu Glu Gly Asn Thr
225                 230                 235                 240

Ile Asn Leu Leu Gln Arg Trp Gln Asn Val Ser His Lys Phe Pro Lys
                245                 250                 255

Asp Leu Phe Met Arg Val Leu Ile Gln Asn Met Gly Phe Gly Asn Glu
            260                 265                 270

Lys Ile Val Gln Val Ser Phe Gln Gly Leu Phe Leu Gly Arg Ala Ser
        275                 280                 285

Glu Leu Thr Pro Leu Leu Asn Gln Thr Phe Pro Glu Phe Gly Leu Asp
    290                 295                 300
```

```
Pro Lys Asn Cys Phe Gln Asp Pro Val Val Asn Cys Asn Glu Leu Pro
305                 310                 315                 320

Phe Ile Lys Lys Glu Cys Phe Glu Val Pro Trp Ile Arg Ser Thr Leu
                325                 330                 335

Tyr Phe Ala Ser Lys Arg Thr Asn Asn Ser Ile Glu Phe Leu Val Asn
            340                 345                 350

Asn Thr Val Ser Gln Thr Lys Asn Tyr Gln Lys Ala Thr Ser Asp Phe
        355                 360                 365

Val Lys Thr Pro Met Gln Glu Glu Val Trp Gly Met Ile Lys Asp Leu
    370                 375                 380

Phe Leu Glu Glu Glu Lys Pro Met Ile Ile Leu Asp Pro Leu Gly Gly
385                 390                 395                 400

Lys Leu Asp Glu Ile Ser Glu Ser Glu Leu Pro Phe Pro His Arg Lys
                405                 410                 415

Gly Asn Leu Phe Asn Ile Gln Tyr Met Val Asn Trp Gly Asp Asn Ser
            420                 425                 430

Glu Ser Ile Ser Ser Lys Lys Ile Lys Trp Leu Arg Glu Leu Tyr Glu
        435                 440                 445

Lys Met Lys Pro Phe Leu Ser His Cys Pro Arg Thr Ala Tyr Leu Asn
    450                 455                 460

Tyr Arg Asp Leu Asp Phe Gly Thr Asn Asp Gly Val Tyr Arg Tyr Ser
465                 470                 475                 480

Lys Ala Lys Val Trp Gly Ala Lys Tyr Phe Asn Glu Asn Phe Glu Arg
                485                 490                 495

Leu Ala Lys Val Lys Ser Lys Val Asp Pro Gly Asn Phe Phe Arg Tyr
            500                 505                 510

Glu Gln Ser Ile Pro Pro Phe Ser Val Ser Thr Trp Ser His Pro Gln
```

```
        515                 520                 525


Phe Glu Lys
    530


<210>  72
<211>  1650
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS94-A0A1S3XA06-truncated alpha factor-no signal peptide-strep
       Tag


<220>
<221>  CDS
<222>  (1)..(1650)

<400>  72
atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca ctt gca atg gcc caa caa gag ttc ttg caa tgt atc tac tct cac         96
Ala Leu Ala Met Ala Gln Gln Glu Phe Leu Gln Cys Ile Tyr Ser His
            20                  25                  30

tcc tcc gag aat att aag aag cac att cat ttc cca aac agc cca act        144
Ser Ser Glu Asn Ile Lys Lys His Ile His Phe Pro Asn Ser Pro Thr
        35                  40                  45

tac tct tcg ttg ttg gaa tac gct caa aag aat cca aga tgg ctg aat        192
Tyr Ser Ser Leu Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Leu Asn
    50                  55                  60

tct tct ttc gcc cat cca att ttc att atc gct cca aag aac gaa tcc        240
Ser Ser Phe Ala His Pro Ile Phe Ile Ile Ala Pro Lys Asn Glu Ser
65                  70                  75                  80

gaa atc cag cca att atc ttg tgc tct caa aag ttc ggc ttg caa atc        288
Glu Ile Gln Pro Ile Ile Leu Cys Ser Gln Lys Phe Gly Leu Gln Ile
                85                  90                  95

aga gtt aag tct ggt ggt cat gat tac gaa ggt ttg tct ttc aga tct        336
Arg Val Lys Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Phe Arg Ser
            100                 105                 110

gtc act aac acc caa ttc gtt atc ttg gac ttg atc aac ttg gac gat        384
Val Thr Asn Thr Gln Phe Val Ile Leu Asp Leu Ile Asn Leu Asp Asp
        115                 120                 125
```

```
atc aga atc gac aag aac gaa gaa act gct tgg att caa act ggt gtt        432
Ile Arg Ile Asp Lys Asn Glu Glu Thr Ala Trp Ile Gln Thr Gly Val
    130                 135                 140

act atg ggt cag ttg tac tac gaa att gcc aag aag tct aag atc ttg        480
Thr Met Gly Gln Leu Tyr Tyr Glu Ile Ala Lys Lys Ser Lys Ile Leu
145                 150                 155                 160

gct ttt cca ggt ggt cta tat cca tct gtt ggt tct ggt ggt ttg att        528
Ala Phe Pro Gly Gly Leu Tyr Pro Ser Val Gly Ser Gly Gly Leu Ile
                165                 170                 175

tca ggt ggt ggt att ggt act ttg atg aga aag ttt ggt ttg tcc gct        576
Ser Gly Gly Gly Ile Gly Thr Leu Met Arg Lys Phe Gly Leu Ser Ala
            180                 185                 190

gat aac gtc att gat gct aga gtt atg gat gtc aac ggt aga atc ttg        624
Asp Asn Val Ile Asp Ala Arg Val Met Asp Val Asn Gly Arg Ile Leu
        195                 200                 205

gac aaa aag tct atg ggc gaa gat atg ttc tgg gct att aga ggt ggt        672
Asp Lys Lys Ser Met Gly Glu Asp Met Phe Trp Ala Ile Arg Gly Gly
    210                 215                 220

ggc ggt tct tct ttt ggt gtt att ttg gct tgg aag atc aag ttg gtt        720
Gly Gly Ser Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val
225                 230                 235                 240

aga atc cca cca aag gtt act gtt ttc acc gtt aga aga aag ttg gaa        768
Arg Ile Pro Pro Lys Val Thr Val Phe Thr Val Arg Arg Lys Leu Glu
                245                 250                 255

ggt aac acc atc aac ttg ttg caa aga tgg caa aac gtt tcc cat aag        816
Gly Asn Thr Ile Asn Leu Leu Gln Arg Trp Gln Asn Val Ser His Lys
            260                 265                 270

ttc cca aag gat ttg ttc atg aga gtc ttg atc caa aac atg ggt ttc        864
Phe Pro Lys Asp Leu Phe Met Arg Val Leu Ile Gln Asn Met Gly Phe
        275                 280                 285

ggt aac gaa aag atc gtt caa gtt tca ttc cag ggt ttg ttt ttg ggt        912
Gly Asn Glu Lys Ile Val Gln Val Ser Phe Gln Gly Leu Phe Leu Gly
    290                 295                 300

aga gct tct gaa ttg acc cct ttg ttg aat caa act ttc cca gaa ttc        960
Arg Ala Ser Glu Leu Thr Pro Leu Leu Asn Gln Thr Phe Pro Glu Phe
305                 310                 315                 320

ggt ttg gac cca aaa aac tgt ttc caa gat cca gtt gtt aac tgc aac       1008
Gly Leu Asp Pro Lys Asn Cys Phe Gln Asp Pro Val Val Asn Cys Asn
                325                 330                 335

gaa ttg ccc ttc att aag aaa gaa tgc ttc gaa gtt cca tgg atc aga       1056
Glu Leu Pro Phe Ile Lys Lys Glu Cys Phe Glu Val Pro Trp Ile Arg
```

```
            340                 345                 350

tct acc ttg tac ttt gct tct aag agg acc aac aac tcc att gaa ttc       1104
Ser Thr Leu Tyr Phe Ala Ser Lys Arg Thr Asn Asn Ser Ile Glu Phe
        355                 360                 365

ttg gtt aac aac acc gtt tct cag acc aag aac tac caa aaa gct act       1152
Leu Val Asn Asn Thr Val Ser Gln Thr Lys Asn Tyr Gln Lys Ala Thr
    370                 375                 380

tcc gat ttc gtt aag acc cca atg caa gaa gag gtt tgg ggt atg atc       1200
Ser Asp Phe Val Lys Thr Pro Met Gln Glu Glu Val Trp Gly Met Ile
385                 390                 395                 400

aaa gac ttg ttc ttg gaa gaa gag aag ccc atg att att ttg gac cct       1248
Lys Asp Leu Phe Leu Glu Glu Glu Lys Pro Met Ile Ile Leu Asp Pro
                405                 410                 415

tta ggt ggt aag ttg gac gaa att tct gaa tcc gaa ttg cca ttt cca       1296
Leu Gly Gly Lys Leu Asp Glu Ile Ser Glu Ser Glu Leu Pro Phe Pro
            420                 425                 430

cac aga aag ggt aac ttg ttc aac atc cag tac atg gtt aat tgg ggt       1344
His Arg Lys Gly Asn Leu Phe Asn Ile Gln Tyr Met Val Asn Trp Gly
        435                 440                 445

gac aac tcc gaa tct atc tcc tcc aaa aaa atc aaa tgg ctg cgt gag       1392
Asp Asn Ser Glu Ser Ile Ser Ser Lys Lys Ile Lys Trp Leu Arg Glu
    450                 455                 460

ttg tac gag aag atg aag cca ttt ttg tct cat tgt cct aga acc gct       1440
Leu Tyr Glu Lys Met Lys Pro Phe Leu Ser His Cys Pro Arg Thr Ala
465                 470                 475                 480

tac ttg aac tac aga gat ttg gac ttc ggt act aat gat ggt gtc tac       1488
Tyr Leu Asn Tyr Arg Asp Leu Asp Phe Gly Thr Asn Asp Gly Val Tyr
                485                 490                 495

aga tac tct aaa gcc aaa gtt tgg ggt gct aag tac ttc aac gaa aac       1536
Arg Tyr Ser Lys Ala Lys Val Trp Gly Ala Lys Tyr Phe Asn Glu Asn
            500                 505                 510

ttt gaa aga ttg gcc aag gtc aag tct aaa gtt gat cca ggt aat ttc       1584
Phe Glu Arg Leu Ala Lys Val Lys Ser Lys Val Asp Pro Gly Asn Phe
        515                 520                 525

ttc agg tac gaa caa tct att cca cca ttc tct gtt tcc acc tgg tca       1632
Phe Arg Tyr Glu Gln Ser Ile Pro Pro Phe Ser Val Ser Thr Trp Ser
    530                 535                 540

cat cca caa ttt gaa aag                                               1650
His Pro Gln Phe Glu Lys
545                 550
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<210> 73
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 73

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


Ala Leu Ala Met Ala Gln Gln Glu Phe Leu Gln Cys Ile Tyr Ser His
            20                  25                  30


Ser Ser Glu Asn Ile Lys Lys His Ile His Phe Pro Asn Ser Pro Thr
        35                  40                  45


Tyr Ser Ser Leu Leu Glu Tyr Ala Gln Lys Asn Pro Arg Trp Leu Asn
    50                  55                  60


Ser Ser Phe Ala His Pro Ile Phe Ile Ile Ala Pro Lys Asn Glu Ser
65                  70                  75                  80


Glu Ile Gln Pro Ile Ile Leu Cys Ser Gln Lys Phe Gly Leu Gln Ile
                85                  90                  95


Arg Val Lys Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Phe Arg Ser
            100                 105                 110


Val Thr Asn Thr Gln Phe Val Ile Leu Asp Leu Ile Asn Leu Asp Asp
        115                 120                 125


Ile Arg Ile Asp Lys Asn Glu Glu Thr Ala Trp Ile Gln Thr Gly Val
    130                 135                 140


Thr Met Gly Gln Leu Tyr Tyr Glu Ile Ala Lys Lys Ser Lys Ile Leu
145                 150                 155                 160


Ala Phe Pro Gly Gly Leu Tyr Pro Ser Val Gly Ser Gly Gly Leu Ile
                165                 170                 175
```

```
Ser Gly Gly Gly Ile Gly Thr Leu Met Arg Lys Phe Gly Leu Ser Ala
            180                 185                 190

Asp Asn Val Ile Asp Ala Arg Val Met Asp Val Asn Gly Arg Ile Leu
        195                 200                 205

Asp Lys Lys Ser Met Gly Glu Asp Met Phe Trp Ala Ile Arg Gly Gly
    210                 215                 220

Gly Gly Ser Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val
225                 230                 235                 240

Arg Ile Pro Pro Lys Val Thr Val Phe Thr Val Arg Arg Lys Leu Glu
                245                 250                 255

Gly Asn Thr Ile Asn Leu Leu Gln Arg Trp Gln Asn Val Ser His Lys
            260                 265                 270

Phe Pro Lys Asp Leu Phe Met Arg Val Leu Ile Gln Asn Met Gly Phe
        275                 280                 285

Gly Asn Glu Lys Ile Val Gln Val Ser Phe Gln Gly Leu Phe Leu Gly
    290                 295                 300

Arg Ala Ser Glu Leu Thr Pro Leu Leu Asn Gln Thr Phe Pro Glu Phe
305                 310                 315                 320

Gly Leu Asp Pro Lys Asn Cys Phe Gln Asp Pro Val Val Asn Cys Asn
                325                 330                 335

Glu Leu Pro Phe Ile Lys Lys Glu Cys Phe Glu Val Pro Trp Ile Arg
            340                 345                 350

Ser Thr Leu Tyr Phe Ala Ser Lys Arg Thr Asn Asn Ser Ile Glu Phe
        355                 360                 365

Leu Val Asn Asn Thr Val Ser Gln Thr Lys Asn Tyr Gln Lys Ala Thr
    370                 375                 380

Ser Asp Phe Val Lys Thr Pro Met Gln Glu Glu Val Trp Gly Met Ile
```

385 390 395 400

Lys Asp Leu Phe Leu Glu Glu Glu Lys Pro Met Ile Ile Leu Asp Pro
405 410 415

Leu Gly Gly Lys Leu Asp Glu Ile Ser Glu Ser Glu Leu Pro Phe Pro
420 425 430

His Arg Lys Gly Asn Leu Phe Asn Ile Gln Tyr Met Val Asn Trp Gly
435 440 445

Asp Asn Ser Glu Ser Ile Ser Ser Lys Lys Ile Lys Trp Leu Arg Glu
450 455 460

Leu Tyr Glu Lys Met Lys Pro Phe Leu Ser His Cys Pro Arg Thr Ala
465 470 475 480

Tyr Leu Asn Tyr Arg Asp Leu Asp Phe Gly Thr Asn Asp Gly Val Tyr
485 490 495

Arg Tyr Ser Lys Ala Lys Val Trp Gly Ala Lys Tyr Phe Asn Glu Asn
500 505 510

Phe Glu Arg Leu Ala Lys Val Lys Ser Lys Val Asp Pro Gly Asn Phe
515 520 525

Phe Arg Tyr Glu Gln Ser Ile Pro Pro Phe Ser Val Ser Thr Trp Ser
530 535 540

His Pro Gln Phe Glu Lys
545 550

<210> 74
<211> 1860
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS94-A0A1S3XA06-full alpha factor-no signal peptide-strep Tag

<220>
<221> CDS

<222> (1)..(1860)

<400> 74

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atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                  10                  15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg gcc caa caa gag ttc ttg        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ala Gln Gln Glu Phe Leu
                85                  90                  95

caa tgt atc tac tct cac tcc tcc gag aat att aag aag cac att cat        336
Gln Cys Ile Tyr Ser His Ser Ser Glu Asn Ile Lys Lys His Ile His
            100                 105                 110

ttc cca aac agc cca act tac tct tcg ttg ttg gaa tac gct caa aag        384
Phe Pro Asn Ser Pro Thr Tyr Ser Ser Leu Leu Glu Tyr Ala Gln Lys
        115                 120                 125

aat cca aga tgg ctg aat tct tct ttc gcc cat cca att ttc att atc        432
Asn Pro Arg Trp Leu Asn Ser Ser Phe Ala His Pro Ile Phe Ile Ile
    130                 135                 140

gct cca aag aac gaa tcc gaa atc cag cca att atc ttg tgc tct caa        480
Ala Pro Lys Asn Glu Ser Glu Ile Gln Pro Ile Ile Leu Cys Ser Gln
145                 150                 155                 160

aag ttc ggc ttg caa atc aga gtt aag tct ggt ggt cat gat tac gaa        528
Lys Phe Gly Leu Gln Ile Arg Val Lys Ser Gly Gly His Asp Tyr Glu
                165                 170                 175

ggt ttg tct ttc aga tct gtc act aac acc caa ttc gtt atc ttg gac        576
Gly Leu Ser Phe Arg Ser Val Thr Asn Thr Gln Phe Val Ile Leu Asp
            180                 185                 190

ttg atc aac ttg gac gat atc aga atc gac aag aac gaa gaa act gct        624
Leu Ile Asn Leu Asp Asp Ile Arg Ile Asp Lys Asn Glu Glu Thr Ala
        195                 200                 205
```

```
tgg att caa act ggt gtt act atg ggt cag ttg tac tac gaa att gcc        672
Trp Ile Gln Thr Gly Val Thr Met Gly Gln Leu Tyr Tyr Glu Ile Ala
    210                 215                 220

aag aag tct aag atc ttg gct ttt cca ggt ggt cta tat cca tct gtt        720
Lys Lys Ser Lys Ile Leu Ala Phe Pro Gly Gly Leu Tyr Pro Ser Val
225                 230                 235                 240

ggt tct ggt ggt ttg att tca ggt ggt ggt att ggt act ttg atg aga        768
Gly Ser Gly Gly Leu Ile Ser Gly Gly Gly Ile Gly Thr Leu Met Arg
                245                 250                 255

aag ttt ggt ttg tcc gct gat aac gtc att gat gct aga gtt atg gat        816
Lys Phe Gly Leu Ser Ala Asp Asn Val Ile Asp Ala Arg Val Met Asp
            260                 265                 270

gtc aac ggt aga atc ttg gac aaa aag tct atg ggc gaa gat atg ttc        864
Val Asn Gly Arg Ile Leu Asp Lys Lys Ser Met Gly Glu Asp Met Phe
        275                 280                 285

tgg gct att aga ggt ggt ggc ggt tct tct ttt ggt gtt att ttg gct        912
Trp Ala Ile Arg Gly Gly Gly Gly Ser Ser Phe Gly Val Ile Leu Ala
    290                 295                 300

tgg aag atc aag ttg gtt aga atc cca cca aag gtt act gtt ttc acc        960
Trp Lys Ile Lys Leu Val Arg Ile Pro Pro Lys Val Thr Val Phe Thr
305                 310                 315                 320

gtt aga aga aag ttg gaa ggt aac acc atc aac ttg ttg caa aga tgg       1008
Val Arg Arg Lys Leu Glu Gly Asn Thr Ile Asn Leu Leu Gln Arg Trp
                325                 330                 335

caa aac gtt tcc cat aag ttc cca aag gat ttg ttc atg aga gtc ttg       1056
Gln Asn Val Ser His Lys Phe Pro Lys Asp Leu Phe Met Arg Val Leu
            340                 345                 350

atc caa aac atg ggt ttc ggt aac gaa aag atc gtt caa gtt tca ttc       1104
Ile Gln Asn Met Gly Phe Gly Asn Glu Lys Ile Val Gln Val Ser Phe
        355                 360                 365

cag ggt ttg ttt ttg ggt aga gct tct gaa ttg acc cct ttg ttg aat       1152
Gln Gly Leu Phe Leu Gly Arg Ala Ser Glu Leu Thr Pro Leu Leu Asn
    370                 375                 380

caa act ttc cca gaa ttc ggt ttg gac cca aaa aac tgt ttc caa gat       1200
Gln Thr Phe Pro Glu Phe Gly Leu Asp Pro Lys Asn Cys Phe Gln Asp
385                 390                 395                 400

cca gtt gtt aac tgc aac gaa ttg ccc ttc att aag aaa gaa tgc ttc       1248
Pro Val Val Asn Cys Asn Glu Leu Pro Phe Ile Lys Lys Glu Cys Phe
                405                 410                 415

gaa gtt cca tgg atc aga tct acc ttg tac ttt gct tct aag agg acc       1296
```

```
Glu Val Pro Trp Ile Arg Ser Thr Leu Tyr Phe Ala Ser Lys Arg Thr
            420                 425                 430

aac aac tcc att gaa ttc ttg gtt aac aac acc gtt tct cag acc aag       1344
Asn Asn Ser Ile Glu Phe Leu Val Asn Asn Thr Val Ser Gln Thr Lys
        435                 440                 445

aac tac caa aaa gct act tcc gat ttc gtt aag acc cca atg caa gaa       1392
Asn Tyr Gln Lys Ala Thr Ser Asp Phe Val Lys Thr Pro Met Gln Glu
    450                 455                 460

gag gtt tgg ggt atg atc aaa gac ttg ttc ttg gaa gaa gag aag ccc       1440
Glu Val Trp Gly Met Ile Lys Asp Leu Phe Leu Glu Glu Glu Lys Pro
465                 470                 475                 480

atg att att ttg gac cct tta ggt ggt aag ttg gac gaa att tct gaa       1488
Met Ile Ile Leu Asp Pro Leu Gly Gly Lys Leu Asp Glu Ile Ser Glu
                485                 490                 495

tcc gaa ttg cca ttt cca cac aga aag ggt aac ttg ttc aac atc cag       1536
Ser Glu Leu Pro Phe Pro His Arg Lys Gly Asn Leu Phe Asn Ile Gln
            500                 505                 510

tac atg gtt aat tgg ggt gac aac tcc gaa tct atc tcc tcc aaa aaa       1584
Tyr Met Val Asn Trp Gly Asp Asn Ser Glu Ser Ile Ser Ser Lys Lys
        515                 520                 525

atc aaa tgg ctg cgt gag ttg tac gag aag atg aag cca ttt ttg tct       1632
Ile Lys Trp Leu Arg Glu Leu Tyr Glu Lys Met Lys Pro Phe Leu Ser
    530                 535                 540

cat tgt cct aga acc gct tac ttg aac tac aga gat ttg gac ttc ggt       1680
His Cys Pro Arg Thr Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Phe Gly
545                 550                 555                 560

act aat gat ggt gtc tac aga tac tct aaa gcc aaa gtt tgg ggt gct       1728
Thr Asn Asp Gly Val Tyr Arg Tyr Ser Lys Ala Lys Val Trp Gly Ala
                565                 570                 575

aag tac ttc aac gaa aac ttt gaa aga ttg gcc aag gtc aag tct aaa       1776
Lys Tyr Phe Asn Glu Asn Phe Glu Arg Leu Ala Lys Val Lys Ser Lys
            580                 585                 590

gtt gat cca ggt aat ttc ttc agg tac gaa caa tct att cca cca ttc       1824
Val Asp Pro Gly Asn Phe Phe Arg Tyr Glu Gln Ser Ile Pro Pro Phe
        595                 600                 605

tct gtt tcc acc tgg tca cat cca caa ttt gaa aag                       1860
Ser Val Ser Thr Trp Ser His Pro Gln Phe Glu Lys
    610                 615                 620
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<210> 75
<211> 620

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 75

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


Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30


Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45


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


Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80


Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ala Gln Gln Glu Phe Leu
                85                  90                  95


Gln Cys Ile Tyr Ser His Ser Ser Glu Asn Ile Lys Lys His Ile His
            100                 105                 110


Phe Pro Asn Ser Pro Thr Tyr Ser Ser Leu Leu Glu Tyr Ala Gln Lys
        115                 120                 125


Asn Pro Arg Trp Leu Asn Ser Ser Phe Ala His Pro Ile Phe Ile Ile
    130                 135                 140


Ala Pro Lys Asn Glu Ser Glu Ile Gln Pro Ile Ile Leu Cys Ser Gln
145                 150                 155                 160


Lys Phe Gly Leu Gln Ile Arg Val Lys Ser Gly Gly His Asp Tyr Glu
                165                 170                 175


Gly Leu Ser Phe Arg Ser Val Thr Asn Thr Gln Phe Val Ile Leu Asp
            180                 185                 190
```

```
Leu Ile Asn Leu Asp Asp Ile Arg Ile Asp Lys Asn Glu Glu Thr Ala
        195                 200                 205

Trp Ile Gln Thr Gly Val Thr Met Gly Gln Leu Tyr Tyr Glu Ile Ala
    210                 215                 220

Lys Lys Ser Lys Ile Leu Ala Phe Pro Gly Gly Leu Tyr Pro Ser Val
225                 230                 235                 240

Gly Ser Gly Gly Leu Ile Ser Gly Gly Gly Ile Gly Thr Leu Met Arg
                245                 250                 255

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

Val Asn Gly Arg Ile Leu Asp Lys Lys Ser Met Gly Glu Asp Met Phe
        275                 280                 285

Trp Ala Ile Arg Gly Gly Gly Gly Ser Ser Phe Gly Val Ile Leu Ala
    290                 295                 300

Trp Lys Ile Lys Leu Val Arg Ile Pro Pro Lys Val Thr Val Phe Thr
305                 310                 315                 320

Val Arg Arg Lys Leu Glu Gly Asn Thr Ile Asn Leu Leu Gln Arg Trp
                325                 330                 335

Gln Asn Val Ser His Lys Phe Pro Lys Asp Leu Phe Met Arg Val Leu
            340                 345                 350

Ile Gln Asn Met Gly Phe Gly Asn Glu Lys Ile Val Gln Val Ser Phe
        355                 360                 365

Gln Gly Leu Phe Leu Gly Arg Ala Ser Glu Leu Thr Pro Leu Leu Asn
    370                 375                 380

Gln Thr Phe Pro Glu Phe Gly Leu Asp Pro Lys Asn Cys Phe Gln Asp
385                 390                 395                 400
```

```
Pro Val Val Asn Cys Asn Glu Leu Pro Phe Ile Lys Lys Glu Cys Phe
                405                 410                 415

Glu Val Pro Trp Ile Arg Ser Thr Leu Tyr Phe Ala Ser Lys Arg Thr
            420                 425                 430

Asn Asn Ser Ile Glu Phe Leu Val Asn Asn Thr Val Ser Gln Thr Lys
        435                 440                 445

Asn Tyr Gln Lys Ala Thr Ser Asp Phe Val Lys Thr Pro Met Gln Glu
    450                 455                 460

Glu Val Trp Gly Met Ile Lys Asp Leu Phe Leu Glu Glu Glu Lys Pro
465                 470                 475                 480

Met Ile Ile Leu Asp Pro Leu Gly Gly Lys Leu Asp Glu Ile Ser Glu
                485                 490                 495

Ser Glu Leu Pro Phe Pro His Arg Lys Gly Asn Leu Phe Asn Ile Gln
            500                 505                 510

Tyr Met Val Asn Trp Gly Asp Asn Ser Glu Ser Ile Ser Ser Lys Lys
        515                 520                 525

Ile Lys Trp Leu Arg Glu Leu Tyr Glu Lys Met Lys Pro Phe Leu Ser
    530                 535                 540

His Cys Pro Arg Thr Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Phe Gly
545                 550                 555                 560

Thr Asn Asp Gly Val Tyr Arg Tyr Ser Lys Ala Lys Val Trp Gly Ala
                565                 570                 575

Lys Tyr Phe Asn Glu Asn Phe Glu Arg Leu Ala Lys Val Lys Ser Lys
            580                 585                 590

Val Asp Pro Gly Asn Phe Phe Arg Tyr Glu Gln Ser Ile Pro Pro Phe
        595                 600                 605

Ser Val Ser Thr Trp Ser His Pro Gln Phe Glu Lys
    610                 615                 620
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<210> 76
<211> 1608
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS99-A0A1S3BDA8

<220>
<221> CDS
<222> (1)..(1608)

<400> 76
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Met Lys Phe Ser Ser Thr Leu Ile Pro Leu Ser Leu Val Phe Ile Val
1 5 10 15

gtc tcc tct gct tct ttg tgt gct tct gct tct cca caa aag tac caa 96
Val Ser Ser Ala Ser Leu Cys Ala Ser Ala Ser Pro Gln Lys Tyr Gln
20 25 30

aat ttc ttg cag tgc ttg tcc gaa cac tct tct aaa tct tac cca atc 144
Asn Phe Leu Gln Cys Leu Ser Glu His Ser Ser Lys Ser Tyr Pro Ile
35 40 45

tcc aag gtt gtc tat acc cca atc aat tcc tct tac tcc tct gtt ttg 192
Ser Lys Val Val Tyr Thr Pro Ile Asn Ser Ser Tyr Ser Ser Val Leu
50 55 60

gac ttc tcc att agg aac ttg ttg ttc tct aaa cca gaa acg cca aag 240
Asp Phe Ser Ile Arg Asn Leu Leu Phe Ser Lys Pro Glu Thr Pro Lys
65 70 75 80

cct ttg ttg att att act cca tct cac gtg tcc cat att caa gct gct 288
Pro Leu Leu Ile Ile Thr Pro Ser His Val Ser His Ile Gln Ala Ala
85 90 95

gtt att tgt tct aag tcc cat ggc ttg caa atc aga act aga tct ggt 336
Val Ile Cys Ser Lys Ser His Gly Leu Gln Ile Arg Thr Arg Ser Gly
100 105 110

ggt cat gat ttc gaa ggt ttg tct tat gtt gct tac aga cca ttc atc 384
Gly His Asp Phe Glu Gly Leu Ser Tyr Val Ala Tyr Arg Pro Phe Ile
115 120 125

gtt gtc gac ttg att aac ttg aga tcc gtt aag gtt gaa gtc gaa aac 432
Val Val Asp Leu Ile Asn Leu Arg Ser Val Lys Val Glu Val Glu Asn
130 135 140

aat act gct tgg gtt gaa tct ggt gct act ttg ggt gag ttg tat tac 480
Asn Thr Ala Trp Val Glu Ser Gly Ala Thr Leu Gly Glu Leu Tyr Tyr

```
145                 150                 155                 160

aga att ggt gaa aag tct agg acc ttg gct ttt cca gct ggt gtt tgt        528
Arg Ile Gly Glu Lys Ser Arg Thr Leu Ala Phe Pro Ala Gly Val Cys
                165                 170                 175

cca act gtt ggt ata ggt ggt cat ttt tct ggt ggt ggt tat ggt ttg        576
Pro Thr Val Gly Ile Gly Gly His Phe Ser Gly Gly Gly Tyr Gly Leu
            180                 185                 190

atg ttg aga aaa ttt ggt ttg gcc gct gat aac gtc att gat gct tat        624
Met Leu Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Ile Asp Ala Tyr
        195                 200                 205

ttg gtt gat gcc aac ggt aag gtt ttg gac aaa gaa tct atg ggc gaa        672
Leu Val Asp Ala Asn Gly Lys Val Leu Asp Lys Glu Ser Met Gly Glu
    210                 215                 220

gat ttg ttc tgg gct att aga ggt ggt ggt ggc ggt tct ttt ggt ata        720
Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly Ile
225                 230                 235                 240

gtt gtt gct tgg aag atc aag ttg gtt cca gtt cca gaa act gtt act        768
Val Val Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Val Thr
                245                 250                 255

att tgc tct acc gac aga aac ttg gaa gaa gat gcc att aag ttg atc        816
Ile Cys Ser Thr Asp Arg Asn Leu Glu Glu Asp Ala Ile Lys Leu Ile
            260                 265                 270

cac aga tgg caa tac gtt ggt aac aaa ttg gac gag aat atc tac ttg        864
His Arg Trp Gln Tyr Val Gly Asn Lys Leu Asp Glu Asn Ile Tyr Leu
        275                 280                 285

ggt atc att ttg act ggt ggt aac gct tct act caa gct ggt att act        912
Gly Ile Ile Leu Thr Gly Gly Asn Ala Ser Thr Gln Ala Gly Ile Thr
    290                 295                 300

aat cca act gcc aga ttc ttc agc ttg ttt ttg ggt aga gct gat gaa        960
Asn Pro Thr Ala Arg Phe Phe Ser Leu Phe Leu Gly Arg Ala Asp Glu
305                 310                 315                 320

ttg gtt act acc ttg tct act atc ttc cca gaa ttg ggt ttg atc aag       1008
Leu Val Thr Thr Leu Ser Thr Ile Phe Pro Glu Leu Gly Leu Ile Lys
                325                 330                 335

caa gat tgt gtt gaa gct tct tgg gtc gaa tcc act ttg att att cca       1056
Gln Asp Cys Val Glu Ala Ser Trp Val Glu Ser Thr Leu Ile Ile Pro
            340                 345                 350

att ggt gtt cag cca atc gaa acc ttg gaa cca tta ttg aac aga act       1104
Ile Gly Val Gln Pro Ile Glu Thr Leu Glu Pro Leu Leu Asn Arg Thr
        355                 360                 365
```

```
ttg acc acc ttg gac tcc act aag att aag tct gat tac atc acc gaa       1152
Leu Thr Thr Leu Asp Ser Thr Lys Ile Lys Ser Asp Tyr Ile Thr Glu
    370                 375                 380

cct att cca gtt gct gct att aag gat atc tgg cag aga ttg aaa acc       1200
Pro Ile Pro Val Ala Ala Ile Lys Asp Ile Trp Gln Arg Leu Lys Thr
385                 390                 395                 400

caa gac att gaa acc tct cag ttg gtt ttt gtt cca tac ggt ggt aga       1248
Gln Asp Ile Glu Thr Ser Gln Leu Val Phe Val Pro Tyr Gly Gly Arg
                405                 410                 415

atg tcc caa atc tct gaa tct gaa act cca ttc tct cat aga gcc aga       1296
Met Ser Gln Ile Ser Glu Ser Glu Thr Pro Phe Ser His Arg Ala Arg
            420                 425                 430

tac ttg ttc aag atc ggt tat gtt gta ggt tgg aag gac caa tct ttg       1344
Tyr Leu Phe Lys Ile Gly Tyr Val Val Gly Trp Lys Asp Gln Ser Leu
        435                 440                 445

aag gct aag aag aga cat atc tcc tgg ttg aga gaa gtt tat gag tac       1392
Lys Ala Lys Lys Arg His Ile Ser Trp Leu Arg Glu Val Tyr Glu Tyr
    450                 455                 460

atg gct cca ttc gtt tct aaa tca cca aga gct gct tac acc aat tac       1440
Met Ala Pro Phe Val Ser Lys Ser Pro Arg Ala Ala Tyr Thr Asn Tyr
465                 470                 475                 480

aga gac ttg gat att ggc tcc aac aac aaa tac ggt aag acc tct tac       1488
Arg Asp Leu Asp Ile Gly Ser Asn Asn Lys Tyr Gly Lys Thr Ser Tyr
                485                 490                 495

aag aga gct tct gtt tgg ggt ttg aag tat ttc ggt aac aac ttc gat       1536
Lys Arg Ala Ser Val Trp Gly Leu Lys Tyr Phe Gly Asn Asn Phe Asp
            500                 505                 510

aga ctg gtt tac gtt aag acc aag gtt gat cca tac gat ttc ttc aga       1584
Arg Leu Val Tyr Val Lys Thr Lys Val Asp Pro Tyr Asp Phe Phe Arg
        515                 520                 525

cac gaa caa tct att ccc acc ttg                                      1608
His Glu Gln Ser Ile Pro Thr Leu
    530                 535
```

<210> 77
<211> 536
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 77

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Met Lys Phe Ser Ser Thr Leu Ile Pro Leu Ser Leu Val Phe Ile Val
1               5                  10                  15

Val Ser Ser Ala Ser Leu Cys Ala Ser Ala Ser Pro Gln Lys Tyr Gln
            20                  25                  30

Asn Phe Leu Gln Cys Leu Ser Glu His Ser Ser Lys Ser Tyr Pro Ile
        35                  40                  45

Ser Lys Val Val Tyr Thr Pro Ile Asn Ser Ser Tyr Ser Ser Val Leu
    50                  55                  60

Asp Phe Ser Ile Arg Asn Leu Leu Phe Ser Lys Pro Glu Thr Pro Lys
65                  70                  75                  80

Pro Leu Leu Ile Ile Thr Pro Ser His Val Ser His Ile Gln Ala Ala
                85                  90                  95

Val Ile Cys Ser Lys Ser His Gly Leu Gln Ile Arg Thr Arg Ser Gly
            100                 105                 110

Gly His Asp Phe Glu Gly Leu Ser Tyr Val Ala Tyr Arg Pro Phe Ile
        115                 120                 125

Val Val Asp Leu Ile Asn Leu Arg Ser Val Lys Val Glu Val Glu Asn
    130                 135                 140

Asn Thr Ala Trp Val Glu Ser Gly Ala Thr Leu Gly Glu Leu Tyr Tyr
145                 150                 155                 160

Arg Ile Gly Glu Lys Ser Arg Thr Leu Ala Phe Pro Ala Gly Val Cys
                165                 170                 175

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

Met Leu Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Ile Asp Ala Tyr
        195                 200                 205

Leu Val Asp Ala Asn Gly Lys Val Leu Asp Lys Glu Ser Met Gly Glu
```

```
    210                 215                 220

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

Val Val Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Val Thr
                245                 250                 255

Ile Cys Ser Thr Asp Arg Asn Leu Glu Glu Asp Ala Ile Lys Leu Ile
            260                 265                 270

His Arg Trp Gln Tyr Val Gly Asn Lys Leu Asp Glu Asn Ile Tyr Leu
        275                 280                 285

Gly Ile Ile Leu Thr Gly Gly Asn Ala Ser Thr Gln Ala Gly Ile Thr
    290                 295                 300

Asn Pro Thr Ala Arg Phe Phe Ser Leu Phe Leu Gly Arg Ala Asp Glu
305                 310                 315                 320

Leu Val Thr Thr Leu Ser Thr Ile Phe Pro Glu Leu Gly Leu Ile Lys
                325                 330                 335

Gln Asp Cys Val Glu Ala Ser Trp Val Glu Ser Thr Leu Ile Ile Pro
            340                 345                 350

Ile Gly Val Gln Pro Ile Glu Thr Leu Glu Pro Leu Leu Asn Arg Thr
        355                 360                 365

Leu Thr Thr Leu Asp Ser Thr Lys Ile Lys Ser Asp Tyr Ile Thr Glu
    370                 375                 380

Pro Ile Pro Val Ala Ala Ile Lys Asp Ile Trp Gln Arg Leu Lys Thr
385                 390                 395                 400

Gln Asp Ile Glu Thr Ser Gln Leu Val Phe Val Pro Tyr Gly Gly Arg
                405                 410                 415

Met Ser Gln Ile Ser Glu Ser Glu Thr Pro Phe Ser His Arg Ala Arg
            420                 425                 430
```

```
Tyr Leu Phe Lys Ile Gly Tyr Val Val Gly Trp Lys Asp Gln Ser Leu
        435                 440                 445


Lys Ala Lys Lys Arg His Ile Ser Trp Leu Arg Glu Val Tyr Glu Tyr
    450                 455                 460


Met Ala Pro Phe Val Ser Lys Ser Pro Arg Ala Ala Tyr Thr Asn Tyr
465                 470                 475                 480


Arg Asp Leu Asp Ile Gly Ser Asn Asn Lys Tyr Gly Lys Thr Ser Tyr
                485                 490                 495


Lys Arg Ala Ser Val Trp Gly Leu Lys Tyr Phe Gly Asn Asn Phe Asp
            500                 505                 510


Arg Leu Val Tyr Val Lys Thr Lys Val Asp Pro Tyr Asp Phe Phe Arg
        515                 520                 525


His Glu Gln Ser Ile Pro Thr Leu
    530                 535


<210>  78
<211>  1536
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS99-A0A1S3BDA8-no signal peptide


<220>
<221>  CDS
<222>  (1)..(1536)

<400>  78
atg gct tct cca caa aag tac caa aat ttc ttg cag tgc ttg tcc gaa         48
Met Ala Ser Pro Gln Lys Tyr Gln Asn Phe Leu Gln Cys Leu Ser Glu
1               5                   10                  15

cac tct tct aaa tct tac cca atc tcc aag gtt gtc tat acc cca atc         96
His Ser Ser Lys Ser Tyr Pro Ile Ser Lys Val Val Tyr Thr Pro Ile
            20                  25                  30

aat tcc tct tac tcc tct gtt ttg gac ttc tcc att agg aac ttg ttg        144
Asn Ser Ser Tyr Ser Ser Val Leu Asp Phe Ser Ile Arg Asn Leu Leu
        35                  40                  45
```

```
ttc tct aaa cca gaa acg cca aag cct ttg ttg att att act cca tct        192
Phe Ser Lys Pro Glu Thr Pro Lys Pro Leu Leu Ile Ile Thr Pro Ser
    50                  55                  60

cac gtg tcc cat att caa gct gct gtt att tgt tct aag tcc cat ggc        240
His Val Ser His Ile Gln Ala Ala Val Ile Cys Ser Lys Ser His Gly
65                  70                  75                  80

ttg caa atc aga act aga tct ggt ggt cat gat ttc gaa ggt ttg tct        288
Leu Gln Ile Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser
                85                  90                  95

tat gtt gct tac aga cca ttc atc gtt gtc gac ttg att aac ttg aga        336
Tyr Val Ala Tyr Arg Pro Phe Ile Val Val Asp Leu Ile Asn Leu Arg
            100                 105                 110

tcc gtt aag gtt gaa gtc gaa aac aat act gct tgg gtt gaa tct ggt        384
Ser Val Lys Val Glu Val Glu Asn Asn Thr Ala Trp Val Glu Ser Gly
        115                 120                 125

gct act ttg ggt gag ttg tat tac aga att ggt gaa aag tct agg acc        432
Ala Thr Leu Gly Glu Leu Tyr Tyr Arg Ile Gly Glu Lys Ser Arg Thr
    130                 135                 140

ttg gct ttt cca gct ggt gtt tgt cca act gtt ggt ata ggt ggt cat        480
Leu Ala Phe Pro Ala Gly Val Cys Pro Thr Val Gly Ile Gly Gly His
145                 150                 155                 160

ttt tct ggt ggt ggt tat ggt ttg atg ttg aga aaa ttt ggt ttg gcc        528
Phe Ser Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe Gly Leu Ala
                165                 170                 175

gct gat aac gtc att gat gct tat ttg gtt gat gcc aac ggt aag gtt        576
Ala Asp Asn Val Ile Asp Ala Tyr Leu Val Asp Ala Asn Gly Lys Val
            180                 185                 190

ttg gac aaa gaa tct atg ggc gaa gat ttg ttc tgg gct att aga ggt        624
Leu Asp Lys Glu Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly
        195                 200                 205

ggt ggt ggc ggt tct ttt ggt ata gtt gtt gct tgg aag atc aag ttg        672
Gly Gly Gly Gly Ser Phe Gly Ile Val Val Ala Trp Lys Ile Lys Leu
    210                 215                 220

gtt cca gtt cca gaa act gtt act att tgc tct acc gac aga aac ttg        720
Val Pro Val Pro Glu Thr Val Thr Ile Cys Ser Thr Asp Arg Asn Leu
225                 230                 235                 240

gaa gaa gat gcc att aag ttg atc cac aga tgg caa tac gtt ggt aac        768
Glu Glu Asp Ala Ile Lys Leu Ile His Arg Trp Gln Tyr Val Gly Asn
                245                 250                 255

aaa ttg gac gag aat atc tac ttg ggt atc att ttg act ggt ggt aac        816
```

```
Lys Leu Asp Glu Asn Ile Tyr Leu Gly Ile Ile Leu Thr Gly Gly Asn
            260                 265                 270

gct tct act caa gct ggt att act aat cca act gcc aga ttc ttc agc        864
Ala Ser Thr Gln Ala Gly Ile Thr Asn Pro Thr Ala Arg Phe Phe Ser
        275                 280                 285

ttg ttt ttg ggt aga gct gat gaa ttg gtt act acc ttg tct act atc        912
Leu Phe Leu Gly Arg Ala Asp Glu Leu Val Thr Thr Leu Ser Thr Ile
    290                 295                 300

ttc cca gaa ttg ggt ttg atc aag caa gat tgt gtt gaa gct tct tgg        960
Phe Pro Glu Leu Gly Leu Ile Lys Gln Asp Cys Val Glu Ala Ser Trp
305                 310                 315                 320

gtc gaa tcc act ttg att att cca att ggt gtt cag cca atc gaa acc       1008
Val Glu Ser Thr Leu Ile Ile Pro Ile Gly Val Gln Pro Ile Glu Thr
                325                 330                 335

ttg gaa cca tta ttg aac aga act ttg acc acc ttg gac tcc act aag       1056
Leu Glu Pro Leu Leu Asn Arg Thr Leu Thr Thr Leu Asp Ser Thr Lys
            340                 345                 350

att aag tct gat tac atc acc gaa cct att cca gtt gct gct att aag       1104
Ile Lys Ser Asp Tyr Ile Thr Glu Pro Ile Pro Val Ala Ala Ile Lys
        355                 360                 365

gat atc tgg cag aga ttg aaa acc caa gac att gaa acc tct cag ttg       1152
Asp Ile Trp Gln Arg Leu Lys Thr Gln Asp Ile Glu Thr Ser Gln Leu
    370                 375                 380

gtt ttt gtt cca tac ggt ggt aga atg tcc caa atc tct gaa tct gaa       1200
Val Phe Val Pro Tyr Gly Gly Arg Met Ser Gln Ile Ser Glu Ser Glu
385                 390                 395                 400

act cca ttc tct cat aga gcc aga tac ttg ttc aag atc ggt tat gtt       1248
Thr Pro Phe Ser His Arg Ala Arg Tyr Leu Phe Lys Ile Gly Tyr Val
                405                 410                 415

gta ggt tgg aag gac caa tct ttg aag gct aag aag aga cat atc tcc       1296
Val Gly Trp Lys Asp Gln Ser Leu Lys Ala Lys Lys Arg His Ile Ser
            420                 425                 430

tgg ttg aga gaa gtt tat gag tac atg gct cca ttc gtt tct aaa tca       1344
Trp Leu Arg Glu Val Tyr Glu Tyr Met Ala Pro Phe Val Ser Lys Ser
        435                 440                 445

cca aga gct gct tac acc aat tac aga gac ttg gat att ggc tcc aac       1392
Pro Arg Ala Ala Tyr Thr Asn Tyr Arg Asp Leu Asp Ile Gly Ser Asn
    450                 455                 460

aac aaa tac ggt aag acc tct tac aag aga gct tct gtt tgg ggt ttg       1440
Asn Lys Tyr Gly Lys Thr Ser Tyr Lys Arg Ala Ser Val Trp Gly Leu
465                 470                 475                 480
```

```
aag tat ttc ggt aac aac ttc gat aga ctg gtt tac gtt aag acc aag       1488
Lys Tyr Phe Gly Asn Asn Phe Asp Arg Leu Val Tyr Val Lys Thr Lys
                485                 490                 495

gtt gat cca tac gat ttc ttc aga cac gaa caa tct att ccc acc ttg       1536
Val Asp Pro Tyr Asp Phe Phe Arg His Glu Gln Ser Ile Pro Thr Leu
            500                 505                 510
```

<210> 79
<211> 512
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 79

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Met Ala Ser Pro Gln Lys Tyr Gln Asn Phe Leu Gln Cys Leu Ser Glu
1               5                   10                  15


His Ser Ser Lys Ser Tyr Pro Ile Ser Lys Val Val Tyr Thr Pro Ile
            20                  25                  30


Asn Ser Ser Tyr Ser Ser Val Leu Asp Phe Ser Ile Arg Asn Leu Leu
        35                  40                  45


Phe Ser Lys Pro Glu Thr Pro Lys Pro Leu Leu Ile Ile Thr Pro Ser
    50                  55                  60


His Val Ser His Ile Gln Ala Ala Val Ile Cys Ser Lys Ser His Gly
65                  70                  75                  80


Leu Gln Ile Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser
                85                  90                  95


Tyr Val Ala Tyr Arg Pro Phe Ile Val Val Asp Leu Ile Asn Leu Arg
            100                 105                 110


Ser Val Lys Val Glu Val Glu Asn Asn Thr Ala Trp Val Glu Ser Gly
        115                 120                 125


Ala Thr Leu Gly Glu Leu Tyr Tyr Arg Ile Gly Glu Lys Ser Arg Thr
    130                 135                 140
```

```
Leu Ala Phe Pro Ala Gly Val Cys Pro Thr Val Gly Ile Gly Gly His
145                 150                 155                 160


Phe Ser Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe Gly Leu Ala
                165                 170                 175


Ala Asp Asn Val Ile Asp Ala Tyr Leu Val Asp Ala Asn Gly Lys Val
            180                 185                 190


Leu Asp Lys Glu Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly
        195                 200                 205


Gly Gly Gly Gly Ser Phe Gly Ile Val Val Ala Trp Lys Ile Lys Leu
    210                 215                 220


Val Pro Val Pro Glu Thr Val Thr Ile Cys Ser Thr Asp Arg Asn Leu
225                 230                 235                 240


Glu Glu Asp Ala Ile Lys Leu Ile His Arg Trp Gln Tyr Val Gly Asn
                245                 250                 255


Lys Leu Asp Glu Asn Ile Tyr Leu Gly Ile Ile Leu Thr Gly Gly Asn
            260                 265                 270


Ala Ser Thr Gln Ala Gly Ile Thr Asn Pro Thr Ala Arg Phe Phe Ser
        275                 280                 285


Leu Phe Leu Gly Arg Ala Asp Glu Leu Val Thr Thr Leu Ser Thr Ile
    290                 295                 300


Phe Pro Glu Leu Gly Leu Ile Lys Gln Asp Cys Val Glu Ala Ser Trp
305                 310                 315                 320


Val Glu Ser Thr Leu Ile Ile Pro Ile Gly Val Gln Pro Ile Glu Thr
                325                 330                 335


Leu Glu Pro Leu Leu Asn Arg Thr Leu Thr Thr Leu Asp Ser Thr Lys
            340                 345                 350
```

```
Ile Lys Ser Asp Tyr Ile Thr Glu Pro Ile Pro Val Ala Ala Ile Lys
        355                 360                 365

Asp Ile Trp Gln Arg Leu Lys Thr Gln Asp Ile Glu Thr Ser Gln Leu
    370                 375                 380

Val Phe Val Pro Tyr Gly Gly Arg Met Ser Gln Ile Ser Glu Ser Glu
385                 390                 395                 400

Thr Pro Phe Ser His Arg Ala Arg Tyr Leu Phe Lys Ile Gly Tyr Val
                405                 410                 415

Val Gly Trp Lys Asp Gln Ser Leu Lys Ala Lys Lys Arg His Ile Ser
            420                 425                 430

Trp Leu Arg Glu Val Tyr Glu Tyr Met Ala Pro Phe Val Ser Lys Ser
        435                 440                 445

Pro Arg Ala Ala Tyr Thr Asn Tyr Arg Asp Leu Asp Ile Gly Ser Asn
    450                 455                 460

Asn Lys Tyr Gly Lys Thr Ser Tyr Lys Arg Ala Ser Val Trp Gly Leu
465                 470                 475                 480

Lys Tyr Phe Gly Asn Asn Phe Asp Arg Leu Val Tyr Val Lys Thr Lys
                485                 490                 495

Val Asp Pro Tyr Asp Phe Phe Arg His Glu Gln Ser Ile Pro Thr Leu
            500                 505                 510


<210>  80
<211>  1560
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS99-A0A1S3BDA8-no signal peptide-strep Tag


<220>
<221>  CDS
<222>  (1)..(1560)

<400>  80
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atg gct tct cca caa aag tac caa aat ttc ttg cag tgc ttg tcc gaa         48
Met Ala Ser Pro Gln Lys Tyr Gln Asn Phe Leu Gln Cys Leu Ser Glu
1               5                   10                  15

cac tct tct aaa tct tac cca atc tcc aag gtt gtc tat acc cca atc         96
His Ser Ser Lys Ser Tyr Pro Ile Ser Lys Val Val Tyr Thr Pro Ile
            20                  25                  30

aat tcc tct tac tcc tct gtt ttg gac ttc tcc att agg aac ttg ttg        144
Asn Ser Ser Tyr Ser Ser Val Leu Asp Phe Ser Ile Arg Asn Leu Leu
        35                  40                  45

ttc tct aaa cca gaa acg cca aag cct ttg ttg att att act cca tct        192
Phe Ser Lys Pro Glu Thr Pro Lys Pro Leu Leu Ile Ile Thr Pro Ser
    50                  55                  60

cac gtg tcc cat att caa gct gct gtt att tgt tct aag tcc cat ggc        240
His Val Ser His Ile Gln Ala Ala Val Ile Cys Ser Lys Ser His Gly
65                  70                  75                  80

ttg caa atc aga act aga tct ggt ggt cat gat ttc gaa ggt ttg tct        288
Leu Gln Ile Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser
                85                  90                  95

tat gtt gct tac aga cca ttc atc gtt gtc gac ttg att aac ttg aga        336
Tyr Val Ala Tyr Arg Pro Phe Ile Val Val Asp Leu Ile Asn Leu Arg
            100                 105                 110

tcc gtt aag gtt gaa gtc gaa aac aat act gct tgg gtt gaa tct ggt        384
Ser Val Lys Val Glu Val Glu Asn Asn Thr Ala Trp Val Glu Ser Gly
        115                 120                 125

gct act ttg ggt gag ttg tat tac aga att ggt gaa aag tct agg acc        432
Ala Thr Leu Gly Glu Leu Tyr Tyr Arg Ile Gly Glu Lys Ser Arg Thr
    130                 135                 140

ttg gct ttt cca gct ggt gtt tgt cca act gtt ggt ata ggt ggt cat        480
Leu Ala Phe Pro Ala Gly Val Cys Pro Thr Val Gly Ile Gly Gly His
145                 150                 155                 160

ttt tct ggt ggt ggt tat ggt ttg atg ttg aga aaa ttt ggt ttg gcc        528
Phe Ser Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe Gly Leu Ala
                165                 170                 175

gct gat aac gtc att gat gct tat ttg gtt gat gcc aac ggt aag gtt        576
Ala Asp Asn Val Ile Asp Ala Tyr Leu Val Asp Ala Asn Gly Lys Val
            180                 185                 190

ttg gac aaa gaa tct atg ggc gaa gat ttg ttc tgg gct att aga ggt        624
Leu Asp Lys Glu Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly
        195                 200                 205

ggt ggt ggc ggt tct ttt ggt ata gtt gtt gct tgg aag atc aag ttg        672
Gly Gly Gly Gly Ser Phe Gly Ile Val Val Ala Trp Lys Ile Lys Leu
```

```
    210                 215                 220

gtt cca gtt cca gaa act gtt act att tgc tct acc gac aga aac ttg        720
Val Pro Val Pro Glu Thr Val Thr Ile Cys Ser Thr Asp Arg Asn Leu
225                 230                 235                 240

gaa gaa gat gcc att aag ttg atc cac aga tgg caa tac gtt ggt aac        768
Glu Glu Asp Ala Ile Lys Leu Ile His Arg Trp Gln Tyr Val Gly Asn
                245                 250                 255

aaa ttg gac gag aat atc tac ttg ggt atc att ttg act ggt ggt aac        816
Lys Leu Asp Glu Asn Ile Tyr Leu Gly Ile Ile Leu Thr Gly Gly Asn
            260                 265                 270

gct tct act caa gct ggt att act aat cca act gcc aga ttc ttc agc        864
Ala Ser Thr Gln Ala Gly Ile Thr Asn Pro Thr Ala Arg Phe Phe Ser
        275                 280                 285

ttg ttt ttg ggt aga gct gat gaa ttg gtt act acc ttg tct act atc        912
Leu Phe Leu Gly Arg Ala Asp Glu Leu Val Thr Thr Leu Ser Thr Ile
    290                 295                 300

ttc cca gaa ttg ggt ttg atc aag caa gat tgt gtt gaa gct tct tgg        960
Phe Pro Glu Leu Gly Leu Ile Lys Gln Asp Cys Val Glu Ala Ser Trp
305                 310                 315                 320

gtc gaa tcc act ttg att att cca att ggt gtt cag cca atc gaa acc       1008
Val Glu Ser Thr Leu Ile Ile Pro Ile Gly Val Gln Pro Ile Glu Thr
                325                 330                 335

ttg gaa cca tta ttg aac aga act ttg acc acc ttg gac tcc act aag       1056
Leu Glu Pro Leu Leu Asn Arg Thr Leu Thr Thr Leu Asp Ser Thr Lys
            340                 345                 350

att aag tct gat tac atc acc gaa cct att cca gtt gct gct att aag       1104
Ile Lys Ser Asp Tyr Ile Thr Glu Pro Ile Pro Val Ala Ala Ile Lys
        355                 360                 365

gat atc tgg cag aga ttg aaa acc caa gac att gaa acc tct cag ttg       1152
Asp Ile Trp Gln Arg Leu Lys Thr Gln Asp Ile Glu Thr Ser Gln Leu
    370                 375                 380

gtt ttt gtt cca tac ggt ggt aga atg tcc caa atc tct gaa tct gaa       1200
Val Phe Val Pro Tyr Gly Gly Arg Met Ser Gln Ile Ser Glu Ser Glu
385                 390                 395                 400

act cca ttc tct cat aga gcc aga tac ttg ttc aag atc ggt tat gtt       1248
Thr Pro Phe Ser His Arg Ala Arg Tyr Leu Phe Lys Ile Gly Tyr Val
                405                 410                 415

gta ggt tgg aag gac caa tct ttg aag gct aag aag aga cat atc tcc       1296
Val Gly Trp Lys Asp Gln Ser Leu Lys Ala Lys Lys Arg His Ile Ser
            420                 425                 430
```

```
tgg ttg aga gaa gtt tat gag tac atg gct cca ttc gtt tct aaa tca       1344
Trp Leu Arg Glu Val Tyr Glu Tyr Met Ala Pro Phe Val Ser Lys Ser
        435                 440                 445

cca aga gct gct tac acc aat tac aga gac ttg gat att ggc tcc aac       1392
Pro Arg Ala Ala Tyr Thr Asn Tyr Arg Asp Leu Asp Ile Gly Ser Asn
    450                 455                 460

aac aaa tac ggt aag acc tct tac aag aga gct tct gtt tgg ggt ttg       1440
Asn Lys Tyr Gly Lys Thr Ser Tyr Lys Arg Ala Ser Val Trp Gly Leu
465                 470                 475                 480

aag tat ttc ggt aac aac ttc gat aga ctg gtt tac gtt aag acc aag       1488
Lys Tyr Phe Gly Asn Asn Phe Asp Arg Leu Val Tyr Val Lys Thr Lys
                485                 490                 495

gtt gat cca tac gat ttc ttc aga cac gaa caa tct att ccc acc ttg       1536
Val Asp Pro Tyr Asp Phe Phe Arg His Glu Gln Ser Ile Pro Thr Leu
            500                 505                 510

tgg tca cat cca caa ttt gaa aag                                      1560
Trp Ser His Pro Gln Phe Glu Lys
        515                 520
```

<210> 81
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 81

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Met Ala Ser Pro Gln Lys Tyr Gln Asn Phe Leu Gln Cys Leu Ser Glu
1               5                   10                  15


His Ser Ser Lys Ser Tyr Pro Ile Ser Lys Val Val Tyr Thr Pro Ile
            20                  25                  30


Asn Ser Ser Tyr Ser Ser Val Leu Asp Phe Ser Ile Arg Asn Leu Leu
        35                  40                  45


Phe Ser Lys Pro Glu Thr Pro Lys Pro Leu Leu Ile Ile Thr Pro Ser
    50                  55                  60


His Val Ser His Ile Gln Ala Ala Val Ile Cys Ser Lys Ser His Gly
65                  70                  75                  80
```

```
Leu Gln Ile Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser
                85                  90                  95

Tyr Val Ala Tyr Arg Pro Phe Ile Val Val Asp Leu Ile Asn Leu Arg
            100                 105                 110

Ser Val Lys Val Glu Val Glu Asn Asn Thr Ala Trp Val Glu Ser Gly
        115                 120                 125

Ala Thr Leu Gly Glu Leu Tyr Tyr Arg Ile Gly Glu Lys Ser Arg Thr
    130                 135                 140

Leu Ala Phe Pro Ala Gly Val Cys Pro Thr Val Gly Ile Gly Gly His
145                 150                 155                 160

Phe Ser Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe Gly Leu Ala
                165                 170                 175

Ala Asp Asn Val Ile Asp Ala Tyr Leu Val Asp Ala Asn Gly Lys Val
            180                 185                 190

Leu Asp Lys Glu Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly
        195                 200                 205

Gly Gly Gly Gly Ser Phe Gly Ile Val Val Ala Trp Lys Ile Lys Leu
    210                 215                 220

Val Pro Val Pro Glu Thr Val Thr Ile Cys Ser Thr Asp Arg Asn Leu
225                 230                 235                 240

Glu Glu Asp Ala Ile Lys Leu Ile His Arg Trp Gln Tyr Val Gly Asn
                245                 250                 255

Lys Leu Asp Glu Asn Ile Tyr Leu Gly Ile Ile Leu Thr Gly Gly Asn
            260                 265                 270

Ala Ser Thr Gln Ala Gly Ile Thr Asn Pro Thr Ala Arg Phe Phe Ser
        275                 280                 285

Leu Phe Leu Gly Arg Ala Asp Glu Leu Val Thr Thr Leu Ser Thr Ile
```

```
    290                 295                 300

Phe Pro Glu Leu Gly Leu Ile Lys Gln Asp Cys Val Glu Ala Ser Trp
305                 310                 315                 320

Val Glu Ser Thr Leu Ile Ile Pro Ile Gly Val Gln Pro Ile Glu Thr
                325                 330                 335

Leu Glu Pro Leu Leu Asn Arg Thr Leu Thr Thr Leu Asp Ser Thr Lys
            340                 345                 350

Ile Lys Ser Asp Tyr Ile Thr Glu Pro Ile Pro Val Ala Ala Ile Lys
        355                 360                 365

Asp Ile Trp Gln Arg Leu Lys Thr Gln Asp Ile Glu Thr Ser Gln Leu
    370                 375                 380

Val Phe Val Pro Tyr Gly Gly Arg Met Ser Gln Ile Ser Glu Ser Glu
385                 390                 395                 400

Thr Pro Phe Ser His Arg Ala Arg Tyr Leu Phe Lys Ile Gly Tyr Val
                405                 410                 415

Val Gly Trp Lys Asp Gln Ser Leu Lys Ala Lys Lys Arg His Ile Ser
            420                 425                 430

Trp Leu Arg Glu Val Tyr Glu Tyr Met Ala Pro Phe Val Ser Lys Ser
        435                 440                 445

Pro Arg Ala Ala Tyr Thr Asn Tyr Arg Asp Leu Asp Ile Gly Ser Asn
    450                 455                 460

Asn Lys Tyr Gly Lys Thr Ser Tyr Lys Arg Ala Ser Val Trp Gly Leu
465                 470                 475                 480

Lys Tyr Phe Gly Asn Asn Phe Asp Arg Leu Val Tyr Val Lys Thr Lys
                485                 490                 495

Val Asp Pro Tyr Asp Phe Phe Arg His Glu Gln Ser Ile Pro Thr Leu
            500                 505                 510
```

```
Trp Ser His Pro Gln Phe Glu Lys
        515                 520


<210>  82
<211>  1617
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS99-A0A1S3BDA8- truncated alpha factor-no signal peptide-strep
       Tag


<220>
<221>  CDS
<222>  (1)..(1617)

<400>  82
atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca ctt gca atg gct tct cca caa aag tac caa aat ttc ttg cag tgc         96
Ala Leu Ala Met Ala Ser Pro Gln Lys Tyr Gln Asn Phe Leu Gln Cys
            20                  25                  30

ttg tcc gaa cac tct tct aaa tct tac cca atc tcc aag gtt gtc tat        144
Leu Ser Glu His Ser Ser Lys Ser Tyr Pro Ile Ser Lys Val Val Tyr
        35                  40                  45

acc cca atc aat tcc tct tac tcc tct gtt ttg gac ttc tcc att agg        192
Thr Pro Ile Asn Ser Ser Tyr Ser Ser Val Leu Asp Phe Ser Ile Arg
    50                  55                  60

aac ttg ttg ttc tct aaa cca gaa acg cca aag cct ttg ttg att att        240
Asn Leu Leu Phe Ser Lys Pro Glu Thr Pro Lys Pro Leu Leu Ile Ile
65                  70                  75                  80

act cca tct cac gtg tcc cat att caa gct gct gtt att tgt tct aag        288
Thr Pro Ser His Val Ser His Ile Gln Ala Ala Val Ile Cys Ser Lys
                85                  90                  95

tcc cat ggc ttg caa atc aga act aga tct ggt ggt cat gat ttc gaa        336
Ser His Gly Leu Gln Ile Arg Thr Arg Ser Gly Gly His Asp Phe Glu
            100                 105                 110

ggt ttg tct tat gtt gct tac aga cca ttc atc gtt gtc gac ttg att        384
Gly Leu Ser Tyr Val Ala Tyr Arg Pro Phe Ile Val Val Asp Leu Ile
        115                 120                 125

aac ttg aga tcc gtt aag gtt gaa gtc gaa aac aat act gct tgg gtt        432
Asn Leu Arg Ser Val Lys Val Glu Val Glu Asn Asn Thr Ala Trp Val
```

```
    130                 135                 140

gaa tct ggt gct act ttg ggt gag ttg tat tac aga att ggt gaa aag        480
Glu Ser Gly Ala Thr Leu Gly Glu Leu Tyr Tyr Arg Ile Gly Glu Lys
145                 150                 155                 160

tct agg acc ttg gct ttt cca gct ggt gtt tgt cca act gtt ggt ata        528
Ser Arg Thr Leu Ala Phe Pro Ala Gly Val Cys Pro Thr Val Gly Ile
                165                 170                 175

ggt ggt cat ttt tct ggt ggt ggt tat ggt ttg atg ttg aga aaa ttt        576
Gly Gly His Phe Ser Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe
            180                 185                 190

ggt ttg gcc gct gat aac gtc att gat gct tat ttg gtt gat gcc aac        624
Gly Leu Ala Ala Asp Asn Val Ile Asp Ala Tyr Leu Val Asp Ala Asn
        195                 200                 205

ggt aag gtt ttg gac aaa gaa tct atg ggc gaa gat ttg ttc tgg gct        672
Gly Lys Val Leu Asp Lys Glu Ser Met Gly Glu Asp Leu Phe Trp Ala
    210                 215                 220

att aga ggt ggt ggt ggc ggt tct ttt ggt ata gtt gtt gct tgg aag        720
Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly Ile Val Val Ala Trp Lys
225                 230                 235                 240

atc aag ttg gtt cca gtt cca gaa act gtt act att tgc tct acc gac        768
Ile Lys Leu Val Pro Val Pro Glu Thr Val Thr Ile Cys Ser Thr Asp
                245                 250                 255

aga aac ttg gaa gaa gat gcc att aag ttg atc cac aga tgg caa tac        816
Arg Asn Leu Glu Glu Asp Ala Ile Lys Leu Ile His Arg Trp Gln Tyr
            260                 265                 270

gtt ggt aac aaa ttg gac gag aat atc tac ttg ggt atc att ttg act        864
Val Gly Asn Lys Leu Asp Glu Asn Ile Tyr Leu Gly Ile Ile Leu Thr
        275                 280                 285

ggt ggt aac gct tct act caa gct ggt att act aat cca act gcc aga        912
Gly Gly Asn Ala Ser Thr Gln Ala Gly Ile Thr Asn Pro Thr Ala Arg
    290                 295                 300

ttc ttc agc ttg ttt ttg ggt aga gct gat gaa ttg gtt act acc ttg        960
Phe Phe Ser Leu Phe Leu Gly Arg Ala Asp Glu Leu Val Thr Thr Leu
305                 310                 315                 320

tct act atc ttc cca gaa ttg ggt ttg atc aag caa gat tgt gtt gaa       1008
Ser Thr Ile Phe Pro Glu Leu Gly Leu Ile Lys Gln Asp Cys Val Glu
                325                 330                 335

gct tct tgg gtc gaa tcc act ttg att att cca att ggt gtt cag cca       1056
Ala Ser Trp Val Glu Ser Thr Leu Ile Ile Pro Ile Gly Val Gln Pro
            340                 345                 350
```

```
atc gaa acc ttg gaa cca tta ttg aac aga act ttg acc acc ttg gac       1104
Ile Glu Thr Leu Glu Pro Leu Leu Asn Arg Thr Leu Thr Thr Leu Asp
        355                 360                 365

tcc act aag att aag tct gat tac atc acc gaa cct att cca gtt gct       1152
Ser Thr Lys Ile Lys Ser Asp Tyr Ile Thr Glu Pro Ile Pro Val Ala
    370                 375                 380

gct att aag gat atc tgg cag aga ttg aaa acc caa gac att gaa acc       1200
Ala Ile Lys Asp Ile Trp Gln Arg Leu Lys Thr Gln Asp Ile Glu Thr
385                 390                 395                 400

tct cag ttg gtt ttt gtt cca tac ggt ggt aga atg tcc caa atc tct       1248
Ser Gln Leu Val Phe Val Pro Tyr Gly Gly Arg Met Ser Gln Ile Ser
                405                 410                 415

gaa tct gaa act cca ttc tct cat aga gcc aga tac ttg ttc aag atc       1296
Glu Ser Glu Thr Pro Phe Ser His Arg Ala Arg Tyr Leu Phe Lys Ile
            420                 425                 430

ggt tat gtt gta ggt tgg aag gac caa tct ttg aag gct aag aag aga       1344
Gly Tyr Val Val Gly Trp Lys Asp Gln Ser Leu Lys Ala Lys Lys Arg
        435                 440                 445

cat atc tcc tgg ttg aga gaa gtt tat gag tac atg gct cca ttc gtt       1392
His Ile Ser Trp Leu Arg Glu Val Tyr Glu Tyr Met Ala Pro Phe Val
    450                 455                 460

tct aaa tca cca aga gct gct tac acc aat tac aga gac ttg gat att       1440
Ser Lys Ser Pro Arg Ala Ala Tyr Thr Asn Tyr Arg Asp Leu Asp Ile
465                 470                 475                 480

ggc tcc aac aac aaa tac ggt aag acc tct tac aag aga gct tct gtt       1488
Gly Ser Asn Asn Lys Tyr Gly Lys Thr Ser Tyr Lys Arg Ala Ser Val
                485                 490                 495

tgg ggt ttg aag tat ttc ggt aac aac ttc gat aga ctg gtt tac gtt       1536
Trp Gly Leu Lys Tyr Phe Gly Asn Asn Phe Asp Arg Leu Val Tyr Val
            500                 505                 510

aag acc aag gtt gat cca tac gat ttc ttc aga cac gaa caa tct att       1584
Lys Thr Lys Val Asp Pro Tyr Asp Phe Phe Arg His Glu Gln Ser Ile
        515                 520                 525

ccc acc ttg tgg tca cat cca caa ttt gaa aag                           1617
Pro Thr Leu Trp Ser His Pro Gln Phe Glu Lys
    530                 535
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<210> 83
<211> 539
<212> PRT
<213> Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  83

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


Ala Leu Ala Met Ala Ser Pro Gln Lys Tyr Gln Asn Phe Leu Gln Cys
            20                  25                  30


Leu Ser Glu His Ser Ser Lys Ser Tyr Pro Ile Ser Lys Val Val Tyr
        35                  40                  45


Thr Pro Ile Asn Ser Ser Tyr Ser Ser Val Leu Asp Phe Ser Ile Arg
    50                  55                  60


Asn Leu Leu Phe Ser Lys Pro Glu Thr Pro Lys Pro Leu Leu Ile Ile
65                  70                  75                  80


Thr Pro Ser His Val Ser His Ile Gln Ala Ala Val Ile Cys Ser Lys
                85                  90                  95


Ser His Gly Leu Gln Ile Arg Thr Arg Ser Gly Gly His Asp Phe Glu
            100                 105                 110


Gly Leu Ser Tyr Val Ala Tyr Arg Pro Phe Ile Val Val Asp Leu Ile
        115                 120                 125


Asn Leu Arg Ser Val Lys Val Glu Val Glu Asn Asn Thr Ala Trp Val
    130                 135                 140


Glu Ser Gly Ala Thr Leu Gly Glu Leu Tyr Tyr Arg Ile Gly Glu Lys
145                 150                 155                 160


Ser Arg Thr Leu Ala Phe Pro Ala Gly Val Cys Pro Thr Val Gly Ile
                165                 170                 175


Gly Gly His Phe Ser Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe
            180                 185                 190


Gly Leu Ala Ala Asp Asn Val Ile Asp Ala Tyr Leu Val Asp Ala Asn
```

```
        195                 200                 205

Gly Lys Val Leu Asp Lys Glu Ser Met Gly Glu Asp Leu Phe Trp Ala
    210                 215                 220

Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly Ile Val Val Ala Trp Lys
225                 230                 235                 240

Ile Lys Leu Val Pro Val Pro Glu Thr Val Thr Ile Cys Ser Thr Asp
                245                 250                 255

Arg Asn Leu Glu Glu Asp Ala Ile Lys Leu Ile His Arg Trp Gln Tyr
            260                 265                 270

Val Gly Asn Lys Leu Asp Glu Asn Ile Tyr Leu Gly Ile Ile Leu Thr
        275                 280                 285

Gly Gly Asn Ala Ser Thr Gln Ala Gly Ile Thr Asn Pro Thr Ala Arg
    290                 295                 300

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

Ser Thr Ile Phe Pro Glu Leu Gly Leu Ile Lys Gln Asp Cys Val Glu
                325                 330                 335

Ala Ser Trp Val Glu Ser Thr Leu Ile Ile Pro Ile Gly Val Gln Pro
            340                 345                 350

Ile Glu Thr Leu Glu Pro Leu Leu Asn Arg Thr Leu Thr Thr Leu Asp
        355                 360                 365

Ser Thr Lys Ile Lys Ser Asp Tyr Ile Thr Glu Pro Ile Pro Val Ala
    370                 375                 380

Ala Ile Lys Asp Ile Trp Gln Arg Leu Lys Thr Gln Asp Ile Glu Thr
385                 390                 395                 400

Ser Gln Leu Val Phe Val Pro Tyr Gly Gly Arg Met Ser Gln Ile Ser
                405                 410                 415
```

```
Glu Ser Glu Thr Pro Phe Ser His Arg Ala Arg Tyr Leu Phe Lys Ile
            420                 425                 430

Gly Tyr Val Val Gly Trp Lys Asp Gln Ser Leu Lys Ala Lys Lys Arg
        435                 440                 445

His Ile Ser Trp Leu Arg Glu Val Tyr Glu Tyr Met Ala Pro Phe Val
    450                 455                 460

Ser Lys Ser Pro Arg Ala Ala Tyr Thr Asn Tyr Arg Asp Leu Asp Ile
465                 470                 475                 480

Gly Ser Asn Asn Lys Tyr Gly Lys Thr Ser Tyr Lys Arg Ala Ser Val
                485                 490                 495

Trp Gly Leu Lys Tyr Phe Gly Asn Asn Phe Asp Arg Leu Val Tyr Val
            500                 505                 510

Lys Thr Lys Val Asp Pro Tyr Asp Phe Phe Arg His Glu Gln Ser Ile
        515                 520                 525

Pro Thr Leu Trp Ser His Pro Gln Phe Glu Lys
    530                 535
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<210> 84
<211> 1827
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS99-A0A1S3BDA8- full alpha factor -no signal peptide-strep Tag

<220>
<221> CDS
<222> (1)..(1827)

<400> 84

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atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30
```

```
att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg gct tct cca caa aag tac        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ala Ser Pro Gln Lys Tyr
                85                  90                  95

caa aat ttc ttg cag tgc ttg tcc gaa cac tct tct aaa tct tac cca        336
Gln Asn Phe Leu Gln Cys Leu Ser Glu His Ser Ser Lys Ser Tyr Pro
            100                 105                 110

atc tcc aag gtt gtc tat acc cca atc aat tcc tct tac tcc tct gtt        384
Ile Ser Lys Val Val Tyr Thr Pro Ile Asn Ser Ser Tyr Ser Ser Val
        115                 120                 125

ttg gac ttc tcc att agg aac ttg ttg ttc tct aaa cca gaa acg cca        432
Leu Asp Phe Ser Ile Arg Asn Leu Leu Phe Ser Lys Pro Glu Thr Pro
    130                 135                 140

aag cct ttg ttg att att act cca tct cac gtg tcc cat att caa gct        480
Lys Pro Leu Leu Ile Ile Thr Pro Ser His Val Ser His Ile Gln Ala
145                 150                 155                 160

gct gtt att tgt tct aag tcc cat ggc ttg caa atc aga act aga tct        528
Ala Val Ile Cys Ser Lys Ser His Gly Leu Gln Ile Arg Thr Arg Ser
                165                 170                 175

ggt ggt cat gat ttc gaa ggt ttg tct tat gtt gct tac aga cca ttc        576
Gly Gly His Asp Phe Glu Gly Leu Ser Tyr Val Ala Tyr Arg Pro Phe
            180                 185                 190

atc gtt gtc gac ttg att aac ttg aga tcc gtt aag gtt gaa gtc gaa        624
Ile Val Val Asp Leu Ile Asn Leu Arg Ser Val Lys Val Glu Val Glu
        195                 200                 205

aac aat act gct tgg gtt gaa tct ggt gct act ttg ggt gag ttg tat        672
Asn Asn Thr Ala Trp Val Glu Ser Gly Ala Thr Leu Gly Glu Leu Tyr
    210                 215                 220

tac aga att ggt gaa aag tct agg acc ttg gct ttt cca gct ggt gtt        720
Tyr Arg Ile Gly Glu Lys Ser Arg Thr Leu Ala Phe Pro Ala Gly Val
225                 230                 235                 240

tgt cca act gtt ggt ata ggt ggt cat ttt tct ggt ggt ggt tat ggt        768
```

```
Cys Pro Thr Val Gly Ile Gly Gly His Phe Ser Gly Gly Gly Tyr Gly
                245                 250                 255

ttg atg ttg aga aaa ttt ggt ttg gcc gct gat aac gtc att gat gct        816
Leu Met Leu Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Ile Asp Ala
            260                 265                 270

tat ttg gtt gat gcc aac ggt aag gtt ttg gac aaa gaa tct atg ggc        864
Tyr Leu Val Asp Ala Asn Gly Lys Val Leu Asp Lys Glu Ser Met Gly
        275                 280                 285

gaa gat ttg ttc tgg gct att aga ggt ggt ggt ggc ggt tct ttt ggt        912
Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly
    290                 295                 300

ata gtt gtt gct tgg aag atc aag ttg gtt cca gtt cca gaa act gtt        960
Ile Val Val Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Val
305                 310                 315                 320

act att tgc tct acc gac aga aac ttg gaa gaa gat gcc att aag ttg       1008
Thr Ile Cys Ser Thr Asp Arg Asn Leu Glu Glu Asp Ala Ile Lys Leu
                325                 330                 335

atc cac aga tgg caa tac gtt ggt aac aaa ttg gac gag aat atc tac       1056
Ile His Arg Trp Gln Tyr Val Gly Asn Lys Leu Asp Glu Asn Ile Tyr
            340                 345                 350

ttg ggt atc att ttg act ggt ggt aac gct tct act caa gct ggt att       1104
Leu Gly Ile Ile Leu Thr Gly Gly Asn Ala Ser Thr Gln Ala Gly Ile
        355                 360                 365

act aat cca act gcc aga ttc ttc agc ttg ttt ttg ggt aga gct gat       1152
Thr Asn Pro Thr Ala Arg Phe Phe Ser Leu Phe Leu Gly Arg Ala Asp
    370                 375                 380

gaa ttg gtt act acc ttg tct act atc ttc cca gaa ttg ggt ttg atc       1200
Glu Leu Val Thr Thr Leu Ser Thr Ile Phe Pro Glu Leu Gly Leu Ile
385                 390                 395                 400

aag caa gat tgt gtt gaa gct tct tgg gtc gaa tcc act ttg att att       1248
Lys Gln Asp Cys Val Glu Ala Ser Trp Val Glu Ser Thr Leu Ile Ile
                405                 410                 415

cca att ggt gtt cag cca atc gaa acc ttg gaa cca tta ttg aac aga       1296
Pro Ile Gly Val Gln Pro Ile Glu Thr Leu Glu Pro Leu Leu Asn Arg
            420                 425                 430

act ttg acc acc ttg gac tcc act aag att aag tct gat tac atc acc       1344
Thr Leu Thr Thr Leu Asp Ser Thr Lys Ile Lys Ser Asp Tyr Ile Thr
        435                 440                 445

gaa cct att cca gtt gct gct att aag gat atc tgg cag aga ttg aaa       1392
Glu Pro Ile Pro Val Ala Ala Ile Lys Asp Ile Trp Gln Arg Leu Lys
    450                 455                 460
```

```
acc caa gac att gaa acc tct cag ttg gtt ttt gtt cca tac ggt ggt       1440
Thr Gln Asp Ile Glu Thr Ser Gln Leu Val Phe Val Pro Tyr Gly Gly
465                 470                 475                 480

aga atg tcc caa atc tct gaa tct gaa act cca ttc tct cat aga gcc       1488
Arg Met Ser Gln Ile Ser Glu Ser Glu Thr Pro Phe Ser His Arg Ala
                485                 490                 495

aga tac ttg ttc aag atc ggt tat gtt gta ggt tgg aag gac caa tct       1536
Arg Tyr Leu Phe Lys Ile Gly Tyr Val Val Gly Trp Lys Asp Gln Ser
            500                 505                 510

ttg aag gct aag aag aga cat atc tcc tgg ttg aga gaa gtt tat gag       1584
Leu Lys Ala Lys Lys Arg His Ile Ser Trp Leu Arg Glu Val Tyr Glu
        515                 520                 525

tac atg gct cca ttc gtt tct aaa tca cca aga gct gct tac acc aat       1632
Tyr Met Ala Pro Phe Val Ser Lys Ser Pro Arg Ala Ala Tyr Thr Asn
    530                 535                 540

tac aga gac ttg gat att ggc tcc aac aac aaa tac ggt aag acc tct       1680
Tyr Arg Asp Leu Asp Ile Gly Ser Asn Asn Lys Tyr Gly Lys Thr Ser
545                 550                 555                 560

tac aag aga gct tct gtt tgg ggt ttg aag tat ttc ggt aac aac ttc       1728
Tyr Lys Arg Ala Ser Val Trp Gly Leu Lys Tyr Phe Gly Asn Asn Phe
                565                 570                 575

gat aga ctg gtt tac gtt aag acc aag gtt gat cca tac gat ttc ttc       1776
Asp Arg Leu Val Tyr Val Lys Thr Lys Val Asp Pro Tyr Asp Phe Phe
            580                 585                 590

aga cac gaa caa tct att ccc acc ttg tgg tca cat cca caa ttt gaa       1824
Arg His Glu Gln Ser Ile Pro Thr Leu Trp Ser His Pro Gln Phe Glu
        595                 600                 605

aag                                                                   1827
Lys
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<210> 85
<211> 609
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 85

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Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15
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Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

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

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ala Ser Pro Gln Lys Tyr
                85                  90                  95

Gln Asn Phe Leu Gln Cys Leu Ser Glu His Ser Ser Lys Ser Tyr Pro
            100                 105                 110

Ile Ser Lys Val Val Tyr Thr Pro Ile Asn Ser Ser Tyr Ser Ser Val
        115                 120                 125

Leu Asp Phe Ser Ile Arg Asn Leu Leu Phe Ser Lys Pro Glu Thr Pro
    130                 135                 140

Lys Pro Leu Leu Ile Ile Thr Pro Ser His Val Ser His Ile Gln Ala
145                 150                 155                 160

Ala Val Ile Cys Ser Lys Ser His Gly Leu Gln Ile Arg Thr Arg Ser
                165                 170                 175

Gly Gly His Asp Phe Glu Gly Leu Ser Tyr Val Ala Tyr Arg Pro Phe
            180                 185                 190

Ile Val Val Asp Leu Ile Asn Leu Arg Ser Val Lys Val Glu Val Glu
        195                 200                 205

Asn Asn Thr Ala Trp Val Glu Ser Gly Ala Thr Leu Gly Glu Leu Tyr
    210                 215                 220
```

```
Tyr Arg Ile Gly Glu Lys Ser Arg Thr Leu Ala Phe Pro Ala Gly Val
225                 230                 235                 240


Cys Pro Thr Val Gly Ile Gly Gly His Phe Ser Gly Gly Gly Tyr Gly
                245                 250                 255


Leu Met Leu Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Ile Asp Ala
            260                 265                 270


Tyr Leu Val Asp Ala Asn Gly Lys Val Leu Asp Lys Glu Ser Met Gly
        275                 280                 285


Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly
    290                 295                 300


Ile Val Val Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Val
305                 310                 315                 320


Thr Ile Cys Ser Thr Asp Arg Asn Leu Glu Glu Asp Ala Ile Lys Leu
                325                 330                 335


Ile His Arg Trp Gln Tyr Val Gly Asn Lys Leu Asp Glu Asn Ile Tyr
            340                 345                 350


Leu Gly Ile Ile Leu Thr Gly Gly Asn Ala Ser Thr Gln Ala Gly Ile
        355                 360                 365


Thr Asn Pro Thr Ala Arg Phe Phe Ser Leu Phe Leu Gly Arg Ala Asp
    370                 375                 380


Glu Leu Val Thr Thr Leu Ser Thr Ile Phe Pro Glu Leu Gly Leu Ile
385                 390                 395                 400


Lys Gln Asp Cys Val Glu Ala Ser Trp Val Glu Ser Thr Leu Ile Ile
                405                 410                 415


Pro Ile Gly Val Gln Pro Ile Glu Thr Leu Glu Pro Leu Leu Asn Arg
            420                 425                 430


Thr Leu Thr Thr Leu Asp Ser Thr Lys Ile Lys Ser Asp Tyr Ile Thr
        435                 440                 445
```

```
Glu Pro Ile Pro Val Ala Ala Ile Lys Asp Ile Trp Gln Arg Leu Lys
    450                 455                 460

Thr Gln Asp Ile Glu Thr Ser Gln Leu Val Phe Val Pro Tyr Gly Gly
465                 470                 475                 480

Arg Met Ser Gln Ile Ser Glu Ser Glu Thr Pro Phe Ser His Arg Ala
                485                 490                 495

Arg Tyr Leu Phe Lys Ile Gly Tyr Val Val Gly Trp Lys Asp Gln Ser
            500                 505                 510

Leu Lys Ala Lys Lys Arg His Ile Ser Trp Leu Arg Glu Val Tyr Glu
        515                 520                 525

Tyr Met Ala Pro Phe Val Ser Lys Ser Pro Arg Ala Ala Tyr Thr Asn
    530                 535                 540

Tyr Arg Asp Leu Asp Ile Gly Ser Asn Asn Lys Tyr Gly Lys Thr Ser
545                 550                 555                 560

Tyr Lys Arg Ala Ser Val Trp Gly Leu Lys Tyr Phe Gly Asn Asn Phe
                565                 570                 575

Asp Arg Leu Val Tyr Val Lys Thr Lys Val Asp Pro Tyr Asp Phe Phe
            580                 585                 590

Arg His Glu Gln Ser Ile Pro Thr Leu Trp Ser His Pro Gln Phe Glu
        595                 600                 605

Lys
```

<210>  86
<211>  1608
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS124-A0A1U8FGM5

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<221> CDS
<222> (1)..(1608)

<400> 86
atg ggt aac ttg caa atc atc tgc gtc ttg ttg ttc tct ttg ttc ttg 48
Met Gly Asn Leu Gln Ile Ile Cys Val Leu Leu Phe Ser Leu Phe Leu
1 5 10 15

gct aag tgc tac tcc aga gaa gat ttc ttg aga tgc ttg ttc aag tcc 96
Ala Lys Cys Tyr Ser Arg Glu Asp Phe Leu Arg Cys Leu Phe Lys Ser
20 25 30

tcc gaa tct aac gtt act caa aac atc tac acc cca aac tca ttg acc 144
Ser Glu Ser Asn Val Thr Gln Asn Ile Tyr Thr Pro Asn Ser Leu Thr
35 40 45

tac tcc tct att ttg aag tac gct caa aaa cac tcc aga tgg gtt aat 192
Tyr Ser Ser Ile Leu Lys Tyr Ala Gln Lys His Ser Arg Trp Val Asn
50 55 60

tct tct cag cca aat ttc att gct tct ccc aca aaa gaa tcc gaa atc 240
Ser Ser Gln Pro Asn Phe Ile Ala Ser Pro Thr Lys Glu Ser Glu Ile
65 70 75 80

aag cca gtt att ttg tgc gct aag aag ttg ggt ctg caa atc aaa atc 288
Lys Pro Val Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile
85 90 95

aaa tcc ggt ggt cat gat tac gag ggt att tct tac aga tct gaa ttc 336
Lys Ser Gly Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Glu Phe
100 105 110

cca ttc gtc atg ttg gac ttg tcc aat ttg aac aag acc gaa atc gac 384
Pro Phe Val Met Leu Asp Leu Ser Asn Leu Asn Lys Thr Glu Ile Asp
115 120 125

ttg aac gaa gaa acc att tgg gtt caa gct ggt gct act ttg ggt caa 432
Leu Asn Glu Glu Thr Ile Trp Val Gln Ala Gly Ala Thr Leu Gly Gln
130 135 140

cta tat tac gct att gcc aac aga tcc aac gtt cat ggt ttt cca ggt 480
Leu Tyr Tyr Ala Ile Ala Asn Arg Ser Asn Val His Gly Phe Pro Gly
145 150 155 160

ggt att tgt ttc tct gtt ggt act ggt ggt ttg att tct ggt ggt ggt 528
Gly Ile Cys Phe Ser Val Gly Thr Gly Gly Leu Ile Ser Gly Gly Gly
165 170 175

tta ggt act atg atg aga aaa ttt ggt ttg gcc gct gat aac gtt gtt 576
Leu Gly Thr Met Met Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Val
180 185 190

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gat gct aga gtt atg gat gtc aac ggt aac atc ttg gac cgt aaa aag        624
Asp Ala Arg Val Met Asp Val Asn Gly Asn Ile Leu Asp Arg Lys Lys
        195                 200                 205

atg aag aac gat ttg ttc tgg gca att aga ggt ggt ggt ggc gct tct        672
Met Lys Asn Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser
    210                 215                 220

ttt ggt gtt att ttg gct tgg aaa ttg aag ttg gtt agg gtt cca gaa        720
Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu
225                 230                 235                 240

aag gtt act gtt ttc acc gtc tgc aaa aag ttc gat gat aac cag aac        768
Lys Val Thr Val Phe Thr Val Cys Lys Lys Phe Asp Asp Asn Gln Asn
                245                 250                 255

ttg atc ctg aag tgg gaa aac att gct cat caa ttg cca gat aag ttg        816
Leu Ile Leu Lys Trp Glu Asn Ile Ala His Gln Leu Pro Asp Lys Leu
            260                 265                 270

gtc atc aga gtt gtt atc caa aac gat ggt aca ggt aac gat aag tac        864
Val Ile Arg Val Val Ile Gln Asn Asp Gly Thr Gly Asn Asp Lys Tyr
        275                 280                 285

gtc gaa atg aga ttt caa gcc ttg tat ttg ggt cca gtt gat gaa ttg        912
Val Glu Met Arg Phe Gln Ala Leu Tyr Leu Gly Pro Val Asp Glu Leu
    290                 295                 300

atc ccc ttg ttg aaa gaa aag ttc cca gaa ttc gac ttg gaa aag aag        960
Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys
305                 310                 315                 320

gat tgc ttg caa gaa cca gtt ggt gat aga tct aac aga tcc tgc att       1008
Asp Cys Leu Gln Glu Pro Val Gly Asp Arg Ser Asn Arg Ser Cys Ile
                325                 330                 335

aac aaa gaa tgc aga gaa acc tct tgg atc ggt tct gtc ttg tac ttt       1056
Asn Lys Glu Cys Arg Glu Thr Ser Trp Ile Gly Ser Val Leu Tyr Phe
            340                 345                 350

tac gaa aga gaa acc acc tcc tca ttg gag gtc tta ttg aaa gaa tcc       1104
Tyr Glu Arg Glu Thr Thr Ser Ser Leu Glu Val Leu Leu Lys Glu Ser
        355                 360                 365

att cca aag cag aag tcc tac tac aaa ggt act tct gat ttc gtc aag       1152
Ile Pro Lys Gln Lys Ser Tyr Tyr Lys Gly Thr Ser Asp Phe Val Lys
    370                 375                 380

acc cag att tct gaa tct ggt tgg gaa atg gtt gaa agg ttg ttg ttg       1200
Thr Gln Ile Ser Glu Ser Gly Trp Glu Met Val Glu Arg Leu Leu Leu
385                 390                 395                 400

gaa gaa gaa tcc cca aga att atc ttg gaa cca tta ggt ggt aag ttg       1248
Glu Glu Glu Ser Pro Arg Ile Ile Leu Glu Pro Leu Gly Gly Lys Leu
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                405                 410                 415

gac gaa atc tcc gaa tca gaa att cca ttt cca cac aga aaa ggc aac       1296
Asp Glu Ile Ser Glu Ser Glu Ile Pro Phe Pro His Arg Lys Gly Asn
            420                 425                 430

ttg tac aac atc caa tac ttg gtt tac tgg cac gac aac aac gaa aac       1344
Leu Tyr Asn Ile Gln Tyr Leu Val Tyr Trp His Asp Asn Asn Glu Asn
        435                 440                 445

gtt tcc tct caa aaa att gcc tgg atg cgt aag ctg tac aaa gaa atg       1392
Val Ser Ser Gln Lys Ile Ala Trp Met Arg Lys Leu Tyr Lys Glu Met
    450                 455                 460

gaa cca tac gtt gct aac tct cca aga act gct tac ttg aac tac aga       1440
Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg
465                 470                 475                 480

gat ttg gac ttc ggt tct aac gat gac aac tac tct tac tcc aaa gct       1488
Asp Leu Asp Phe Gly Ser Asn Asp Asp Asn Tyr Ser Tyr Ser Lys Ala
                485                 490                 495

aaa atc tgg ggc gaa aag tac ttc aac tac aac ttt gaa aga ctg gcc       1536
Lys Ile Trp Gly Glu Lys Tyr Phe Asn Tyr Asn Phe Glu Arg Leu Ala
            500                 505                 510

aag gtt aag tct aag gtt gat cca aac aac ttc ttc aga acc gaa caa       1584
Lys Val Lys Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Thr Glu Gln
        515                 520                 525

tct att ccc ttg tac caa acc tac                                      1608
Ser Ile Pro Leu Tyr Gln Thr Tyr
    530                 535
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<210>  87
<211>  536
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  87

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Met Gly Asn Leu Gln Ile Ile Cys Val Leu Leu Phe Ser Leu Phe Leu
1               5                   10                  15


Ala Lys Cys Tyr Ser Arg Glu Asp Phe Leu Arg Cys Leu Phe Lys Ser
            20                  25                  30


Ser Glu Ser Asn Val Thr Gln Asn Ile Tyr Thr Pro Asn Ser Leu Thr
```

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        35                  40                  45

Tyr Ser Ser Ile Leu Lys Tyr Ala Gln Lys His Ser Arg Trp Val Asn
    50                  55                  60

Ser Ser Gln Pro Asn Phe Ile Ala Ser Pro Thr Lys Glu Ser Glu Ile
65                  70                  75                  80

Lys Pro Val Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile
                85                  90                  95

Lys Ser Gly Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Glu Phe
            100                 105                 110

Pro Phe Val Met Leu Asp Leu Ser Asn Leu Asn Lys Thr Glu Ile Asp
        115                 120                 125

Leu Asn Glu Glu Thr Ile Trp Val Gln Ala Gly Ala Thr Leu Gly Gln
    130                 135                 140

Leu Tyr Tyr Ala Ile Ala Asn Arg Ser Asn Val His Gly Phe Pro Gly
145                 150                 155                 160

Gly Ile Cys Phe Ser Val Gly Thr Gly Gly Leu Ile Ser Gly Gly Gly
                165                 170                 175

Leu Gly Thr Met Met Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Val
            180                 185                 190

Asp Ala Arg Val Met Asp Val Asn Gly Asn Ile Leu Asp Arg Lys Lys
        195                 200                 205

Met Lys Asn Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser
    210                 215                 220

Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu
225                 230                 235                 240

Lys Val Thr Val Phe Thr Val Cys Lys Lys Phe Asp Asp Asn Gln Asn
                245                 250                 255
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Leu Ile Leu Lys Trp Glu Asn Ile Ala His Gln Leu Pro Asp Lys Leu
            260                 265                 270

Val Ile Arg Val Val Ile Gln Asn Asp Gly Thr Gly Asn Asp Lys Tyr
        275                 280                 285

Val Glu Met Arg Phe Gln Ala Leu Tyr Leu Gly Pro Val Asp Glu Leu
    290                 295                 300

Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys
305                 310                 315                 320

Asp Cys Leu Gln Glu Pro Val Gly Asp Arg Ser Asn Arg Ser Cys Ile
                325                 330                 335

Asn Lys Glu Cys Arg Glu Thr Ser Trp Ile Gly Ser Val Leu Tyr Phe
            340                 345                 350

Tyr Glu Arg Glu Thr Thr Ser Ser Leu Glu Val Leu Leu Lys Glu Ser
        355                 360                 365

Ile Pro Lys Gln Lys Ser Tyr Tyr Lys Gly Thr Ser Asp Phe Val Lys
    370                 375                 380

Thr Gln Ile Ser Glu Ser Gly Trp Glu Met Val Glu Arg Leu Leu Leu
385                 390                 395                 400

Glu Glu Glu Ser Pro Arg Ile Ile Leu Glu Pro Leu Gly Gly Lys Leu
                405                 410                 415

Asp Glu Ile Ser Glu Ser Glu Ile Pro Phe Pro His Arg Lys Gly Asn
            420                 425                 430

Leu Tyr Asn Ile Gln Tyr Leu Val Tyr Trp His Asp Asn Asn Glu Asn
        435                 440                 445

Val Ser Ser Gln Lys Ile Ala Trp Met Arg Lys Leu Tyr Lys Glu Met
    450                 455                 460

Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg
```

```
465                 470                 475                 480

Asp Leu Asp Phe Gly Ser Asn Asp Asp Asn Tyr Ser Tyr Ser Lys Ala
                485                 490                 495

Lys Ile Trp Gly Glu Lys Tyr Phe Asn Tyr Asn Phe Glu Arg Leu Ala
            500                 505                 510

Lys Val Lys Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Thr Glu Gln
        515                 520                 525

Ser Ile Pro Leu Tyr Gln Thr Tyr
    530                 535
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<210> 88
<211> 1551
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS124-A0A1U8FGM5-no signal peptide

<220>
<221> CDS
<222> (1)..(1551)

<400> 88

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atg tcc aga gaa gat ttc ttg aga tgc ttg ttc aag tcc tcc gaa tct         48
Met Ser Arg Glu Asp Phe Leu Arg Cys Leu Phe Lys Ser Ser Glu Ser
1               5                   10                  15

aac gtt act caa aac atc tac acc cca aac tca ttg acc tac tcc tct         96
Asn Val Thr Gln Asn Ile Tyr Thr Pro Asn Ser Leu Thr Tyr Ser Ser
            20                  25                  30

att ttg aag tac gct caa aaa cac tcc aga tgg gtt aat tct tct cag        144
Ile Leu Lys Tyr Ala Gln Lys His Ser Arg Trp Val Asn Ser Ser Gln
        35                  40                  45

cca aat ttc att gct tct ccc aca aaa gaa tcc gaa atc aag cca gtt        192
Pro Asn Phe Ile Ala Ser Pro Thr Lys Glu Ser Glu Ile Lys Pro Val
    50                  55                  60

att ttg tgc gct aag aag ttg ggt ctg caa atc aaa atc aaa tcc ggt        240
Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile Lys Ser Gly
65                  70                  75                  80

ggt cat gat tac gag ggt att tct tac aga tct gaa ttc cca ttc gtc        288
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Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Glu Phe Pro Phe Val
                85                  90                  95

atg ttg gac ttg tcc aat ttg aac aag acc gaa atc gac ttg aac gaa        336
Met Leu Asp Leu Ser Asn Leu Asn Lys Thr Glu Ile Asp Leu Asn Glu
            100                 105                 110

gaa acc att tgg gtt caa gct ggt gct act ttg ggt caa cta tat tac        384
Glu Thr Ile Trp Val Gln Ala Gly Ala Thr Leu Gly Gln Leu Tyr Tyr
        115                 120                 125

gct att gcc aac aga tcc aac gtt cat ggt ttt cca ggt ggt att tgt        432
Ala Ile Ala Asn Arg Ser Asn Val His Gly Phe Pro Gly Gly Ile Cys
    130                 135                 140

ttc tct gtt ggt act ggt ggt ttg att tct ggt ggt ggt tta ggt act        480
Phe Ser Val Gly Thr Gly Gly Leu Ile Ser Gly Gly Gly Leu Gly Thr
145                 150                 155                 160

atg atg aga aaa ttt ggt ttg gcc gct gat aac gtt gtt gat gct aga        528
Met Met Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Val Asp Ala Arg
                165                 170                 175

gtt atg gat gtc aac ggt aac atc ttg gac cgt aaa aag atg aag aac        576
Val Met Asp Val Asn Gly Asn Ile Leu Asp Arg Lys Lys Met Lys Asn
            180                 185                 190

gat ttg ttc tgg gca att aga ggt ggt ggt ggc gct tct ttt ggt gtt        624
Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Val
        195                 200                 205

att ttg gct tgg aaa ttg aag ttg gtt agg gtt cca gaa aag gtt act        672
Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu Lys Val Thr
    210                 215                 220

gtt ttc acc gtc tgc aaa aag ttc gat gat aac cag aac ttg atc ctg        720
Val Phe Thr Val Cys Lys Lys Phe Asp Asp Asn Gln Asn Leu Ile Leu
225                 230                 235                 240

aag tgg gaa aac att gct cat caa ttg cca gat aag ttg gtc atc aga        768
Lys Trp Glu Asn Ile Ala His Gln Leu Pro Asp Lys Leu Val Ile Arg
                245                 250                 255

gtt gtt atc caa aac gat ggt aca ggt aac gat aag tac gtc gaa atg        816
Val Val Ile Gln Asn Asp Gly Thr Gly Asn Asp Lys Tyr Val Glu Met
            260                 265                 270

aga ttt caa gcc ttg tat ttg ggt cca gtt gat gaa ttg atc ccc ttg        864
Arg Phe Gln Ala Leu Tyr Leu Gly Pro Val Asp Glu Leu Ile Pro Leu
        275                 280                 285

ttg aaa gaa aag ttc cca gaa ttc gac ttg gaa aag aag gat tgc ttg        912
Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys Asp Cys Leu
    290                 295                 300
```

```
caa gaa cca gtt ggt gat aga tct aac aga tcc tgc att aac aaa gaa        960
Gln Glu Pro Val Gly Asp Arg Ser Asn Arg Ser Cys Ile Asn Lys Glu
305                 310                 315                 320

tgc aga gaa acc tct tgg atc ggt tct gtc ttg tac ttt tac gaa aga       1008
Cys Arg Glu Thr Ser Trp Ile Gly Ser Val Leu Tyr Phe Tyr Glu Arg
                325                 330                 335

gaa acc acc tcc tca ttg gag gtc tta ttg aaa gaa tcc att cca aag       1056
Glu Thr Thr Ser Ser Leu Glu Val Leu Leu Lys Glu Ser Ile Pro Lys
            340                 345                 350

cag aag tcc tac tac aaa ggt act tct gat ttc gtc aag acc cag att       1104
Gln Lys Ser Tyr Tyr Lys Gly Thr Ser Asp Phe Val Lys Thr Gln Ile
        355                 360                 365

tct gaa tct ggt tgg gaa atg gtt gaa agg ttg ttg ttg gaa gaa gaa       1152
Ser Glu Ser Gly Trp Glu Met Val Glu Arg Leu Leu Leu Glu Glu Glu
    370                 375                 380

tcc cca aga att atc ttg gaa cca tta ggt ggt aag ttg gac gaa atc       1200
Ser Pro Arg Ile Ile Leu Glu Pro Leu Gly Gly Lys Leu Asp Glu Ile
385                 390                 395                 400

tcc gaa tca gaa att cca ttt cca cac aga aaa ggc aac ttg tac aac       1248
Ser Glu Ser Glu Ile Pro Phe Pro His Arg Lys Gly Asn Leu Tyr Asn
                405                 410                 415

atc caa tac ttg gtt tac tgg cac gac aac aac gaa aac gtt tcc tct       1296
Ile Gln Tyr Leu Val Tyr Trp His Asp Asn Asn Glu Asn Val Ser Ser
            420                 425                 430

caa aaa att gcc tgg atg cgt aag ctg tac aaa gaa atg gaa cca tac       1344
Gln Lys Ile Ala Trp Met Arg Lys Leu Tyr Lys Glu Met Glu Pro Tyr
        435                 440                 445

gtt gct aac tct cca aga act gct tac ttg aac tac aga gat ttg gac       1392
Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg Asp Leu Asp
    450                 455                 460

ttc ggt tct aac gat gac aac tac tct tac tcc aaa gct aaa atc tgg       1440
Phe Gly Ser Asn Asp Asp Asn Tyr Ser Tyr Ser Lys Ala Lys Ile Trp
465                 470                 475                 480

ggc gaa aag tac ttc aac tac aac ttt gaa aga ctg gcc aag gtt aag       1488
Gly Glu Lys Tyr Phe Asn Tyr Asn Phe Glu Arg Leu Ala Lys Val Lys
                485                 490                 495

tct aag gtt gat cca aac aac ttc ttc aga acc gaa caa tct att ccc       1536
Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Thr Glu Gln Ser Ile Pro
            500                 505                 510

ttg tac caa acc tac                                                  1551
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Leu Tyr Gln Thr Tyr
515

<210> 89
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 89

Met Ser Arg Glu Asp Phe Leu Arg Cys Leu Phe Lys Ser Ser Glu Ser
1 5 10 15

Asn Val Thr Gln Asn Ile Tyr Thr Pro Asn Ser Leu Thr Tyr Ser Ser
20 25 30

Ile Leu Lys Tyr Ala Gln Lys His Ser Arg Trp Val Asn Ser Ser Gln
35 40 45

Pro Asn Phe Ile Ala Ser Pro Thr Lys Glu Ser Glu Ile Lys Pro Val
50 55 60

Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile Lys Ser Gly
65 70 75 80

Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Glu Phe Pro Phe Val
85 90 95

Met Leu Asp Leu Ser Asn Leu Asn Lys Thr Glu Ile Asp Leu Asn Glu
100 105 110

Glu Thr Ile Trp Val Gln Ala Gly Ala Thr Leu Gly Gln Leu Tyr Tyr
115 120 125

Ala Ile Ala Asn Arg Ser Asn Val His Gly Phe Pro Gly Gly Ile Cys
130 135 140

Phe Ser Val Gly Thr Gly Gly Leu Ile Ser Gly Gly Gly Leu Gly Thr
145 150 155 160

```
Met Met Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Val Asp Ala Arg
                165                 170                 175

Val Met Asp Val Asn Gly Asn Ile Leu Asp Arg Lys Lys Met Lys Asn
            180                 185                 190

Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Val
        195                 200                 205

Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu Lys Val Thr
    210                 215                 220

Val Phe Thr Val Cys Lys Lys Phe Asp Asp Asn Gln Asn Leu Ile Leu
225                 230                 235                 240

Lys Trp Glu Asn Ile Ala His Gln Leu Pro Asp Lys Leu Val Ile Arg
                245                 250                 255

Val Val Ile Gln Asn Asp Gly Thr Gly Asn Asp Lys Tyr Val Glu Met
            260                 265                 270

Arg Phe Gln Ala Leu Tyr Leu Gly Pro Val Asp Glu Leu Ile Pro Leu
        275                 280                 285

Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys Asp Cys Leu
    290                 295                 300

Gln Glu Pro Val Gly Asp Arg Ser Asn Arg Ser Cys Ile Asn Lys Glu
305                 310                 315                 320

Cys Arg Glu Thr Ser Trp Ile Gly Ser Val Leu Tyr Phe Tyr Glu Arg
                325                 330                 335

Glu Thr Thr Ser Ser Leu Glu Val Leu Leu Lys Glu Ser Ile Pro Lys
            340                 345                 350

Gln Lys Ser Tyr Tyr Lys Gly Thr Ser Asp Phe Val Lys Thr Gln Ile
        355                 360                 365

Ser Glu Ser Gly Trp Glu Met Val Glu Arg Leu Leu Leu Glu Glu Glu
    370                 375                 380
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```
Ser Pro Arg Ile Ile Leu Glu Pro Leu Gly Gly Lys Leu Asp Glu Ile
385                 390                 395                 400


Ser Glu Ser Glu Ile Pro Phe Pro His Arg Lys Gly Asn Leu Tyr Asn
                405                 410                 415


Ile Gln Tyr Leu Val Tyr Trp His Asp Asn Asn Glu Asn Val Ser Ser
            420                 425                 430


Gln Lys Ile Ala Trp Met Arg Lys Leu Tyr Lys Glu Met Glu Pro Tyr
        435                 440                 445


Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg Asp Leu Asp
    450                 455                 460


Phe Gly Ser Asn Asp Asp Asn Tyr Ser Tyr Ser Lys Ala Lys Ile Trp
465                 470                 475                 480


Gly Glu Lys Tyr Phe Asn Tyr Asn Phe Glu Arg Leu Ala Lys Val Lys
                485                 490                 495


Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Thr Glu Gln Ser Ile Pro
            500                 505                 510


Leu Tyr Gln Thr Tyr
        515


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<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS124-A0A1U8FGM5-no signal peptide-strep Tag


<220>
<221>  CDS
<222>  (1)..(1575)

<400>  90
atg tcc aga gaa gat ttc ttg aga tgc ttg ttc aag tcc tcc gaa tct         48
Met Ser Arg Glu Asp Phe Leu Arg Cys Leu Phe Lys Ser Ser Glu Ser
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1               5                   10                  15

aac gtt act caa aac atc tac acc cca aac tca ttg acc tac tcc tct         96
Asn Val Thr Gln Asn Ile Tyr Thr Pro Asn Ser Leu Thr Tyr Ser Ser
            20                  25                  30

att ttg aag tac gct caa aaa cac tcc aga tgg gtt aat tct tct cag        144
Ile Leu Lys Tyr Ala Gln Lys His Ser Arg Trp Val Asn Ser Ser Gln
        35                  40                  45

cca aat ttc att gct tct ccc aca aaa gaa tcc gaa atc aag cca gtt        192
Pro Asn Phe Ile Ala Ser Pro Thr Lys Glu Ser Glu Ile Lys Pro Val
    50                  55                  60

att ttg tgc gct aag aag ttg ggt ctg caa atc aaa atc aaa tcc ggt        240
Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile Lys Ser Gly
65                  70                  75                  80

ggt cat gat tac gag ggt att tct tac aga tct gaa ttc cca ttc gtc        288
Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Glu Phe Pro Phe Val
                85                  90                  95

atg ttg gac ttg tcc aat ttg aac aag acc gaa atc gac ttg aac gaa        336
Met Leu Asp Leu Ser Asn Leu Asn Lys Thr Glu Ile Asp Leu Asn Glu
            100                 105                 110

gaa acc att tgg gtt caa gct ggt gct act ttg ggt caa cta tat tac        384
Glu Thr Ile Trp Val Gln Ala Gly Ala Thr Leu Gly Gln Leu Tyr Tyr
        115                 120                 125

gct att gcc aac aga tcc aac gtt cat ggt ttt cca ggt ggt att tgt        432
Ala Ile Ala Asn Arg Ser Asn Val His Gly Phe Pro Gly Gly Ile Cys
    130                 135                 140

ttc tct gtt ggt act ggt ggt ttg att tct ggt ggt ggt tta ggt act        480
Phe Ser Val Gly Thr Gly Gly Leu Ile Ser Gly Gly Gly Leu Gly Thr
145                 150                 155                 160

atg atg aga aaa ttt ggt ttg gcc gct gat aac gtt gtt gat gct aga        528
Met Met Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Val Asp Ala Arg
                165                 170                 175

gtt atg gat gtc aac ggt aac atc ttg gac cgt aaa aag atg aag aac        576
Val Met Asp Val Asn Gly Asn Ile Leu Asp Arg Lys Lys Met Lys Asn
            180                 185                 190

gat ttg ttc tgg gca att aga ggt ggt ggt ggc gct tct ttt ggt gtt        624
Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Val
        195                 200                 205

att ttg gct tgg aaa ttg aag ttg gtt agg gtt cca gaa aag gtt act        672
Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu Lys Val Thr
    210                 215                 220
```

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gtt ttc acc gtc tgc aaa aag ttc gat gat aac cag aac ttg atc ctg        720
Val Phe Thr Val Cys Lys Lys Phe Asp Asp Asn Gln Asn Leu Ile Leu
225                 230                 235                 240

aag tgg gaa aac att gct cat caa ttg cca gat aag ttg gtc atc aga        768
Lys Trp Glu Asn Ile Ala His Gln Leu Pro Asp Lys Leu Val Ile Arg
                245                 250                 255

gtt gtt atc caa aac gat ggt aca ggt aac gat aag tac gtc gaa atg        816
Val Val Ile Gln Asn Asp Gly Thr Gly Asn Asp Lys Tyr Val Glu Met
            260                 265                 270

aga ttt caa gcc ttg tat ttg ggt cca gtt gat gaa ttg atc ccc ttg        864
Arg Phe Gln Ala Leu Tyr Leu Gly Pro Val Asp Glu Leu Ile Pro Leu
        275                 280                 285

ttg aaa gaa aag ttc cca gaa ttc gac ttg gaa aag aag gat tgc ttg        912
Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys Asp Cys Leu
    290                 295                 300

caa gaa cca gtt ggt gat aga tct aac aga tcc tgc att aac aaa gaa        960
Gln Glu Pro Val Gly Asp Arg Ser Asn Arg Ser Cys Ile Asn Lys Glu
305                 310                 315                 320

tgc aga gaa acc tct tgg atc ggt tct gtc ttg tac ttt tac gaa aga       1008
Cys Arg Glu Thr Ser Trp Ile Gly Ser Val Leu Tyr Phe Tyr Glu Arg
                325                 330                 335

gaa acc acc tcc tca ttg gag gtc tta ttg aaa gaa tcc att cca aag       1056
Glu Thr Thr Ser Ser Leu Glu Val Leu Leu Lys Glu Ser Ile Pro Lys
            340                 345                 350

cag aag tcc tac tac aaa ggt act tct gat ttc gtc aag acc cag att       1104
Gln Lys Ser Tyr Tyr Lys Gly Thr Ser Asp Phe Val Lys Thr Gln Ile
        355                 360                 365

tct gaa tct ggt tgg gaa atg gtt gaa agg ttg ttg ttg gaa gaa gaa       1152
Ser Glu Ser Gly Trp Glu Met Val Glu Arg Leu Leu Leu Glu Glu Glu
    370                 375                 380

tcc cca aga att atc ttg gaa cca tta ggt ggt aag ttg gac gaa atc       1200
Ser Pro Arg Ile Ile Leu Glu Pro Leu Gly Gly Lys Leu Asp Glu Ile
385                 390                 395                 400

tcc gaa tca gaa att cca ttt cca cac aga aaa ggc aac ttg tac aac       1248
Ser Glu Ser Glu Ile Pro Phe Pro His Arg Lys Gly Asn Leu Tyr Asn
                405                 410                 415

atc caa tac ttg gtt tac tgg cac gac aac aac gaa aac gtt tcc tct       1296
Ile Gln Tyr Leu Val Tyr Trp His Asp Asn Asn Glu Asn Val Ser Ser
            420                 425                 430

caa aaa att gcc tgg atg cgt aag ctg tac aaa gaa atg gaa cca tac       1344
Gln Lys Ile Ala Trp Met Arg Lys Leu Tyr Lys Glu Met Glu Pro Tyr
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        435                 440                 445

gtt gct aac tct cca aga act gct tac ttg aac tac aga gat ttg gac       1392
Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg Asp Leu Asp
    450                 455                 460

ttc ggt tct aac gat gac aac tac tct tac tcc aaa gct aaa atc tgg       1440
Phe Gly Ser Asn Asp Asp Asn Tyr Ser Tyr Ser Lys Ala Lys Ile Trp
465                 470                 475                 480

ggc gaa aag tac ttc aac tac aac ttt gaa aga ctg gcc aag gtt aag       1488
Gly Glu Lys Tyr Phe Asn Tyr Asn Phe Glu Arg Leu Ala Lys Val Lys
                485                 490                 495

tct aag gtt gat cca aac aac ttc ttc aga acc gaa caa tct att ccc       1536
Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Thr Glu Gln Ser Ile Pro
            500                 505                 510

ttg tac caa acc tac tgg tca cat cca caa ttt gaa aag                   1575
Leu Tyr Gln Thr Tyr Trp Ser His Pro Gln Phe Glu Lys
        515                 520                 525


<210>  91
<211>  525
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  91

Met Ser Arg Glu Asp Phe Leu Arg Cys Leu Phe Lys Ser Ser Glu Ser
1               5                   10                  15


Asn Val Thr Gln Asn Ile Tyr Thr Pro Asn Ser Leu Thr Tyr Ser Ser
            20                  25                  30


Ile Leu Lys Tyr Ala Gln Lys His Ser Arg Trp Val Asn Ser Ser Gln
        35                  40                  45


Pro Asn Phe Ile Ala Ser Pro Thr Lys Glu Ser Glu Ile Lys Pro Val
    50                  55                  60


Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile Lys Ser Gly
65                  70                  75                  80


Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Glu Phe Pro Phe Val
```

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                85                  90                  95

Met Leu Asp Leu Ser Asn Leu Asn Lys Thr Glu Ile Asp Leu Asn Glu
            100                 105                 110

Glu Thr Ile Trp Val Gln Ala Gly Ala Thr Leu Gly Gln Leu Tyr Tyr
        115                 120                 125

Ala Ile Ala Asn Arg Ser Asn Val His Gly Phe Pro Gly Gly Ile Cys
    130                 135                 140

Phe Ser Val Gly Thr Gly Gly Leu Ile Ser Gly Gly Gly Leu Gly Thr
145                 150                 155                 160

Met Met Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Val Asp Ala Arg
                165                 170                 175

Val Met Asp Val Asn Gly Asn Ile Leu Asp Arg Lys Lys Met Lys Asn
            180                 185                 190

Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Val
        195                 200                 205

Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu Lys Val Thr
    210                 215                 220

Val Phe Thr Val Cys Lys Lys Phe Asp Asp Asn Gln Asn Leu Ile Leu
225                 230                 235                 240

Lys Trp Glu Asn Ile Ala His Gln Leu Pro Asp Lys Leu Val Ile Arg
                245                 250                 255

Val Val Ile Gln Asn Asp Gly Thr Gly Asn Asp Lys Tyr Val Glu Met
            260                 265                 270

Arg Phe Gln Ala Leu Tyr Leu Gly Pro Val Asp Glu Leu Ile Pro Leu
        275                 280                 285

Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys Asp Cys Leu
    290                 295                 300
```

```
Gln Glu Pro Val Gly Asp Arg Ser Asn Arg Ser Cys Ile Asn Lys Glu
305                 310                 315                 320

Cys Arg Glu Thr Ser Trp Ile Gly Ser Val Leu Tyr Phe Tyr Glu Arg
                325                 330                 335

Glu Thr Thr Ser Ser Leu Glu Val Leu Leu Lys Glu Ser Ile Pro Lys
            340                 345                 350

Gln Lys Ser Tyr Tyr Lys Gly Thr Ser Asp Phe Val Lys Thr Gln Ile
        355                 360                 365

Ser Glu Ser Gly Trp Glu Met Val Glu Arg Leu Leu Leu Glu Glu Glu
    370                 375                 380

Ser Pro Arg Ile Ile Leu Glu Pro Leu Gly Gly Lys Leu Asp Glu Ile
385                 390                 395                 400

Ser Glu Ser Glu Ile Pro Phe Pro His Arg Lys Gly Asn Leu Tyr Asn
                405                 410                 415

Ile Gln Tyr Leu Val Tyr Trp His Asp Asn Asn Glu Asn Val Ser Ser
            420                 425                 430

Gln Lys Ile Ala Trp Met Arg Lys Leu Tyr Lys Glu Met Glu Pro Tyr
        435                 440                 445

Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg Asp Leu Asp
    450                 455                 460

Phe Gly Ser Asn Asp Asp Asn Tyr Ser Tyr Ser Lys Ala Lys Ile Trp
465                 470                 475                 480

Gly Glu Lys Tyr Phe Asn Tyr Asn Phe Glu Arg Leu Ala Lys Val Lys
                485                 490                 495

Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Thr Glu Gln Ser Ile Pro
            500                 505                 510

Leu Tyr Gln Thr Tyr Trp Ser His Pro Gln Phe Glu Lys
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        515                 520                 525


<210>  92
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS124-A0A1U8FGM5- truncated alpha factor - no signal
       peptide-strep Tag


<220>
<221>  CDS
<222>  (1)..(1632)

<400>  92
atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca ctt gca atg tcc aga gaa gat ttc ttg aga tgc ttg ttc aag tcc         96
Ala Leu Ala Met Ser Arg Glu Asp Phe Leu Arg Cys Leu Phe Lys Ser
            20                  25                  30

tcc gaa tct aac gtt act caa aac atc tac acc cca aac tca ttg acc        144
Ser Glu Ser Asn Val Thr Gln Asn Ile Tyr Thr Pro Asn Ser Leu Thr
        35                  40                  45

tac tcc tct att ttg aag tac gct caa aaa cac tcc aga tgg gtt aat        192
Tyr Ser Ser Ile Leu Lys Tyr Ala Gln Lys His Ser Arg Trp Val Asn
    50                  55                  60

tct tct cag cca aat ttc att gct tct ccc aca aaa gaa tcc gaa atc        240
Ser Ser Gln Pro Asn Phe Ile Ala Ser Pro Thr Lys Glu Ser Glu Ile
65                  70                  75                  80

aag cca gtt att ttg tgc gct aag aag ttg ggt ctg caa atc aaa atc        288
Lys Pro Val Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile
                85                  90                  95

aaa tcc ggt ggt cat gat tac gag ggt att tct tac aga tct gaa ttc        336
Lys Ser Gly Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Glu Phe
            100                 105                 110

cca ttc gtc atg ttg gac ttg tcc aat ttg aac aag acc gaa atc gac        384
Pro Phe Val Met Leu Asp Leu Ser Asn Leu Asn Lys Thr Glu Ile Asp
        115                 120                 125

ttg aac gaa gaa acc att tgg gtt caa gct ggt gct act ttg ggt caa        432
Leu Asn Glu Glu Thr Ile Trp Val Gln Ala Gly Ala Thr Leu Gly Gln
    130                 135                 140
```

```
cta tat tac gct att gcc aac aga tcc aac gtt cat ggt ttt cca ggt        480
Leu Tyr Tyr Ala Ile Ala Asn Arg Ser Asn Val His Gly Phe Pro Gly
145                 150                 155                 160

ggt att tgt ttc tct gtt ggt act ggt ggt ttg att tct ggt ggt ggt        528
Gly Ile Cys Phe Ser Val Gly Thr Gly Gly Leu Ile Ser Gly Gly Gly
                165                 170                 175

tta ggt act atg atg aga aaa ttt ggt ttg gcc gct gat aac gtt gtt        576
Leu Gly Thr Met Met Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Val
            180                 185                 190

gat gct aga gtt atg gat gtc aac ggt aac atc ttg gac cgt aaa aag        624
Asp Ala Arg Val Met Asp Val Asn Gly Asn Ile Leu Asp Arg Lys Lys
        195                 200                 205

atg aag aac gat ttg ttc tgg gca att aga ggt ggt ggt ggc gct tct        672
Met Lys Asn Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser
    210                 215                 220

ttt ggt gtt att ttg gct tgg aaa ttg aag ttg gtt agg gtt cca gaa        720
Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu
225                 230                 235                 240

aag gtt act gtt ttc acc gtc tgc aaa aag ttc gat gat aac cag aac        768
Lys Val Thr Val Phe Thr Val Cys Lys Lys Phe Asp Asp Asn Gln Asn
                245                 250                 255

ttg atc ctg aag tgg gaa aac att gct cat caa ttg cca gat aag ttg        816
Leu Ile Leu Lys Trp Glu Asn Ile Ala His Gln Leu Pro Asp Lys Leu
            260                 265                 270

gtc atc aga gtt gtt atc caa aac gat ggt aca ggt aac gat aag tac        864
Val Ile Arg Val Val Ile Gln Asn Asp Gly Thr Gly Asn Asp Lys Tyr
        275                 280                 285

gtc gaa atg aga ttt caa gcc ttg tat ttg ggt cca gtt gat gaa ttg        912
Val Glu Met Arg Phe Gln Ala Leu Tyr Leu Gly Pro Val Asp Glu Leu
    290                 295                 300

atc ccc ttg ttg aaa gaa aag ttc cca gaa ttc gac ttg gaa aag aag        960
Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys
305                 310                 315                 320

gat tgc ttg caa gaa cca gtt ggt gat aga tct aac aga tcc tgc att       1008
Asp Cys Leu Gln Glu Pro Val Gly Asp Arg Ser Asn Arg Ser Cys Ile
                325                 330                 335

aac aaa gaa tgc aga gaa acc tct tgg atc ggt tct gtc ttg tac ttt       1056
Asn Lys Glu Cys Arg Glu Thr Ser Trp Ile Gly Ser Val Leu Tyr Phe
            340                 345                 350

tac gaa aga gaa acc acc tcc tca ttg gag gtc tta ttg aaa gaa tcc       1104
Tyr Glu Arg Glu Thr Thr Ser Ser Leu Glu Val Leu Leu Lys Glu Ser
```

```
        355                 360                 365

att cca aag cag aag tcc tac tac aaa ggt act tct gat ttc gtc aag       1152
Ile Pro Lys Gln Lys Ser Tyr Tyr Lys Gly Thr Ser Asp Phe Val Lys
    370                 375                 380

acc cag att tct gaa tct ggt tgg gaa atg gtt gaa agg ttg ttg ttg       1200
Thr Gln Ile Ser Glu Ser Gly Trp Glu Met Val Glu Arg Leu Leu Leu
385                 390                 395                 400

gaa gaa gaa tcc cca aga att atc ttg gaa cca tta ggt ggt aag ttg       1248
Glu Glu Glu Ser Pro Arg Ile Ile Leu Glu Pro Leu Gly Gly Lys Leu
                405                 410                 415

gac gaa atc tcc gaa tca gaa att cca ttt cca cac aga aaa ggc aac       1296
Asp Glu Ile Ser Glu Ser Glu Ile Pro Phe Pro His Arg Lys Gly Asn
            420                 425                 430

ttg tac aac atc caa tac ttg gtt tac tgg cac gac aac aac gaa aac       1344
Leu Tyr Asn Ile Gln Tyr Leu Val Tyr Trp His Asp Asn Asn Glu Asn
        435                 440                 445

gtt tcc tct caa aaa att gcc tgg atg cgt aag ctg tac aaa gaa atg       1392
Val Ser Ser Gln Lys Ile Ala Trp Met Arg Lys Leu Tyr Lys Glu Met
    450                 455                 460

gaa cca tac gtt gct aac tct cca aga act gct tac ttg aac tac aga       1440
Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg
465                 470                 475                 480

gat ttg gac ttc ggt tct aac gat gac aac tac tct tac tcc aaa gct       1488
Asp Leu Asp Phe Gly Ser Asn Asp Asp Asn Tyr Ser Tyr Ser Lys Ala
                485                 490                 495

aaa atc tgg ggc gaa aag tac ttc aac tac aac ttt gaa aga ctg gcc       1536
Lys Ile Trp Gly Glu Lys Tyr Phe Asn Tyr Asn Phe Glu Arg Leu Ala
            500                 505                 510

aag gtt aag tct aag gtt gat cca aac aac ttc ttc aga acc gaa caa       1584
Lys Val Lys Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Thr Glu Gln
        515                 520                 525

tct att ccc ttg tac caa acc tac tgg tca cat cca caa ttt gaa aag       1632
Ser Ile Pro Leu Tyr Gln Thr Tyr Trp Ser His Pro Gln Phe Glu Lys
    530                 535                 540
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<210> 93
<211> 544
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 93

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

Ala Leu Ala Met Ser Arg Glu Asp Phe Leu Arg Cys Leu Phe Lys Ser
            20                  25                  30

Ser Glu Ser Asn Val Thr Gln Asn Ile Tyr Thr Pro Asn Ser Leu Thr
        35                  40                  45

Tyr Ser Ser Ile Leu Lys Tyr Ala Gln Lys His Ser Arg Trp Val Asn
    50                  55                  60

Ser Ser Gln Pro Asn Phe Ile Ala Ser Pro Thr Lys Glu Ser Glu Ile
65                  70                  75                  80

Lys Pro Val Ile Leu Cys Ala Lys Lys Leu Gly Leu Gln Ile Lys Ile
                85                  90                  95

Lys Ser Gly Gly His Asp Tyr Glu Gly Ile Ser Tyr Arg Ser Glu Phe
            100                 105                 110

Pro Phe Val Met Leu Asp Leu Ser Asn Leu Asn Lys Thr Glu Ile Asp
        115                 120                 125

Leu Asn Glu Glu Thr Ile Trp Val Gln Ala Gly Ala Thr Leu Gly Gln
    130                 135                 140

Leu Tyr Tyr Ala Ile Ala Asn Arg Ser Asn Val His Gly Phe Pro Gly
145                 150                 155                 160

Gly Ile Cys Phe Ser Val Gly Thr Gly Gly Leu Ile Ser Gly Gly Gly
                165                 170                 175

Leu Gly Thr Met Met Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Val
            180                 185                 190

Asp Ala Arg Val Met Asp Val Asn Gly Asn Ile Leu Asp Arg Lys Lys
        195                 200                 205
```

```
Met Lys Asn Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser
    210                 215                 220

Phe Gly Val Ile Leu Ala Trp Lys Leu Lys Leu Val Arg Val Pro Glu
225                 230                 235                 240

Lys Val Thr Val Phe Thr Val Cys Lys Lys Phe Asp Asp Asn Gln Asn
                245                 250                 255

Leu Ile Leu Lys Trp Glu Asn Ile Ala His Gln Leu Pro Asp Lys Leu
            260                 265                 270

Val Ile Arg Val Val Ile Gln Asn Asp Gly Thr Gly Asn Asp Lys Tyr
        275                 280                 285

Val Glu Met Arg Phe Gln Ala Leu Tyr Leu Gly Pro Val Asp Glu Leu
    290                 295                 300

Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu Phe Asp Leu Glu Lys Lys
305                 310                 315                 320

Asp Cys Leu Gln Glu Pro Val Gly Asp Arg Ser Asn Arg Ser Cys Ile
                325                 330                 335

Asn Lys Glu Cys Arg Glu Thr Ser Trp Ile Gly Ser Val Leu Tyr Phe
            340                 345                 350

Tyr Glu Arg Glu Thr Thr Ser Ser Leu Glu Val Leu Leu Lys Glu Ser
        355                 360                 365

Ile Pro Lys Gln Lys Ser Tyr Tyr Lys Gly Thr Ser Asp Phe Val Lys
    370                 375                 380

Thr Gln Ile Ser Glu Ser Gly Trp Glu Met Val Glu Arg Leu Leu Leu
385                 390                 395                 400

Glu Glu Glu Ser Pro Arg Ile Ile Leu Glu Pro Leu Gly Gly Lys Leu
                405                 410                 415

Asp Glu Ile Ser Glu Ser Glu Ile Pro Phe Pro His Arg Lys Gly Asn
```

```
            420                 425                 430

Leu Tyr Asn Ile Gln Tyr Leu Val Tyr Trp His Asp Asn Asn Glu Asn
        435                 440                 445

Val Ser Ser Gln Lys Ile Ala Trp Met Arg Lys Leu Tyr Lys Glu Met
    450                 455                 460

Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr Ala Tyr Leu Asn Tyr Arg
465                 470                 475                 480

Asp Leu Asp Phe Gly Ser Asn Asp Asp Asn Tyr Ser Tyr Ser Lys Ala
                485                 490                 495

Lys Ile Trp Gly Glu Lys Tyr Phe Asn Tyr Asn Phe Glu Arg Leu Ala
            500                 505                 510

Lys Val Lys Ser Lys Val Asp Pro Asn Asn Phe Phe Arg Thr Glu Gln
        515                 520                 525

Ser Ile Pro Leu Tyr Gln Thr Tyr Trp Ser His Pro Gln Phe Glu Lys
    530                 535                 540


<210>  94
<211>  1842
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS124-A0A1U8FGM5- full alpha factor -no signal peptide-strep Tag


<220>
<221>  CDS
<222>  (1)..(1842)

<400>  94
atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
```

```
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg tcc aga gaa gat ttc ttg        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ser Arg Glu Asp Phe Leu
                85                  90                  95

aga tgc ttg ttc aag tcc tcc gaa tct aac gtt act caa aac atc tac        336
Arg Cys Leu Phe Lys Ser Ser Glu Ser Asn Val Thr Gln Asn Ile Tyr
            100                 105                 110

acc cca aac tca ttg acc tac tcc tct att ttg aag tac gct caa aaa        384
Thr Pro Asn Ser Leu Thr Tyr Ser Ser Ile Leu Lys Tyr Ala Gln Lys
        115                 120                 125

cac tcc aga tgg gtt aat tct tct cag cca aat ttc att gct tct ccc        432
His Ser Arg Trp Val Asn Ser Ser Gln Pro Asn Phe Ile Ala Ser Pro
    130                 135                 140

aca aaa gaa tcc gaa atc aag cca gtt att ttg tgc gct aag aag ttg        480
Thr Lys Glu Ser Glu Ile Lys Pro Val Ile Leu Cys Ala Lys Lys Leu
145                 150                 155                 160

ggt ctg caa atc aaa atc aaa tcc ggt ggt cat gat tac gag ggt att        528
Gly Leu Gln Ile Lys Ile Lys Ser Gly Gly His Asp Tyr Glu Gly Ile
                165                 170                 175

tct tac aga tct gaa ttc cca ttc gtc atg ttg gac ttg tcc aat ttg        576
Ser Tyr Arg Ser Glu Phe Pro Phe Val Met Leu Asp Leu Ser Asn Leu
            180                 185                 190

aac aag acc gaa atc gac ttg aac gaa gaa acc att tgg gtt caa gct        624
Asn Lys Thr Glu Ile Asp Leu Asn Glu Glu Thr Ile Trp Val Gln Ala
        195                 200                 205

ggt gct act ttg ggt caa cta tat tac gct att gcc aac aga tcc aac        672
Gly Ala Thr Leu Gly Gln Leu Tyr Tyr Ala Ile Ala Asn Arg Ser Asn
    210                 215                 220

gtt cat ggt ttt cca ggt ggt att tgt ttc tct gtt ggt act ggt ggt        720
Val His Gly Phe Pro Gly Gly Ile Cys Phe Ser Val Gly Thr Gly Gly
225                 230                 235                 240

ttg att tct ggt ggt ggt tta ggt act atg atg aga aaa ttt ggt ttg        768
Leu Ile Ser Gly Gly Gly Leu Gly Thr Met Met Arg Lys Phe Gly Leu
                245                 250                 255
```

```
gcc gct gat aac gtt gtt gat gct aga gtt atg gat gtc aac ggt aac        816
Ala Ala Asp Asn Val Val Asp Ala Arg Val Met Asp Val Asn Gly Asn
            260                 265                 270

atc ttg gac cgt aaa aag atg aag aac gat ttg ttc tgg gca att aga        864
Ile Leu Asp Arg Lys Lys Met Lys Asn Asp Leu Phe Trp Ala Ile Arg
        275                 280                 285

ggt ggt ggt ggc gct tct ttt ggt gtt att ttg gct tgg aaa ttg aag        912
Gly Gly Gly Gly Ala Ser Phe Gly Val Ile Leu Ala Trp Lys Leu Lys
    290                 295                 300

ttg gtt agg gtt cca gaa aag gtt act gtt ttc acc gtc tgc aaa aag        960
Leu Val Arg Val Pro Glu Lys Val Thr Val Phe Thr Val Cys Lys Lys
305                 310                 315                 320

ttc gat gat aac cag aac ttg atc ctg aag tgg gaa aac att gct cat       1008
Phe Asp Asp Asn Gln Asn Leu Ile Leu Lys Trp Glu Asn Ile Ala His
                325                 330                 335

caa ttg cca gat aag ttg gtc atc aga gtt gtt atc caa aac gat ggt       1056
Gln Leu Pro Asp Lys Leu Val Ile Arg Val Val Ile Gln Asn Asp Gly
            340                 345                 350

aca ggt aac gat aag tac gtc gaa atg aga ttt caa gcc ttg tat ttg       1104
Thr Gly Asn Asp Lys Tyr Val Glu Met Arg Phe Gln Ala Leu Tyr Leu
        355                 360                 365

ggt cca gtt gat gaa ttg atc ccc ttg ttg aaa gaa aag ttc cca gaa       1152
Gly Pro Val Asp Glu Leu Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu
    370                 375                 380

ttc gac ttg gaa aag aag gat tgc ttg caa gaa cca gtt ggt gat aga       1200
Phe Asp Leu Glu Lys Lys Asp Cys Leu Gln Glu Pro Val Gly Asp Arg
385                 390                 395                 400

tct aac aga tcc tgc att aac aaa gaa tgc aga gaa acc tct tgg atc       1248
Ser Asn Arg Ser Cys Ile Asn Lys Glu Cys Arg Glu Thr Ser Trp Ile
                405                 410                 415

ggt tct gtc ttg tac ttt tac gaa aga gaa acc acc tcc tca ttg gag       1296
Gly Ser Val Leu Tyr Phe Tyr Glu Arg Glu Thr Thr Ser Ser Leu Glu
            420                 425                 430

gtc tta ttg aaa gaa tcc att cca aag cag aag tcc tac tac aaa ggt       1344
Val Leu Leu Lys Glu Ser Ile Pro Lys Gln Lys Ser Tyr Tyr Lys Gly
        435                 440                 445

act tct gat ttc gtc aag acc cag att tct gaa tct ggt tgg gaa atg       1392
Thr Ser Asp Phe Val Lys Thr Gln Ile Ser Glu Ser Gly Trp Glu Met
    450                 455                 460

gtt gaa agg ttg ttg ttg gaa gaa gaa tcc cca aga att atc ttg gaa       1440
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```
Val Glu Arg Leu Leu Leu Glu Glu Glu Ser Pro Arg Ile Ile Leu Glu
465                 470                 475                 480

cca tta ggt ggt aag ttg gac gaa atc tcc gaa tca gaa att cca ttt       1488
Pro Leu Gly Gly Lys Leu Asp Glu Ile Ser Glu Ser Glu Ile Pro Phe
                485                 490                 495

cca cac aga aaa ggc aac ttg tac aac atc caa tac ttg gtt tac tgg       1536
Pro His Arg Lys Gly Asn Leu Tyr Asn Ile Gln Tyr Leu Val Tyr Trp
            500                 505                 510

cac gac aac aac gaa aac gtt tcc tct caa aaa att gcc tgg atg cgt       1584
His Asp Asn Asn Glu Asn Val Ser Ser Gln Lys Ile Ala Trp Met Arg
        515                 520                 525

aag ctg tac aaa gaa atg gaa cca tac gtt gct aac tct cca aga act       1632
Lys Leu Tyr Lys Glu Met Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr
    530                 535                 540

gct tac ttg aac tac aga gat ttg gac ttc ggt tct aac gat gac aac       1680
Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Phe Gly Ser Asn Asp Asp Asn
545                 550                 555                 560

tac tct tac tcc aaa gct aaa atc tgg ggc gaa aag tac ttc aac tac       1728
Tyr Ser Tyr Ser Lys Ala Lys Ile Trp Gly Glu Lys Tyr Phe Asn Tyr
                565                 570                 575

aac ttt gaa aga ctg gcc aag gtt aag tct aag gtt gat cca aac aac       1776
Asn Phe Glu Arg Leu Ala Lys Val Lys Ser Lys Val Asp Pro Asn Asn
            580                 585                 590

ttc ttc aga acc gaa caa tct att ccc ttg tac caa acc tac tgg tca       1824
Phe Phe Arg Thr Glu Gln Ser Ile Pro Leu Tyr Gln Thr Tyr Trp Ser
        595                 600                 605

cat cca caa ttt gaa aag                                              1842
His Pro Gln Phe Glu Lys
    610
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<210>  95
<211>  614
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  95

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Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15
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Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

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

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ser Arg Glu Asp Phe Leu
                85                  90                  95

Arg Cys Leu Phe Lys Ser Ser Glu Ser Asn Val Thr Gln Asn Ile Tyr
            100                 105                 110

Thr Pro Asn Ser Leu Thr Tyr Ser Ser Ile Leu Lys Tyr Ala Gln Lys
        115                 120                 125

His Ser Arg Trp Val Asn Ser Ser Gln Pro Asn Phe Ile Ala Ser Pro
    130                 135                 140

Thr Lys Glu Ser Glu Ile Lys Pro Val Ile Leu Cys Ala Lys Lys Leu
145                 150                 155                 160

Gly Leu Gln Ile Lys Ile Lys Ser Gly Gly His Asp Tyr Glu Gly Ile
                165                 170                 175

Ser Tyr Arg Ser Glu Phe Pro Phe Val Met Leu Asp Leu Ser Asn Leu
            180                 185                 190

Asn Lys Thr Glu Ile Asp Leu Asn Glu Glu Thr Ile Trp Val Gln Ala
        195                 200                 205

Gly Ala Thr Leu Gly Gln Leu Tyr Tyr Ala Ile Ala Asn Arg Ser Asn
    210                 215                 220

Val His Gly Phe Pro Gly Gly Ile Cys Phe Ser Val Gly Thr Gly Gly
225                 230                 235                 240
```

```
Leu Ile Ser Gly Gly Gly Leu Gly Thr Met Met Arg Lys Phe Gly Leu
                245                 250                 255

Ala Ala Asp Asn Val Val Asp Ala Arg Val Met Asp Val Asn Gly Asn
            260                 265                 270

Ile Leu Asp Arg Lys Lys Met Lys Asn Asp Leu Phe Trp Ala Ile Arg
        275                 280                 285

Gly Gly Gly Gly Ala Ser Phe Gly Val Ile Leu Ala Trp Lys Leu Lys
    290                 295                 300

Leu Val Arg Val Pro Glu Lys Val Thr Val Phe Thr Val Cys Lys Lys
305                 310                 315                 320

Phe Asp Asp Asn Gln Asn Leu Ile Leu Lys Trp Glu Asn Ile Ala His
                325                 330                 335

Gln Leu Pro Asp Lys Leu Val Ile Arg Val Val Ile Gln Asn Asp Gly
            340                 345                 350

Thr Gly Asn Asp Lys Tyr Val Glu Met Arg Phe Gln Ala Leu Tyr Leu
        355                 360                 365

Gly Pro Val Asp Glu Leu Ile Pro Leu Leu Lys Glu Lys Phe Pro Glu
    370                 375                 380

Phe Asp Leu Glu Lys Lys Asp Cys Leu Gln Glu Pro Val Gly Asp Arg
385                 390                 395                 400

Ser Asn Arg Ser Cys Ile Asn Lys Glu Cys Arg Glu Thr Ser Trp Ile
                405                 410                 415

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

Val Leu Leu Lys Glu Ser Ile Pro Lys Gln Lys Ser Tyr Tyr Lys Gly
        435                 440                 445
```

```
Thr Ser Asp Phe Val Lys Thr Gln Ile Ser Glu Ser Gly Trp Glu Met
    450                 455                 460

Val Glu Arg Leu Leu Leu Glu Glu Glu Ser Pro Arg Ile Ile Leu Glu
465                 470                 475                 480

Pro Leu Gly Gly Lys Leu Asp Glu Ile Ser Glu Ser Glu Ile Pro Phe
                485                 490                 495

Pro His Arg Lys Gly Asn Leu Tyr Asn Ile Gln Tyr Leu Val Tyr Trp
            500                 505                 510

His Asp Asn Asn Glu Asn Val Ser Ser Gln Lys Ile Ala Trp Met Arg
        515                 520                 525

Lys Leu Tyr Lys Glu Met Glu Pro Tyr Val Ala Asn Ser Pro Arg Thr
    530                 535                 540

Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Phe Gly Ser Asn Asp Asp Asn
545                 550                 555                 560

Tyr Ser Tyr Ser Lys Ala Lys Ile Trp Gly Glu Lys Tyr Phe Asn Tyr
                565                 570                 575

Asn Phe Glu Arg Leu Ala Lys Val Lys Ser Lys Val Asp Pro Asn Asn
            580                 585                 590

Phe Phe Arg Thr Glu Gln Ser Ile Pro Leu Tyr Gln Thr Tyr Trp Ser
        595                 600                 605

His Pro Gln Phe Glu Lys
    610
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<210> 96
<211> 1641
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS133-A0A1U8MHW2

<220>

<221> CDS
<222> (1)..(1641)

<400> 96
atg ttc cca ttc ttg ttc gtc gtc ttg ttg tct ttg tct tgg aga atc 48
Met Phe Pro Phe Leu Phe Val Val Leu Leu Ser Leu Ser Trp Arg Ile
1 5 10 15

aat gct tct gct ttg cca gtt caa gaa ttc cta cat tgc ttg tct ttg 96
Asn Ala Ser Ala Leu Pro Val Gln Glu Phe Leu His Cys Leu Ser Leu
20 25 30

aga tcc cca aac tct tct att gcc aag ttg gtc tat acc cag aac aac 144
Arg Ser Pro Asn Ser Ser Ile Ala Lys Leu Val Tyr Thr Gln Asn Asn
35 40 45

tct tct tac tcc tct gtt ttg aaa tcc gct gct caa aac ttc aga ttc 192
Ser Ser Tyr Ser Ser Val Leu Lys Ser Ala Ala Gln Asn Phe Arg Phe
50 55 60

act act cca tct act cca act cca ttg gct ata gtt act cca ttg cat 240
Thr Thr Pro Ser Thr Pro Thr Pro Leu Ala Ile Val Thr Pro Leu His
65 70 75 80

gcc tct cat att caa gct gct gtt tac tgt tgt aga aaa cac ggt tta 288
Ala Ser His Ile Gln Ala Ala Val Tyr Cys Cys Arg Lys His Gly Leu
85 90 95

caa gtc aga act aga tct ggt ggt cat gat ttt gaa ggt ttg tct tac 336
Gln Val Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser Tyr
100 105 110

act tcc gct tac aag gtt cca ttc gtt gtt atc gat ttg gtc aac ttg 384
Thr Ser Ala Tyr Lys Val Pro Phe Val Val Ile Asp Leu Val Asn Leu
115 120 125

aga tcc gtt aga gtt aac gtt gaa aaa gct act gct tgg gtt gaa tct 432
Arg Ser Val Arg Val Asn Val Glu Lys Ala Thr Ala Trp Val Glu Ser
130 135 140

ggt gct act gtt ggt gaa tta tac gac gaa att gcc aga aag tct aag 480
Gly Ala Thr Val Gly Glu Leu Tyr Asp Glu Ile Ala Arg Lys Ser Lys
145 150 155 160

acc ttg ggt ttt cca gct ggt att tgt cca act tta ggt gtt ggt ggt 528
Thr Leu Gly Phe Pro Ala Gly Ile Cys Pro Thr Leu Gly Val Gly Gly
165 170 175

cac ttg tct ggt ggt ggt tat ggt ttg ttg ttt aga aag tat ggt ttg 576
His Leu Ser Gly Gly Gly Tyr Gly Leu Leu Phe Arg Lys Tyr Gly Leu
180 185 190

ggt gcc gat aac gtc att gat gct aga ttg att gat gtc aag ggt cgt 624
Gly Ala Asp Asn Val Ile Asp Ala Arg Leu Ile Asp Val Lys Gly Arg

```
        195                 200                 205

atc ttg gac aaa aag tct atg ggt gaa gat ttg ttt tgg gcc att aga        672
Ile Leu Asp Lys Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg
    210                 215                 220

ggt ggt ggt ggc ggt act ttt ggt ata gtt ttg gct tgg aaa ttg aag        720
Gly Gly Gly Gly Gly Thr Phe Gly Ile Val Leu Ala Trp Lys Leu Lys
225                 230                 235                 240

ttg gtt gct gtt cca gct aac gtt act gtt ttc act gtt aga aag act        768
Leu Val Ala Val Pro Ala Asn Val Thr Val Phe Thr Val Arg Lys Thr
                245                 250                 255

ttg gaa caa aac gcc act aag ttg gtt cat aga tgg caa tct att gcc        816
Leu Glu Gln Asn Ala Thr Lys Leu Val His Arg Trp Gln Ser Ile Ala
            260                 265                 270

cac aag ttc cca aaa gaa atg cac ttg tct att gct att gct agg gct        864
His Lys Phe Pro Lys Glu Met His Leu Ser Ile Ala Ile Ala Arg Ala
        275                 280                 285

aac tct tcc gaa gat gaa gaa aag atg act atc caa gct tct ttc acc        912
Asn Ser Ser Glu Asp Glu Glu Lys Met Thr Ile Gln Ala Ser Phe Thr
    290                 295                 300

tct act ttc ttg ggt tcc att gat gaa ttg atc cca ttg atg gaa gaa        960
Ser Thr Phe Leu Gly Ser Ile Asp Glu Leu Ile Pro Leu Met Glu Glu
305                 310                 315                 320

aag ttc cca gaa ttg ggt tta gtc aaa gaa gat tgc cta gaa atg tct       1008
Lys Phe Pro Glu Leu Gly Leu Val Lys Glu Asp Cys Leu Glu Met Ser
                325                 330                 335

tgg gct gag tct aac ttg tac agc ttt ttg ttc ttg ctg aga tct cca       1056
Trp Ala Glu Ser Asn Leu Tyr Ser Phe Leu Phe Leu Leu Arg Ser Pro
            340                 345                 350

tct gaa acc ctg ttg aat aga aac cag aag tcc tct atc tcc aaa acc       1104
Ser Glu Thr Leu Leu Asn Arg Asn Gln Lys Ser Ser Ile Ser Lys Thr
        355                 360                 365

ttt ttc aag gcc aag tcc gat ttt gtc aaa cag cca att cca gaa tct       1152
Phe Phe Lys Ala Lys Ser Asp Phe Val Lys Gln Pro Ile Pro Glu Ser
    370                 375                 380

gct ttc gaa ggt tta tgg tcc aag ttt tat gaa gat gag gct aag tcc       1200
Ala Phe Glu Gly Leu Trp Ser Lys Phe Tyr Glu Asp Glu Ala Lys Ser
385                 390                 395                 400

gcc atc atg gtt ttt gtt gct ttt ggt ggt aag atg gac gaa atc ttg       1248
Ala Ile Met Val Phe Val Ala Phe Gly Gly Lys Met Asp Glu Ile Leu
                405                 410                 415
```

```
gaa act gaa tac cca tat cca cat aga gcc ggt aac tta tac act atc       1296
Glu Thr Glu Tyr Pro Tyr Pro His Arg Ala Gly Asn Leu Tyr Thr Ile
            420                 425                 430

ttg tac act gtt gac tgg gaa gag aaa gag aac atc aac tct gaa aag       1344
Leu Tyr Thr Val Asp Trp Glu Glu Lys Glu Asn Ile Asn Ser Glu Lys
        435                 440                 445

ttc atg tcc tgg atg aga aga gtc tac aat tac atg act ccc tac gtt       1392
Phe Met Ser Trp Met Arg Arg Val Tyr Asn Tyr Met Thr Pro Tyr Val
    450                 455                 460

tct aag tct cca aga gaa gct tac atc aac tac aga gat ttg gac atc       1440
Ser Lys Ser Pro Arg Glu Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile
465                 470                 475                 480

ggt aca aac aag atc aac aac aga aag aga tct tac gct aag gct aga       1488
Gly Thr Asn Lys Ile Asn Asn Arg Lys Arg Ser Tyr Ala Lys Ala Arg
                485                 490                 495

gta tgg ggt gtt aag tac ttt aag aac aac ttc aac agg ctg gtt aac       1536
Val Trp Gly Val Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Asn
            500                 505                 510

gtc aag act ata gtt gac cca cag aat ttc ttc aga cac gaa caa tct       1584
Val Lys Thr Ile Val Asp Pro Gln Asn Phe Phe Arg His Glu Gln Ser
        515                 520                 525

att cca cca cta ttc ttg tcc tgg aaa aga tcc gat cat aag aag cac       1632
Ile Pro Pro Leu Phe Leu Ser Trp Lys Arg Ser Asp His Lys Lys His
    530                 535                 540

ttg tcc tcc                                                          1641
Leu Ser Ser
545
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<210> 97
<211> 547
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 97

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Met Phe Pro Phe Leu Phe Val Val Leu Leu Ser Leu Ser Trp Arg Ile
1               5                   10                  15


Asn Ala Ser Ala Leu Pro Val Gln Glu Phe Leu His Cys Leu Ser Leu
            20                  25                  30
```

```
Arg Ser Pro Asn Ser Ser Ile Ala Lys Leu Val Tyr Thr Gln Asn Asn
        35                  40                  45

Ser Ser Tyr Ser Ser Val Leu Lys Ser Ala Ala Gln Asn Phe Arg Phe
    50                  55                  60

Thr Thr Pro Ser Thr Pro Thr Pro Leu Ala Ile Val Thr Pro Leu His
65                  70                  75                  80

Ala Ser His Ile Gln Ala Ala Val Tyr Cys Cys Arg Lys His Gly Leu
                85                  90                  95

Gln Val Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser Tyr
            100                 105                 110

Thr Ser Ala Tyr Lys Val Pro Phe Val Val Ile Asp Leu Val Asn Leu
        115                 120                 125

Arg Ser Val Arg Val Asn Val Glu Lys Ala Thr Ala Trp Val Glu Ser
    130                 135                 140

Gly Ala Thr Val Gly Glu Leu Tyr Asp Glu Ile Ala Arg Lys Ser Lys
145                 150                 155                 160

Thr Leu Gly Phe Pro Ala Gly Ile Cys Pro Thr Leu Gly Val Gly Gly
                165                 170                 175

His Leu Ser Gly Gly Gly Tyr Gly Leu Leu Phe Arg Lys Tyr Gly Leu
            180                 185                 190

Gly Ala Asp Asn Val Ile Asp Ala Arg Leu Ile Asp Val Lys Gly Arg
        195                 200                 205

Ile Leu Asp Lys Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg
    210                 215                 220

Gly Gly Gly Gly Gly Thr Phe Gly Ile Val Leu Ala Trp Lys Leu Lys
225                 230                 235                 240

Leu Val Ala Val Pro Ala Asn Val Thr Val Phe Thr Val Arg Lys Thr
```

```
                245                 250                 255

Leu Glu Gln Asn Ala Thr Lys Leu Val His Arg Trp Gln Ser Ile Ala
            260                 265                 270

His Lys Phe Pro Lys Glu Met His Leu Ser Ile Ala Ile Ala Arg Ala
        275                 280                 285

Asn Ser Ser Glu Asp Glu Glu Lys Met Thr Ile Gln Ala Ser Phe Thr
    290                 295                 300

Ser Thr Phe Leu Gly Ser Ile Asp Glu Leu Ile Pro Leu Met Glu Glu
305                 310                 315                 320

Lys Phe Pro Glu Leu Gly Leu Val Lys Glu Asp Cys Leu Glu Met Ser
                325                 330                 335

Trp Ala Glu Ser Asn Leu Tyr Ser Phe Leu Phe Leu Leu Arg Ser Pro
            340                 345                 350

Ser Glu Thr Leu Leu Asn Arg Asn Gln Lys Ser Ser Ile Ser Lys Thr
        355                 360                 365

Phe Phe Lys Ala Lys Ser Asp Phe Val Lys Gln Pro Ile Pro Glu Ser
    370                 375                 380

Ala Phe Glu Gly Leu Trp Ser Lys Phe Tyr Glu Asp Glu Ala Lys Ser
385                 390                 395                 400

Ala Ile Met Val Phe Val Ala Phe Gly Gly Lys Met Asp Glu Ile Leu
                405                 410                 415

Glu Thr Glu Tyr Pro Tyr Pro His Arg Ala Gly Asn Leu Tyr Thr Ile
            420                 425                 430

Leu Tyr Thr Val Asp Trp Glu Glu Lys Glu Asn Ile Asn Ser Glu Lys
        435                 440                 445

Phe Met Ser Trp Met Arg Arg Val Tyr Asn Tyr Met Thr Pro Tyr Val
    450                 455                 460
```

```
Ser Lys Ser Pro Arg Glu Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile
465                 470                 475                 480


Gly Thr Asn Lys Ile Asn Asn Arg Lys Arg Ser Tyr Ala Lys Ala Arg
                485                 490                 495


Val Trp Gly Val Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Asn
            500                 505                 510


Val Lys Thr Ile Val Asp Pro Gln Asn Phe Phe Arg His Glu Gln Ser
        515                 520                 525


Ile Pro Pro Leu Phe Leu Ser Trp Lys Arg Ser Asp His Lys Lys His
    530                 535                 540


Leu Ser Ser
545


<210>  98
<211>  1587
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS133-A0A1U8MHW2- no signal peptide


<220>
<221>  CDS
<222>  (1)..(1587)

<400>  98
atg gct ttg cca gtt caa gaa ttc cta cat tgc ttg tct ttg aga tcc         48
Met Ala Leu Pro Val Gln Glu Phe Leu His Cys Leu Ser Leu Arg Ser
1               5                   10                  15

cca aac tct tct att gcc aag ttg gtc tat acc cag aac aac tct tct         96
Pro Asn Ser Ser Ile Ala Lys Leu Val Tyr Thr Gln Asn Asn Ser Ser
            20                  25                  30

tac tcc tct gtt ttg aaa tcc gct gct caa aac ttc aga ttc act act        144
Tyr Ser Ser Val Leu Lys Ser Ala Ala Gln Asn Phe Arg Phe Thr Thr
        35                  40                  45

cca tct act cca act cca ttg gct ata gtt act cca ttg cat gcc tct        192
Pro Ser Thr Pro Thr Pro Leu Ala Ile Val Thr Pro Leu His Ala Ser
    50                  55                  60
```

```
cat att caa gct gct gtt tac tgt tgt aga aaa cac ggt tta caa gtc        240
His Ile Gln Ala Ala Val Tyr Cys Cys Arg Lys His Gly Leu Gln Val
65                  70                  75                  80

aga act aga tct ggt ggt cat gat ttt gaa ggt ttg tct tac act tcc        288
Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser Tyr Thr Ser
                85                  90                  95

gct tac aag gtt cca ttc gtt gtt atc gat ttg gtc aac ttg aga tcc        336
Ala Tyr Lys Val Pro Phe Val Val Ile Asp Leu Val Asn Leu Arg Ser
            100                 105                 110

gtt aga gtt aac gtt gaa aaa gct act gct tgg gtt gaa tct ggt gct        384
Val Arg Val Asn Val Glu Lys Ala Thr Ala Trp Val Glu Ser Gly Ala
        115                 120                 125

act gtt ggt gaa tta tac gac gaa att gcc aga aag tct aag acc ttg        432
Thr Val Gly Glu Leu Tyr Asp Glu Ile Ala Arg Lys Ser Lys Thr Leu
    130                 135                 140

ggt ttt cca gct ggt att tgt cca act tta ggt gtt ggt ggt cac ttg        480
Gly Phe Pro Ala Gly Ile Cys Pro Thr Leu Gly Val Gly Gly His Leu
145                 150                 155                 160

tct ggt ggt ggt tat ggt ttg ttg ttt aga aag tat ggt ttg ggt gcc        528
Ser Gly Gly Gly Tyr Gly Leu Leu Phe Arg Lys Tyr Gly Leu Gly Ala
                165                 170                 175

gat aac gtc att gat gct aga ttg att gat gtc aag ggt cgt atc ttg        576
Asp Asn Val Ile Asp Ala Arg Leu Ile Asp Val Lys Gly Arg Ile Leu
            180                 185                 190

gac aaa aag tct atg ggt gaa gat ttg ttt tgg gcc att aga ggt ggt        624
Asp Lys Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly
        195                 200                 205

ggt ggc ggt act ttt ggt ata gtt ttg gct tgg aaa ttg aag ttg gtt        672
Gly Gly Gly Thr Phe Gly Ile Val Leu Ala Trp Lys Leu Lys Leu Val
    210                 215                 220

gct gtt cca gct aac gtt act gtt ttc act gtt aga aag act ttg gaa        720
Ala Val Pro Ala Asn Val Thr Val Phe Thr Val Arg Lys Thr Leu Glu
225                 230                 235                 240

caa aac gcc act aag ttg gtt cat aga tgg caa tct att gcc cac aag        768
Gln Asn Ala Thr Lys Leu Val His Arg Trp Gln Ser Ile Ala His Lys
                245                 250                 255

ttc cca aaa gaa atg cac ttg tct att gct att gct agg gct aac tct        816
Phe Pro Lys Glu Met His Leu Ser Ile Ala Ile Ala Arg Ala Asn Ser
            260                 265                 270

tcc gaa gat gaa gaa aag atg act atc caa gct tct ttc acc tct act        864
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```
Ser Glu Asp Glu Glu Lys Met Thr Ile Gln Ala Ser Phe Thr Ser Thr
        275                 280                 285

ttc ttg ggt tcc att gat gaa ttg atc cca ttg atg gaa gaa aag ttc        912
Phe Leu Gly Ser Ile Asp Glu Leu Ile Pro Leu Met Glu Glu Lys Phe
    290                 295                 300

cca gaa ttg ggt tta gtc aaa gaa gat tgc cta gaa atg tct tgg gct        960
Pro Glu Leu Gly Leu Val Lys Glu Asp Cys Leu Glu Met Ser Trp Ala
305                 310                 315                 320

gag tct aac ttg tac agc ttt ttg ttc ttg ctg aga tct cca tct gaa       1008
Glu Ser Asn Leu Tyr Ser Phe Leu Phe Leu Leu Arg Ser Pro Ser Glu
                325                 330                 335

acc ctg ttg aat aga aac cag aag tcc tct atc tcc aaa acc ttt ttc       1056
Thr Leu Leu Asn Arg Asn Gln Lys Ser Ser Ile Ser Lys Thr Phe Phe
            340                 345                 350

aag gcc aag tcc gat ttt gtc aaa cag cca att cca gaa tct gct ttc       1104
Lys Ala Lys Ser Asp Phe Val Lys Gln Pro Ile Pro Glu Ser Ala Phe
        355                 360                 365

gaa ggt tta tgg tcc aag ttt tat gaa gat gag gct aag tcc gcc atc       1152
Glu Gly Leu Trp Ser Lys Phe Tyr Glu Asp Glu Ala Lys Ser Ala Ile
    370                 375                 380

atg gtt ttt gtt gct ttt ggt ggt aag atg gac gaa atc ttg gaa act       1200
Met Val Phe Val Ala Phe Gly Gly Lys Met Asp Glu Ile Leu Glu Thr
385                 390                 395                 400

gaa tac cca tat cca cat aga gcc ggt aac tta tac act atc ttg tac       1248
Glu Tyr Pro Tyr Pro His Arg Ala Gly Asn Leu Tyr Thr Ile Leu Tyr
                405                 410                 415

act gtt gac tgg gaa gag aaa gag aac atc aac tct gaa aag ttc atg       1296
Thr Val Asp Trp Glu Glu Lys Glu Asn Ile Asn Ser Glu Lys Phe Met
            420                 425                 430

tcc tgg atg aga aga gtc tac aat tac atg act ccc tac gtt tct aag       1344
Ser Trp Met Arg Arg Val Tyr Asn Tyr Met Thr Pro Tyr Val Ser Lys
        435                 440                 445

tct cca aga gaa gct tac atc aac tac aga gat ttg gac atc ggt aca       1392
Ser Pro Arg Glu Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile Gly Thr
    450                 455                 460

aac aag atc aac aac aga aag aga tct tac gct aag gct aga gta tgg       1440
Asn Lys Ile Asn Asn Arg Lys Arg Ser Tyr Ala Lys Ala Arg Val Trp
465                 470                 475                 480

ggt gtt aag tac ttt aag aac aac ttc aac agg ctg gtt aac gtc aag       1488
Gly Val Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Asn Val Lys
                485                 490                 495
```

```
act ata gtt gac cca cag aat ttc ttc aga cac gaa caa tct att cca       1536
Thr Ile Val Asp Pro Gln Asn Phe Phe Arg His Glu Gln Ser Ile Pro
            500                 505                 510

cca cta ttc ttg tcc tgg aaa aga tcc gat cat aag aag cac ttg tcc       1584
Pro Leu Phe Leu Ser Trp Lys Arg Ser Asp His Lys Lys His Leu Ser
        515                 520                 525

tcc                                                                   1587
Ser
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<210> 99
<211> 529
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 99

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Met Ala Leu Pro Val Gln Glu Phe Leu His Cys Leu Ser Leu Arg Ser
1               5                   10                  15


Pro Asn Ser Ser Ile Ala Lys Leu Val Tyr Thr Gln Asn Asn Ser Ser
            20                  25                  30


Tyr Ser Ser Val Leu Lys Ser Ala Ala Gln Asn Phe Arg Phe Thr Thr
        35                  40                  45


Pro Ser Thr Pro Thr Pro Leu Ala Ile Val Thr Pro Leu His Ala Ser
    50                  55                  60


His Ile Gln Ala Ala Val Tyr Cys Cys Arg Lys His Gly Leu Gln Val
65                  70                  75                  80


Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser Tyr Thr Ser
                85                  90                  95


Ala Tyr Lys Val Pro Phe Val Val Ile Asp Leu Val Asn Leu Arg Ser
            100                 105                 110


Val Arg Val Asn Val Glu Lys Ala Thr Ala Trp Val Glu Ser Gly Ala
        115                 120                 125
```

```
Thr Val Gly Glu Leu Tyr Asp Glu Ile Ala Arg Lys Ser Lys Thr Leu
    130                 135                 140

Gly Phe Pro Ala Gly Ile Cys Pro Thr Leu Gly Val Gly Gly His Leu
145                 150                 155                 160

Ser Gly Gly Gly Tyr Gly Leu Leu Phe Arg Lys Tyr Gly Leu Gly Ala
                165                 170                 175

Asp Asn Val Ile Asp Ala Arg Leu Ile Asp Val Lys Gly Arg Ile Leu
            180                 185                 190

Asp Lys Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly
        195                 200                 205

Gly Gly Gly Thr Phe Gly Ile Val Leu Ala Trp Lys Leu Lys Leu Val
    210                 215                 220

Ala Val Pro Ala Asn Val Thr Val Phe Thr Val Arg Lys Thr Leu Glu
225                 230                 235                 240

Gln Asn Ala Thr Lys Leu Val His Arg Trp Gln Ser Ile Ala His Lys
                245                 250                 255

Phe Pro Lys Glu Met His Leu Ser Ile Ala Ile Ala Arg Ala Asn Ser
            260                 265                 270

Ser Glu Asp Glu Glu Lys Met Thr Ile Gln Ala Ser Phe Thr Ser Thr
        275                 280                 285

Phe Leu Gly Ser Ile Asp Glu Leu Ile Pro Leu Met Glu Glu Lys Phe
    290                 295                 300

Pro Glu Leu Gly Leu Val Lys Glu Asp Cys Leu Glu Met Ser Trp Ala
305                 310                 315                 320

Glu Ser Asn Leu Tyr Ser Phe Leu Phe Leu Leu Arg Ser Pro Ser Glu
                325                 330                 335
```

```
Thr Leu Leu Asn Arg Asn Gln Lys Ser Ser Ile Ser Lys Thr Phe Phe
            340                 345                 350

Lys Ala Lys Ser Asp Phe Val Lys Gln Pro Ile Pro Glu Ser Ala Phe
        355                 360                 365

Glu Gly Leu Trp Ser Lys Phe Tyr Glu Asp Glu Ala Lys Ser Ala Ile
    370                 375                 380

Met Val Phe Val Ala Phe Gly Gly Lys Met Asp Glu Ile Leu Glu Thr
385                 390                 395                 400

Glu Tyr Pro Tyr Pro His Arg Ala Gly Asn Leu Tyr Thr Ile Leu Tyr
                405                 410                 415

Thr Val Asp Trp Glu Glu Lys Glu Asn Ile Asn Ser Glu Lys Phe Met
            420                 425                 430

Ser Trp Met Arg Arg Val Tyr Asn Tyr Met Thr Pro Tyr Val Ser Lys
        435                 440                 445

Ser Pro Arg Glu Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile Gly Thr
    450                 455                 460

Asn Lys Ile Asn Asn Arg Lys Arg Ser Tyr Ala Lys Ala Arg Val Trp
465                 470                 475                 480

Gly Val Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Asn Val Lys
                485                 490                 495

Thr Ile Val Asp Pro Gln Asn Phe Phe Arg His Glu Gln Ser Ile Pro
            500                 505                 510

Pro Leu Phe Leu Ser Trp Lys Arg Ser Asp His Lys Lys His Leu Ser
        515                 520                 525

Ser
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<210>  100
<211>  1611

<212> DNA
<213> Artificial Sequence

<220>
<223> CBS133-A0A1U8MHW2- no signal peptide-strep Tag

<220>
<221> CDS
<222> (1)..(1611)

<400> 100
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Met Ala Leu Pro Val Gln Glu Phe Leu His Cys Leu Ser Leu Arg Ser
1 5 10 15

cca aac tct tct att gcc aag ttg gtc tat acc cag aac aac tct tct 96
Pro Asn Ser Ser Ile Ala Lys Leu Val Tyr Thr Gln Asn Asn Ser Ser
20 25 30

tac tcc tct gtt ttg aaa tcc gct gct caa aac ttc aga ttc act act 144
Tyr Ser Ser Val Leu Lys Ser Ala Ala Gln Asn Phe Arg Phe Thr Thr
35 40 45

cca tct act cca act cca ttg gct ata gtt act cca ttg cat gcc tct 192
Pro Ser Thr Pro Thr Pro Leu Ala Ile Val Thr Pro Leu His Ala Ser
50 55 60

cat att caa gct gct gtt tac tgt tgt aga aaa cac ggt tta caa gtc 240
His Ile Gln Ala Ala Val Tyr Cys Cys Arg Lys His Gly Leu Gln Val
65 70 75 80

aga act aga tct ggt ggt cat gat ttt gaa ggt ttg tct tac act tcc 288
Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser Tyr Thr Ser
85 90 95

gct tac aag gtt cca ttc gtt gtt atc gat ttg gtc aac ttg aga tcc 336
Ala Tyr Lys Val Pro Phe Val Val Ile Asp Leu Val Asn Leu Arg Ser
100 105 110

gtt aga gtt aac gtt gaa aaa gct act gct tgg gtt gaa tct ggt gct 384
Val Arg Val Asn Val Glu Lys Ala Thr Ala Trp Val Glu Ser Gly Ala
115 120 125

act gtt ggt gaa tta tac gac gaa att gcc aga aag tct aag acc ttg 432
Thr Val Gly Glu Leu Tyr Asp Glu Ile Ala Arg Lys Ser Lys Thr Leu
130 135 140

ggt ttt cca gct ggt att tgt cca act tta ggt gtt ggt ggt cac ttg 480
Gly Phe Pro Ala Gly Ile Cys Pro Thr Leu Gly Val Gly Gly His Leu
145 150 155 160

tct ggt ggt ggt tat ggt ttg ttg ttt aga aag tat ggt ttg ggt gcc 528
Ser Gly Gly Gly Tyr Gly Leu Leu Phe Arg Lys Tyr Gly Leu Gly Ala

```
                165                 170                 175

gat aac gtc att gat gct aga ttg att gat gtc aag ggt cgt atc ttg        576
Asp Asn Val Ile Asp Ala Arg Leu Ile Asp Val Lys Gly Arg Ile Leu
            180                 185                 190

gac aaa aag tct atg ggt gaa gat ttg ttt tgg gcc att aga ggt ggt        624
Asp Lys Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly
        195                 200                 205

ggt ggc ggt act ttt ggt ata gtt ttg gct tgg aaa ttg aag ttg gtt        672
Gly Gly Gly Thr Phe Gly Ile Val Leu Ala Trp Lys Leu Lys Leu Val
    210                 215                 220

gct gtt cca gct aac gtt act gtt ttc act gtt aga aag act ttg gaa        720
Ala Val Pro Ala Asn Val Thr Val Phe Thr Val Arg Lys Thr Leu Glu
225                 230                 235                 240

caa aac gcc act aag ttg gtt cat aga tgg caa tct att gcc cac aag        768
Gln Asn Ala Thr Lys Leu Val His Arg Trp Gln Ser Ile Ala His Lys
                245                 250                 255

ttc cca aaa gaa atg cac ttg tct att gct att gct agg gct aac tct        816
Phe Pro Lys Glu Met His Leu Ser Ile Ala Ile Ala Arg Ala Asn Ser
            260                 265                 270

tcc gaa gat gaa gaa aag atg act atc caa gct tct ttc acc tct act        864
Ser Glu Asp Glu Glu Lys Met Thr Ile Gln Ala Ser Phe Thr Ser Thr
        275                 280                 285

ttc ttg ggt tcc att gat gaa ttg atc cca ttg atg gaa gaa aag ttc        912
Phe Leu Gly Ser Ile Asp Glu Leu Ile Pro Leu Met Glu Glu Lys Phe
    290                 295                 300

cca gaa ttg ggt tta gtc aaa gaa gat tgc cta gaa atg tct tgg gct        960
Pro Glu Leu Gly Leu Val Lys Glu Asp Cys Leu Glu Met Ser Trp Ala
305                 310                 315                 320

gag tct aac ttg tac agc ttt ttg ttc ttg ctg aga tct cca tct gaa       1008
Glu Ser Asn Leu Tyr Ser Phe Leu Phe Leu Leu Arg Ser Pro Ser Glu
                325                 330                 335

acc ctg ttg aat aga aac cag aag tcc tct atc tcc aaa acc ttt ttc       1056
Thr Leu Leu Asn Arg Asn Gln Lys Ser Ser Ile Ser Lys Thr Phe Phe
            340                 345                 350

aag gcc aag tcc gat ttt gtc aaa cag cca att cca gaa tct gct ttc       1104
Lys Ala Lys Ser Asp Phe Val Lys Gln Pro Ile Pro Glu Ser Ala Phe
        355                 360                 365

gaa ggt tta tgg tcc aag ttt tat gaa gat gag gct aag tcc gcc atc       1152
Glu Gly Leu Trp Ser Lys Phe Tyr Glu Asp Glu Ala Lys Ser Ala Ile
    370                 375                 380
```

```
atg gtt ttt gtt gct ttt ggt ggt aag atg gac gaa atc ttg gaa act       1200
Met Val Phe Val Ala Phe Gly Gly Lys Met Asp Glu Ile Leu Glu Thr
385                 390                 395                 400

gaa tac cca tat cca cat aga gcc ggt aac tta tac act atc ttg tac       1248
Glu Tyr Pro Tyr Pro His Arg Ala Gly Asn Leu Tyr Thr Ile Leu Tyr
                405                 410                 415

act gtt gac tgg gaa gag aaa gag aac atc aac tct gaa aag ttc atg       1296
Thr Val Asp Trp Glu Glu Lys Glu Asn Ile Asn Ser Glu Lys Phe Met
            420                 425                 430

tcc tgg atg aga aga gtc tac aat tac atg act ccc tac gtt tct aag       1344
Ser Trp Met Arg Arg Val Tyr Asn Tyr Met Thr Pro Tyr Val Ser Lys
        435                 440                 445

tct cca aga gaa gct tac atc aac tac aga gat ttg gac atc ggt aca       1392
Ser Pro Arg Glu Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile Gly Thr
    450                 455                 460

aac aag atc aac aac aga aag aga tct tac gct aag gct aga gta tgg       1440
Asn Lys Ile Asn Asn Arg Lys Arg Ser Tyr Ala Lys Ala Arg Val Trp
465                 470                 475                 480

ggt gtt aag tac ttt aag aac aac ttc aac agg ctg gtt aac gtc aag       1488
Gly Val Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Asn Val Lys
                485                 490                 495

act ata gtt gac cca cag aat ttc ttc aga cac gaa caa tct att cca       1536
Thr Ile Val Asp Pro Gln Asn Phe Phe Arg His Glu Gln Ser Ile Pro
            500                 505                 510

cca cta ttc ttg tcc tgg aaa aga tcc gat cat aag aag cac ttg tcc       1584
Pro Leu Phe Leu Ser Trp Lys Arg Ser Asp His Lys Lys His Leu Ser
        515                 520                 525

tcc tgg tca cat cca caa ttt gaa aag                                  1611
Ser Trp Ser His Pro Gln Phe Glu Lys
    530                 535
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<210> 101
<211> 537
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 101

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Met Ala Leu Pro Val Gln Glu Phe Leu His Cys Leu Ser Leu Arg Ser
1               5                   10                  15
```

```
Pro Asn Ser Ser Ile Ala Lys Leu Val Tyr Thr Gln Asn Asn Ser Ser
            20                  25                  30

Tyr Ser Ser Val Leu Lys Ser Ala Ala Gln Asn Phe Arg Phe Thr Thr
        35                  40                  45

Pro Ser Thr Pro Thr Pro Leu Ala Ile Val Thr Pro Leu His Ala Ser
    50                  55                  60

His Ile Gln Ala Ala Val Tyr Cys Cys Arg Lys His Gly Leu Gln Val
65                  70                  75                  80

Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser Tyr Thr Ser
                85                  90                  95

Ala Tyr Lys Val Pro Phe Val Val Ile Asp Leu Val Asn Leu Arg Ser
            100                 105                 110

Val Arg Val Asn Val Glu Lys Ala Thr Ala Trp Val Glu Ser Gly Ala
        115                 120                 125

Thr Val Gly Glu Leu Tyr Asp Glu Ile Ala Arg Lys Ser Lys Thr Leu
    130                 135                 140

Gly Phe Pro Ala Gly Ile Cys Pro Thr Leu Gly Val Gly Gly His Leu
145                 150                 155                 160

Ser Gly Gly Gly Tyr Gly Leu Leu Phe Arg Lys Tyr Gly Leu Gly Ala
                165                 170                 175

Asp Asn Val Ile Asp Ala Arg Leu Ile Asp Val Lys Gly Arg Ile Leu
            180                 185                 190

Asp Lys Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly
        195                 200                 205

Gly Gly Gly Thr Phe Gly Ile Val Leu Ala Trp Lys Leu Lys Leu Val
    210                 215                 220

Ala Val Pro Ala Asn Val Thr Val Phe Thr Val Arg Lys Thr Leu Glu
```

```
225                 230                 235                 240

Gln Asn Ala Thr Lys Leu Val His Arg Trp Gln Ser Ile Ala His Lys
                245                 250                 255

Phe Pro Lys Glu Met His Leu Ser Ile Ala Ile Ala Arg Ala Asn Ser
            260                 265                 270

Ser Glu Asp Glu Glu Lys Met Thr Ile Gln Ala Ser Phe Thr Ser Thr
        275                 280                 285

Phe Leu Gly Ser Ile Asp Glu Leu Ile Pro Leu Met Glu Glu Lys Phe
    290                 295                 300

Pro Glu Leu Gly Leu Val Lys Glu Asp Cys Leu Glu Met Ser Trp Ala
305                 310                 315                 320

Glu Ser Asn Leu Tyr Ser Phe Leu Phe Leu Leu Arg Ser Pro Ser Glu
                325                 330                 335

Thr Leu Leu Asn Arg Asn Gln Lys Ser Ser Ile Ser Lys Thr Phe Phe
            340                 345                 350

Lys Ala Lys Ser Asp Phe Val Lys Gln Pro Ile Pro Glu Ser Ala Phe
        355                 360                 365

Glu Gly Leu Trp Ser Lys Phe Tyr Glu Asp Glu Ala Lys Ser Ala Ile
    370                 375                 380

Met Val Phe Val Ala Phe Gly Gly Lys Met Asp Glu Ile Leu Glu Thr
385                 390                 395                 400

Glu Tyr Pro Tyr Pro His Arg Ala Gly Asn Leu Tyr Thr Ile Leu Tyr
                405                 410                 415

Thr Val Asp Trp Glu Glu Lys Glu Asn Ile Asn Ser Glu Lys Phe Met
            420                 425                 430

Ser Trp Met Arg Arg Val Tyr Asn Tyr Met Thr Pro Tyr Val Ser Lys
        435                 440                 445
```

```
Ser Pro Arg Glu Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile Gly Thr
    450                 455                 460

Asn Lys Ile Asn Asn Arg Lys Arg Ser Tyr Ala Lys Ala Arg Val Trp
465                 470                 475                 480

Gly Val Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Asn Val Lys
                485                 490                 495

Thr Ile Val Asp Pro Gln Asn Phe Phe Arg His Glu Gln Ser Ile Pro
            500                 505                 510

Pro Leu Phe Leu Ser Trp Lys Arg Ser Asp His Lys Lys His Leu Ser
        515                 520                 525

Ser Trp Ser His Pro Gln Phe Glu Lys
    530                 535
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<210> 102
<211> 1668
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS133-A0A1U8MHW2-truncated alpha factor - no signal peptide-strep Tag

<220>
<221> CDS
<222> (1)..(1668)

<400> 102

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atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca ctt gca atg gct ttg cca gtt caa gaa ttc cta cat tgc ttg tct         96
Ala Leu Ala Met Ala Leu Pro Val Gln Glu Phe Leu His Cys Leu Ser
            20                  25                  30

ttg aga tcc cca aac tct tct att gcc aag ttg gtc tat acc cag aac        144
Leu Arg Ser Pro Asn Ser Ser Ile Ala Lys Leu Val Tyr Thr Gln Asn
        35                  40                  45

aac tct tct tac tcc tct gtt ttg aaa tcc gct gct caa aac ttc aga        192
Asn Ser Ser Tyr Ser Ser Val Leu Lys Ser Ala Ala Gln Asn Phe Arg
```

```
    50                  55                  60

ttc act act cca tct act cca act cca ttg gct ata gtt act cca ttg        240
Phe Thr Thr Pro Ser Thr Pro Thr Pro Leu Ala Ile Val Thr Pro Leu
65                  70                  75                  80

cat gcc tct cat att caa gct gct gtt tac tgt tgt aga aaa cac ggt        288
His Ala Ser His Ile Gln Ala Ala Val Tyr Cys Cys Arg Lys His Gly
                85                  90                  95

tta caa gtc aga act aga tct ggt ggt cat gat ttt gaa ggt ttg tct        336
Leu Gln Val Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser
            100                 105                 110

tac act tcc gct tac aag gtt cca ttc gtt gtt atc gat ttg gtc aac        384
Tyr Thr Ser Ala Tyr Lys Val Pro Phe Val Val Ile Asp Leu Val Asn
        115                 120                 125

ttg aga tcc gtt aga gtt aac gtt gaa aaa gct act gct tgg gtt gaa        432
Leu Arg Ser Val Arg Val Asn Val Glu Lys Ala Thr Ala Trp Val Glu
    130                 135                 140

tct ggt gct act gtt ggt gaa tta tac gac gaa att gcc aga aag tct        480
Ser Gly Ala Thr Val Gly Glu Leu Tyr Asp Glu Ile Ala Arg Lys Ser
145                 150                 155                 160

aag acc ttg ggt ttt cca gct ggt att tgt cca act tta ggt gtt ggt        528
Lys Thr Leu Gly Phe Pro Ala Gly Ile Cys Pro Thr Leu Gly Val Gly
                165                 170                 175

ggt cac ttg tct ggt ggt ggt tat ggt ttg ttg ttt aga aag tat ggt        576
Gly His Leu Ser Gly Gly Gly Tyr Gly Leu Leu Phe Arg Lys Tyr Gly
            180                 185                 190

ttg ggt gcc gat aac gtc att gat gct aga ttg att gat gtc aag ggt        624
Leu Gly Ala Asp Asn Val Ile Asp Ala Arg Leu Ile Asp Val Lys Gly
        195                 200                 205

cgt atc ttg gac aaa aag tct atg ggt gaa gat ttg ttt tgg gcc att        672
Arg Ile Leu Asp Lys Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Ile
    210                 215                 220

aga ggt ggt ggt ggc ggt act ttt ggt ata gtt ttg gct tgg aaa ttg        720
Arg Gly Gly Gly Gly Gly Thr Phe Gly Ile Val Leu Ala Trp Lys Leu
225                 230                 235                 240

aag ttg gtt gct gtt cca gct aac gtt act gtt ttc act gtt aga aag        768
Lys Leu Val Ala Val Pro Ala Asn Val Thr Val Phe Thr Val Arg Lys
                245                 250                 255

act ttg gaa caa aac gcc act aag ttg gtt cat aga tgg caa tct att        816
Thr Leu Glu Gln Asn Ala Thr Lys Leu Val His Arg Trp Gln Ser Ile
            260                 265                 270
```

```
gcc cac aag ttc cca aaa gaa atg cac ttg tct att gct att gct agg        864
Ala His Lys Phe Pro Lys Glu Met His Leu Ser Ile Ala Ile Ala Arg
        275                 280                 285

gct aac tct tcc gaa gat gaa gaa aag atg act atc caa gct tct ttc        912
Ala Asn Ser Ser Glu Asp Glu Glu Lys Met Thr Ile Gln Ala Ser Phe
    290                 295                 300

acc tct act ttc ttg ggt tcc att gat gaa ttg atc cca ttg atg gaa        960
Thr Ser Thr Phe Leu Gly Ser Ile Asp Glu Leu Ile Pro Leu Met Glu
305                 310                 315                 320

gaa aag ttc cca gaa ttg ggt tta gtc aaa gaa gat tgc cta gaa atg       1008
Glu Lys Phe Pro Glu Leu Gly Leu Val Lys Glu Asp Cys Leu Glu Met
                325                 330                 335

tct tgg gct gag tct aac ttg tac agc ttt ttg ttc ttg ctg aga tct       1056
Ser Trp Ala Glu Ser Asn Leu Tyr Ser Phe Leu Phe Leu Leu Arg Ser
            340                 345                 350

cca tct gaa acc ctg ttg aat aga aac cag aag tcc tct atc tcc aaa       1104
Pro Ser Glu Thr Leu Leu Asn Arg Asn Gln Lys Ser Ser Ile Ser Lys
        355                 360                 365

acc ttt ttc aag gcc aag tcc gat ttt gtc aaa cag cca att cca gaa       1152
Thr Phe Phe Lys Ala Lys Ser Asp Phe Val Lys Gln Pro Ile Pro Glu
    370                 375                 380

tct gct ttc gaa ggt tta tgg tcc aag ttt tat gaa gat gag gct aag       1200
Ser Ala Phe Glu Gly Leu Trp Ser Lys Phe Tyr Glu Asp Glu Ala Lys
385                 390                 395                 400

tcc gcc atc atg gtt ttt gtt gct ttt ggt ggt aag atg gac gaa atc       1248
Ser Ala Ile Met Val Phe Val Ala Phe Gly Gly Lys Met Asp Glu Ile
                405                 410                 415

ttg gaa act gaa tac cca tat cca cat aga gcc ggt aac tta tac act       1296
Leu Glu Thr Glu Tyr Pro Tyr Pro His Arg Ala Gly Asn Leu Tyr Thr
            420                 425                 430

atc ttg tac act gtt gac tgg gaa gag aaa gag aac atc aac tct gaa       1344
Ile Leu Tyr Thr Val Asp Trp Glu Glu Lys Glu Asn Ile Asn Ser Glu
        435                 440                 445

aag ttc atg tcc tgg atg aga aga gtc tac aat tac atg act ccc tac       1392
Lys Phe Met Ser Trp Met Arg Arg Val Tyr Asn Tyr Met Thr Pro Tyr
    450                 455                 460

gtt tct aag tct cca aga gaa gct tac atc aac tac aga gat ttg gac       1440
Val Ser Lys Ser Pro Arg Glu Ala Tyr Ile Asn Tyr Arg Asp Leu Asp
465                 470                 475                 480

atc ggt aca aac aag atc aac aac aga aag aga tct tac gct aag gct       1488
Ile Gly Thr Asn Lys Ile Asn Asn Arg Lys Arg Ser Tyr Ala Lys Ala
```

```
                485                 490                 495

aga gta tgg ggt gtt aag tac ttt aag aac aac ttc aac agg ctg gtt       1536
Arg Val Trp Gly Val Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val
            500                 505                 510

aac gtc aag act ata gtt gac cca cag aat ttc ttc aga cac gaa caa       1584
Asn Val Lys Thr Ile Val Asp Pro Gln Asn Phe Phe Arg His Glu Gln
        515                 520                 525

tct att cca cca cta ttc ttg tcc tgg aaa aga tcc gat cat aag aag       1632
Ser Ile Pro Pro Leu Phe Leu Ser Trp Lys Arg Ser Asp His Lys Lys
    530                 535                 540

cac ttg tcc tcc tgg tca cat cca caa ttt gaa aag                       1668
His Leu Ser Ser Trp Ser His Pro Gln Phe Glu Lys
545                 550                 555
```

<210> 103
<211> 556
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 103

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


Ala Leu Ala Met Ala Leu Pro Val Gln Glu Phe Leu His Cys Leu Ser
            20                  25                  30


Leu Arg Ser Pro Asn Ser Ser Ile Ala Lys Leu Val Tyr Thr Gln Asn
        35                  40                  45


Asn Ser Ser Tyr Ser Ser Val Leu Lys Ser Ala Ala Gln Asn Phe Arg
    50                  55                  60


Phe Thr Thr Pro Ser Thr Pro Thr Pro Leu Ala Ile Val Thr Pro Leu
65                  70                  75                  80


His Ala Ser His Ile Gln Ala Ala Val Tyr Cys Cys Arg Lys His Gly
                85                  90                  95


Leu Gln Val Arg Thr Arg Ser Gly Gly His Asp Phe Glu Gly Leu Ser
```

```
            100                 105                 110

Tyr Thr Ser Ala Tyr Lys Val Pro Phe Val Val Ile Asp Leu Val Asn
        115                 120                 125

Leu Arg Ser Val Arg Val Asn Val Glu Lys Ala Thr Ala Trp Val Glu
    130                 135                 140

Ser Gly Ala Thr Val Gly Glu Leu Tyr Asp Glu Ile Ala Arg Lys Ser
145                 150                 155                 160

Lys Thr Leu Gly Phe Pro Ala Gly Ile Cys Pro Thr Leu Gly Val Gly
                165                 170                 175

Gly His Leu Ser Gly Gly Gly Tyr Gly Leu Leu Phe Arg Lys Tyr Gly
            180                 185                 190

Leu Gly Ala Asp Asn Val Ile Asp Ala Arg Leu Ile Asp Val Lys Gly
        195                 200                 205

Arg Ile Leu Asp Lys Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Ile
    210                 215                 220

Arg Gly Gly Gly Gly Gly Thr Phe Gly Ile Val Leu Ala Trp Lys Leu
225                 230                 235                 240

Lys Leu Val Ala Val Pro Ala Asn Val Thr Val Phe Thr Val Arg Lys
                245                 250                 255

Thr Leu Glu Gln Asn Ala Thr Lys Leu Val His Arg Trp Gln Ser Ile
            260                 265                 270

Ala His Lys Phe Pro Lys Glu Met His Leu Ser Ile Ala Ile Ala Arg
        275                 280                 285

Ala Asn Ser Ser Glu Asp Glu Glu Lys Met Thr Ile Gln Ala Ser Phe
    290                 295                 300

Thr Ser Thr Phe Leu Gly Ser Ile Asp Glu Leu Ile Pro Leu Met Glu
305                 310                 315                 320
```

```
Glu Lys Phe Pro Glu Leu Gly Leu Val Lys Glu Asp Cys Leu Glu Met
                325                 330                 335

Ser Trp Ala Glu Ser Asn Leu Tyr Ser Phe Leu Phe Leu Leu Arg Ser
            340                 345                 350

Pro Ser Glu Thr Leu Leu Asn Arg Asn Gln Lys Ser Ser Ile Ser Lys
        355                 360                 365

Thr Phe Phe Lys Ala Lys Ser Asp Phe Val Lys Gln Pro Ile Pro Glu
    370                 375                 380

Ser Ala Phe Glu Gly Leu Trp Ser Lys Phe Tyr Glu Asp Glu Ala Lys
385                 390                 395                 400

Ser Ala Ile Met Val Phe Val Ala Phe Gly Gly Lys Met Asp Glu Ile
                405                 410                 415

Leu Glu Thr Glu Tyr Pro Tyr Pro His Arg Ala Gly Asn Leu Tyr Thr
            420                 425                 430

Ile Leu Tyr Thr Val Asp Trp Glu Glu Lys Glu Asn Ile Asn Ser Glu
        435                 440                 445

Lys Phe Met Ser Trp Met Arg Arg Val Tyr Asn Tyr Met Thr Pro Tyr
    450                 455                 460

Val Ser Lys Ser Pro Arg Glu Ala Tyr Ile Asn Tyr Arg Asp Leu Asp
465                 470                 475                 480

Ile Gly Thr Asn Lys Ile Asn Asn Arg Lys Arg Ser Tyr Ala Lys Ala
                485                 490                 495

Arg Val Trp Gly Val Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val
            500                 505                 510

Asn Val Lys Thr Ile Val Asp Pro Gln Asn Phe Phe Arg His Glu Gln
        515                 520                 525

Ser Ile Pro Pro Leu Phe Leu Ser Trp Lys Arg Ser Asp His Lys Lys
```

```
    530                 535                 540


His Leu Ser Ser Trp Ser His Pro Gln Phe Glu Lys
545                 550                 555


<210>  104
<211>  1878
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS133-A0A1U8MHW2-full alpha factor -no signal peptide-strep Tag


<220>
<221>  CDS
<222>  (1)..(1878)

<400>  104
atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg gct ttg cca gtt caa gaa        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ala Leu Pro Val Gln Glu
                85                  90                  95

ttc cta cat tgc ttg tct ttg aga tcc cca aac tct tct att gcc aag        336
Phe Leu His Cys Leu Ser Leu Arg Ser Pro Asn Ser Ser Ile Ala Lys
            100                 105                 110

ttg gtc tat acc cag aac aac tct tct tac tcc tct gtt ttg aaa tcc        384
Leu Val Tyr Thr Gln Asn Asn Ser Ser Tyr Ser Ser Val Leu Lys Ser
        115                 120                 125

gct gct caa aac ttc aga ttc act act cca tct act cca act cca ttg        432
```

```
Ala Ala Gln Asn Phe Arg Phe Thr Thr Pro Ser Thr Pro Thr Pro Leu
    130                 135                 140

gct ata gtt act cca ttg cat gcc tct cat att caa gct gct gtt tac        480
Ala Ile Val Thr Pro Leu His Ala Ser His Ile Gln Ala Ala Val Tyr
145                 150                 155                 160

tgt tgt aga aaa cac ggt tta caa gtc aga act aga tct ggt ggt cat        528
Cys Cys Arg Lys His Gly Leu Gln Val Arg Thr Arg Ser Gly Gly His
                165                 170                 175

gat ttt gaa ggt ttg tct tac act tcc gct tac aag gtt cca ttc gtt        576
Asp Phe Glu Gly Leu Ser Tyr Thr Ser Ala Tyr Lys Val Pro Phe Val
            180                 185                 190

gtt atc gat ttg gtc aac ttg aga tcc gtt aga gtt aac gtt gaa aaa        624
Val Ile Asp Leu Val Asn Leu Arg Ser Val Arg Val Asn Val Glu Lys
        195                 200                 205

gct act gct tgg gtt gaa tct ggt gct act gtt ggt gaa tta tac gac        672
Ala Thr Ala Trp Val Glu Ser Gly Ala Thr Val Gly Glu Leu Tyr Asp
    210                 215                 220

gaa att gcc aga aag tct aag acc ttg ggt ttt cca gct ggt att tgt        720
Glu Ile Ala Arg Lys Ser Lys Thr Leu Gly Phe Pro Ala Gly Ile Cys
225                 230                 235                 240

cca act tta ggt gtt ggt ggt cac ttg tct ggt ggt ggt tat ggt ttg        768
Pro Thr Leu Gly Val Gly Gly His Leu Ser Gly Gly Gly Tyr Gly Leu
                245                 250                 255

ttg ttt aga aag tat ggt ttg ggt gcc gat aac gtc att gat gct aga        816
Leu Phe Arg Lys Tyr Gly Leu Gly Ala Asp Asn Val Ile Asp Ala Arg
            260                 265                 270

ttg att gat gtc aag ggt cgt atc ttg gac aaa aag tct atg ggt gaa        864
Leu Ile Asp Val Lys Gly Arg Ile Leu Asp Lys Lys Ser Met Gly Glu
        275                 280                 285

gat ttg ttt tgg gcc att aga ggt ggt ggt ggc ggt act ttt ggt ata        912
Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Thr Phe Gly Ile
    290                 295                 300

gtt ttg gct tgg aaa ttg aag ttg gtt gct gtt cca gct aac gtt act        960
Val Leu Ala Trp Lys Leu Lys Leu Val Ala Val Pro Ala Asn Val Thr
305                 310                 315                 320

gtt ttc act gtt aga aag act ttg gaa caa aac gcc act aag ttg gtt       1008
Val Phe Thr Val Arg Lys Thr Leu Glu Gln Asn Ala Thr Lys Leu Val
                325                 330                 335

cat aga tgg caa tct att gcc cac aag ttc cca aaa gaa atg cac ttg       1056
His Arg Trp Gln Ser Ile Ala His Lys Phe Pro Lys Glu Met His Leu
            340                 345                 350
```

```
tct att gct att gct agg gct aac tct tcc gaa gat gaa gaa aag atg       1104
Ser Ile Ala Ile Ala Arg Ala Asn Ser Ser Glu Asp Glu Glu Lys Met
        355                 360                 365

act atc caa gct tct ttc acc tct act ttc ttg ggt tcc att gat gaa       1152
Thr Ile Gln Ala Ser Phe Thr Ser Thr Phe Leu Gly Ser Ile Asp Glu
    370                 375                 380

ttg atc cca ttg atg gaa gaa aag ttc cca gaa ttg ggt tta gtc aaa       1200
Leu Ile Pro Leu Met Glu Glu Lys Phe Pro Glu Leu Gly Leu Val Lys
385                 390                 395                 400

gaa gat tgc cta gaa atg tct tgg gct gag tct aac ttg tac agc ttt       1248
Glu Asp Cys Leu Glu Met Ser Trp Ala Glu Ser Asn Leu Tyr Ser Phe
                405                 410                 415

ttg ttc ttg ctg aga tct cca tct gaa acc ctg ttg aat aga aac cag       1296
Leu Phe Leu Leu Arg Ser Pro Ser Glu Thr Leu Leu Asn Arg Asn Gln
            420                 425                 430

aag tcc tct atc tcc aaa acc ttt ttc aag gcc aag tcc gat ttt gtc       1344
Lys Ser Ser Ile Ser Lys Thr Phe Phe Lys Ala Lys Ser Asp Phe Val
        435                 440                 445

aaa cag cca att cca gaa tct gct ttc gaa ggt tta tgg tcc aag ttt       1392
Lys Gln Pro Ile Pro Glu Ser Ala Phe Glu Gly Leu Trp Ser Lys Phe
    450                 455                 460

tat gaa gat gag gct aag tcc gcc atc atg gtt ttt gtt gct ttt ggt       1440
Tyr Glu Asp Glu Ala Lys Ser Ala Ile Met Val Phe Val Ala Phe Gly
465                 470                 475                 480

ggt aag atg gac gaa atc ttg gaa act gaa tac cca tat cca cat aga       1488
Gly Lys Met Asp Glu Ile Leu Glu Thr Glu Tyr Pro Tyr Pro His Arg
                485                 490                 495

gcc ggt aac tta tac act atc ttg tac act gtt gac tgg gaa gag aaa       1536
Ala Gly Asn Leu Tyr Thr Ile Leu Tyr Thr Val Asp Trp Glu Glu Lys
            500                 505                 510

gag aac atc aac tct gaa aag ttc atg tcc tgg atg aga aga gtc tac       1584
Glu Asn Ile Asn Ser Glu Lys Phe Met Ser Trp Met Arg Arg Val Tyr
        515                 520                 525

aat tac atg act ccc tac gtt tct aag tct cca aga gaa gct tac atc       1632
Asn Tyr Met Thr Pro Tyr Val Ser Lys Ser Pro Arg Glu Ala Tyr Ile
    530                 535                 540

aac tac aga gat ttg gac atc ggt aca aac aag atc aac aac aga aag       1680
Asn Tyr Arg Asp Leu Asp Ile Gly Thr Asn Lys Ile Asn Asn Arg Lys
545                 550                 555                 560

aga tct tac gct aag gct aga gta tgg ggt gtt aag tac ttt aag aac       1728
```

```
Arg Ser Tyr Ala Lys Ala Arg Val Trp Gly Val Lys Tyr Phe Lys Asn
                565                 570                 575

aac ttc aac agg ctg gtt aac gtc aag act ata gtt gac cca cag aat       1776
Asn Phe Asn Arg Leu Val Asn Val Lys Thr Ile Val Asp Pro Gln Asn
            580                 585                 590

ttc ttc aga cac gaa caa tct att cca cca cta ttc ttg tcc tgg aaa       1824
Phe Phe Arg His Glu Gln Ser Ile Pro Pro Leu Phe Leu Ser Trp Lys
        595                 600                 605

aga tcc gat cat aag aag cac ttg tcc tcc tgg tca cat cca caa ttt       1872
Arg Ser Asp His Lys Lys His Leu Ser Ser Trp Ser His Pro Gln Phe
    610                 615                 620

gaa aag                                                              1878
Glu Lys
625
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<210> 105
<211> 626
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 105

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

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

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

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ala Leu Pro Val Gln Glu
                85                  90                  95
```

```
Phe Leu His Cys Leu Ser Leu Arg Ser Pro Asn Ser Ser Ile Ala Lys
            100                 105                 110

Leu Val Tyr Thr Gln Asn Asn Ser Ser Tyr Ser Ser Val Leu Lys Ser
        115                 120                 125

Ala Ala Gln Asn Phe Arg Phe Thr Thr Pro Ser Thr Pro Thr Pro Leu
    130                 135                 140

Ala Ile Val Thr Pro Leu His Ala Ser His Ile Gln Ala Ala Val Tyr
145                 150                 155                 160

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

Asp Phe Glu Gly Leu Ser Tyr Thr Ser Ala Tyr Lys Val Pro Phe Val
            180                 185                 190

Val Ile Asp Leu Val Asn Leu Arg Ser Val Arg Val Asn Val Glu Lys
        195                 200                 205

Ala Thr Ala Trp Val Glu Ser Gly Ala Thr Val Gly Glu Leu Tyr Asp
    210                 215                 220

Glu Ile Ala Arg Lys Ser Lys Thr Leu Gly Phe Pro Ala Gly Ile Cys
225                 230                 235                 240

Pro Thr Leu Gly Val Gly Gly His Leu Ser Gly Gly Gly Tyr Gly Leu
                245                 250                 255

Leu Phe Arg Lys Tyr Gly Leu Gly Ala Asp Asn Val Ile Asp Ala Arg
            260                 265                 270

Leu Ile Asp Val Lys Gly Arg Ile Leu Asp Lys Lys Ser Met Gly Glu
        275                 280                 285

Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Thr Phe Gly Ile
    290                 295                 300

Val Leu Ala Trp Lys Leu Lys Leu Val Ala Val Pro Ala Asn Val Thr
305                 310                 315                 320
```

```
Val Phe Thr Val Arg Lys Thr Leu Glu Gln Asn Ala Thr Lys Leu Val
                325                 330                 335

His Arg Trp Gln Ser Ile Ala His Lys Phe Pro Lys Glu Met His Leu
            340                 345                 350

Ser Ile Ala Ile Ala Arg Ala Asn Ser Ser Glu Asp Glu Glu Lys Met
        355                 360                 365

Thr Ile Gln Ala Ser Phe Thr Ser Thr Phe Leu Gly Ser Ile Asp Glu
    370                 375                 380

Leu Ile Pro Leu Met Glu Glu Lys Phe Pro Glu Leu Gly Leu Val Lys
385                 390                 395                 400

Glu Asp Cys Leu Glu Met Ser Trp Ala Glu Ser Asn Leu Tyr Ser Phe
                405                 410                 415

Leu Phe Leu Leu Arg Ser Pro Ser Glu Thr Leu Leu Asn Arg Asn Gln
            420                 425                 430

Lys Ser Ser Ile Ser Lys Thr Phe Phe Lys Ala Lys Ser Asp Phe Val
        435                 440                 445

Lys Gln Pro Ile Pro Glu Ser Ala Phe Glu Gly Leu Trp Ser Lys Phe
    450                 455                 460

Tyr Glu Asp Glu Ala Lys Ser Ala Ile Met Val Phe Val Ala Phe Gly
465                 470                 475                 480

Gly Lys Met Asp Glu Ile Leu Glu Thr Glu Tyr Pro Tyr Pro His Arg
                485                 490                 495

Ala Gly Asn Leu Tyr Thr Ile Leu Tyr Thr Val Asp Trp Glu Glu Lys
            500                 505                 510

Glu Asn Ile Asn Ser Glu Lys Phe Met Ser Trp Met Arg Arg Val Tyr
        515                 520                 525
```

```
Asn Tyr Met Thr Pro Tyr Val Ser Lys Ser Pro Arg Glu Ala Tyr Ile
    530                 535                 540

Asn Tyr Arg Asp Leu Asp Ile Gly Thr Asn Lys Ile Asn Asn Arg Lys
545                 550                 555                 560

Arg Ser Tyr Ala Lys Ala Arg Val Trp Gly Val Lys Tyr Phe Lys Asn
                565                 570                 575

Asn Phe Asn Arg Leu Val Asn Val Lys Thr Ile Val Asp Pro Gln Asn
            580                 585                 590

Phe Phe Arg His Glu Gln Ser Ile Pro Pro Leu Phe Leu Ser Trp Lys
        595                 600                 605

Arg Ser Asp His Lys Lys His Leu Ser Ser Trp Ser His Pro Gln Phe
    610                 615                 620

Glu Lys
625
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<210> 106
<211> 1638
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS134-A0A1J3CT99

<220>
<221> CDS
<222> (1)..(1638)

<400> 106

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atg agg atc tct aag cca att cca gtc atc tcc tac att ttg ttc ttg         48
Met Arg Ile Ser Lys Pro Ile Pro Val Ile Ser Tyr Ile Leu Phe Leu
1               5                   10                  15

gcc caa tac ttc tca ttg cac aca aaa gaa cct acc tct tct acc tca         96
Ala Gln Tyr Phe Ser Leu His Thr Lys Glu Pro Thr Ser Ser Thr Ser
            20                  25                  30

ttg caa gat gat ttc atc aag tgc ttg cac aga aac acc aat gtt gat        144
Leu Gln Asp Asp Phe Ile Lys Cys Leu His Arg Asn Thr Asn Val Asp
        35                  40                  45
```

```
ttc cca ttg gac aag act ttc ttc act cca caa aga aac tcc tcc aac        192
Phe Pro Leu Asp Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser Ser Asn
    50                  55                  60

ttc aaa gaa gtt ttg aac acc acc gtc tgg aat caa aga tat atg act        240
Phe Lys Glu Val Leu Asn Thr Thr Val Trp Asn Gln Arg Tyr Met Thr
65                  70                  75                  80

aag tct atg ccc aag cca gag ttc att ttt aag cca gtt cat gaa tcc        288
Lys Ser Met Pro Lys Pro Glu Phe Ile Phe Lys Pro Val His Glu Ser
                85                  90                  95

cat gtc caa gcc tct att att tgc tct aag aag ttg aga atc cac ttc        336
His Val Gln Ala Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile His Phe
            100                 105                 110

aga gtt aga tct ggt ggt cat gat tat gag ggt ttg tct tac gtt tct        384
Arg Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val Ser
        115                 120                 125

caa atg gaa act cca ttc gtc ttg atc gat ttg tgg aag ttg aag caa        432
Gln Met Glu Thr Pro Phe Val Leu Ile Asp Leu Trp Lys Leu Lys Gln
    130                 135                 140

atc aac gtc gac atc gaa gat aat tct gct tgg gtt caa gct ggt gct        480
Ile Asn Val Asp Ile Glu Asp Asn Ser Ala Trp Val Gln Ala Gly Ala
145                 150                 155                 160

act act ggt gag ttg tat tat aga att gct gcc aag tct aag gtt cat        528
Thr Thr Gly Glu Leu Tyr Tyr Arg Ile Ala Ala Lys Ser Lys Val His
                165                 170                 175

ggt ttt cca gct ggt ttg tgt tct act gtt ggt ata ggt ggt cat atc        576
Gly Phe Pro Ala Gly Leu Cys Ser Thr Val Gly Ile Gly Gly His Ile
            180                 185                 190

act ggt ggt ggt tat ggt act ttg atg aga aag tat ggt ttg tcc acc        624
Thr Gly Gly Gly Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu Ser Thr
        195                 200                 205

gat aac gtt ttg gat gct aga atc gtt gat gct aat ggt cag ttg ttg        672
Asp Asn Val Leu Asp Ala Arg Ile Val Asp Ala Asn Gly Gln Leu Leu
    210                 215                 220

aac aga act gct atg ggt gaa gat ttg ttc tgg gct att aga ggt ggt        720
Asn Arg Thr Ala Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly
225                 230                 235                 240

ggt ggc ggt tca ttt ggt gtt att ttg gct tgg aag atc aag ttg gtt        768
Gly Gly Gly Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val
                245                 250                 255

cca gtt cca gaa act ttg acc att ttc act att acc aag acc ttg gaa        816
Pro Val Pro Glu Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr Leu Glu
```

```
            260                 265                 270

caa gat gcc ggt ttc aag att ttg tct aag tgg caa aga atc gtc gac        864
Gln Asp Ala Gly Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile Val Asp
        275                 280                 285

aag ttg gta gaa gaa ttg tcc atc aga gtc ttg ttc aga aac act ggt        912
Lys Leu Val Glu Glu Leu Ser Ile Arg Val Leu Phe Arg Asn Thr Gly
    290                 295                 300

aac aag act gtt act act acc tac aga ggt gaa ttc ttg ggt gaa aaa        960
Asn Lys Thr Val Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly Glu Lys
305                 310                 315                 320

ggt aca ttg atg gaa gtc atg aag aag tgc ttt cca gaa ttg ggt ttg       1008
Gly Thr Leu Met Glu Val Met Lys Lys Cys Phe Pro Glu Leu Gly Leu
                325                 330                 335

act caa gag gat tgc att gaa atg tct tgg atc gaa act gtt gtc aac       1056
Thr Gln Glu Asp Cys Ile Glu Met Ser Trp Ile Glu Thr Val Val Asn
            340                 345                 350

aat gct ggt ttt act act aga cca cct cca cca ttg gaa att ttg ttg       1104
Asn Ala Gly Phe Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile Leu Leu
        355                 360                 365

caa cca tct tct cca tac ggt aga cca tac ttc aaa gct aag tct gat       1152
Gln Pro Ser Ser Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys Ser Asp
    370                 375                 380

ttc gtc aaa gaa ccc att cca gtt ttg ggt tta aag ggt atg ttc aag       1200
Phe Val Lys Glu Pro Ile Pro Val Leu Gly Leu Lys Gly Met Phe Lys
385                 390                 395                 400

aga atg atc gaa gag gat gcc tct ttc ttg att tgg aaa cca tac ggt       1248
Arg Met Ile Glu Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro Tyr Gly
                405                 410                 415

ggt atg atg gct aga att cca gaa tcc gaa att cca ttt cca cac aga       1296
Gly Met Met Ala Arg Ile Pro Glu Ser Glu Ile Pro Phe Pro His Arg
            420                 425                 430

aac ggt act atc ttc aag atc cat tac ttc acc aag tgg tct gaa aac       1344
Asn Gly Thr Ile Phe Lys Ile His Tyr Phe Thr Lys Trp Ser Glu Asn
        435                 440                 445

ggt tct tct tct gat gac aaa cac atg aag tgg atc agg gaa ctg tat       1392
Gly Ser Ser Ser Asp Asp Lys His Met Lys Trp Ile Arg Glu Leu Tyr
    450                 455                 460

tct tat atg acc cca tac gtt tct tct aac cca aga caa gct tac gtt       1440
Ser Tyr Met Thr Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala Tyr Val
465                 470                 475                 480
```

```
aac tac aga gat ttg gac atc ggt cag aac aag aag aat gac tct gaa       1488
Asn Tyr Arg Asp Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp Ser Glu
                485                 490                 495

gat aac ttt aga agg gct caa att tgg ggt gct aag tac ttt aag aac       1536
Asp Asn Phe Arg Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe Lys Asn
            500                 505                 510

aac ttc aac agg ctg gtc aag atc aag aca aaa gtt gat cca gaa aac       1584
Asn Phe Asn Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn
        515                 520                 525

ttg ttc agg cac gaa caa tct att cca cca tta cca att aga agg cag       1632
Leu Phe Arg His Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg Arg Gln
    530                 535                 540

acc tct                                                              1638
Thr Ser
545
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<210> 107
<211> 546
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 107

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Met Arg Ile Ser Lys Pro Ile Pro Val Ile Ser Tyr Ile Leu Phe Leu
1               5                   10                  15


Ala Gln Tyr Phe Ser Leu His Thr Lys Glu Pro Thr Ser Ser Thr Ser
            20                  25                  30


Leu Gln Asp Asp Phe Ile Lys Cys Leu His Arg Asn Thr Asn Val Asp
        35                  40                  45


Phe Pro Leu Asp Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser Ser Asn
    50                  55                  60


Phe Lys Glu Val Leu Asn Thr Thr Val Trp Asn Gln Arg Tyr Met Thr
65                  70                  75                  80


Lys Ser Met Pro Lys Pro Glu Phe Ile Phe Lys Pro Val His Glu Ser
                85                  90                  95
```

```
His Val Gln Ala Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile His Phe
            100                 105                 110

Arg Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val Ser
        115                 120                 125

Gln Met Glu Thr Pro Phe Val Leu Ile Asp Leu Trp Lys Leu Lys Gln
    130                 135                 140

Ile Asn Val Asp Ile Glu Asp Asn Ser Ala Trp Val Gln Ala Gly Ala
145                 150                 155                 160

Thr Thr Gly Glu Leu Tyr Tyr Arg Ile Ala Ala Lys Ser Lys Val His
                165                 170                 175

Gly Phe Pro Ala Gly Leu Cys Ser Thr Val Gly Ile Gly Gly His Ile
            180                 185                 190

Thr Gly Gly Gly Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu Ser Thr
        195                 200                 205

Asp Asn Val Leu Asp Ala Arg Ile Val Asp Ala Asn Gly Gln Leu Leu
    210                 215                 220

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

Gly Gly Gly Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val
                245                 250                 255

Pro Val Pro Glu Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr Leu Glu
            260                 265                 270

Gln Asp Ala Gly Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile Val Asp
        275                 280                 285

Lys Leu Val Glu Glu Leu Ser Ile Arg Val Leu Phe Arg Asn Thr Gly
    290                 295                 300

Asn Lys Thr Val Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly Glu Lys
```

```
305                 310                 315                 320

Gly Thr Leu Met Glu Val Met Lys Lys Cys Phe Pro Glu Leu Gly Leu
                325                 330                 335

Thr Gln Glu Asp Cys Ile Glu Met Ser Trp Ile Glu Thr Val Val Asn
            340                 345                 350

Asn Ala Gly Phe Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile Leu Leu
        355                 360                 365

Gln Pro Ser Ser Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys Ser Asp
    370                 375                 380

Phe Val Lys Glu Pro Ile Pro Val Leu Gly Leu Lys Gly Met Phe Lys
385                 390                 395                 400

Arg Met Ile Glu Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro Tyr Gly
                405                 410                 415

Gly Met Met Ala Arg Ile Pro Glu Ser Glu Ile Pro Phe Pro His Arg
            420                 425                 430

Asn Gly Thr Ile Phe Lys Ile His Tyr Phe Thr Lys Trp Ser Glu Asn
        435                 440                 445

Gly Ser Ser Ser Asp Asp Lys His Met Lys Trp Ile Arg Glu Leu Tyr
    450                 455                 460

Ser Tyr Met Thr Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala Tyr Val
465                 470                 475                 480

Asn Tyr Arg Asp Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp Ser Glu
                485                 490                 495

Asp Asn Phe Arg Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe Lys Asn
            500                 505                 510

Asn Phe Asn Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn
        515                 520                 525
```

```
Leu Phe Arg His Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg Arg Gln
    530                 535                 540


Thr Ser
545


<210>  108
<211>  1569
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS134-A0A1J3CT99- no signal peptide


<220>
<221>  CDS
<222>  (1)..(1569)

<400>  108
atg aaa gaa cct acc tct tct acc tca ttg caa gat gat ttc atc aag         48
Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp Phe Ile Lys
1               5                   10                  15

tgc ttg cac aga aac acc aat gtt gat ttc cca ttg gac aag act ttc         96
Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp Lys Thr Phe
            20                  25                  30

ttc act cca caa aga aac tcc tcc aac ttc aaa gaa gtt ttg aac acc        144
Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val Leu Asn Thr
        35                  40                  45

acc gtc tgg aat caa aga tat atg act aag tct atg ccc aag cca gag        192
Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro Lys Pro Glu
    50                  55                  60

ttc att ttt aag cca gtt cat gaa tcc cat gtc caa gcc tct att att        240
Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala Ser Ile Ile
65                  70                  75                  80

tgc tct aag aag ttg aga atc cac ttc aga gtt aga tct ggt ggt cat        288
Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser Gly Gly His
                85                  90                  95

gat tat gag ggt ttg tct tac gtt tct caa atg gaa act cca ttc gtc        336
Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr Pro Phe Val
            100                 105                 110

ttg atc gat ttg tgg aag ttg aag caa atc aac gtc gac atc gaa gat        384
Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp Ile Glu Asp
        115                 120                 125
```

```
aat tct gct tgg gtt caa gct ggt gct act act ggt gag ttg tat tat        432
Asn Ser Ala Trp Val Gln Ala Gly Ala Thr Thr Gly Glu Leu Tyr Tyr
    130                 135                 140

aga att gct gcc aag tct aag gtt cat ggt ttt cca gct ggt ttg tgt        480
Arg Ile Ala Ala Lys Ser Lys Val His Gly Phe Pro Ala Gly Leu Cys
145                 150                 155                 160

tct act gtt ggt ata ggt ggt cat atc act ggt ggt ggt tat ggt act        528
Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly Tyr Gly Thr
                165                 170                 175

ttg atg aga aag tat ggt ttg tcc acc gat aac gtt ttg gat gct aga        576
Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu Asp Ala Arg
            180                 185                 190

atc gtt gat gct aat ggt cag ttg ttg aac aga act gct atg ggt gaa        624
Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala Met Gly Glu
        195                 200                 205

gat ttg ttc tgg gct att aga ggt ggt ggt ggc ggt tca ttt ggt gtt        672
Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly Val
    210                 215                 220

att ttg gct tgg aag atc aag ttg gtt cca gtt cca gaa act ttg acc        720
Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Leu Thr
225                 230                 235                 240

att ttc act att acc aag acc ttg gaa caa gat gcc ggt ttc aag att        768
Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly Phe Lys Ile
                245                 250                 255

ttg tct aag tgg caa aga atc gtc gac aag ttg gta gaa gaa ttg tcc        816
Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu Glu Leu Ser
            260                 265                 270

atc aga gtc ttg ttc aga aac act ggt aac aag act gtt act act acc        864
Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val Thr Thr Thr
        275                 280                 285

tac aga ggt gaa ttc ttg ggt gaa aaa ggt aca ttg atg gaa gtc atg        912
Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met Glu Val Met
    290                 295                 300

aag aag tgc ttt cca gaa ttg ggt ttg act caa gag gat tgc att gaa        960
Lys Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp Cys Ile Glu
305                 310                 315                 320

atg tct tgg atc gaa act gtt gtc aac aat gct ggt ttt act act aga       1008
Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe Thr Thr Arg
                325                 330                 335

cca cct cca cca ttg gaa att ttg ttg caa cca tct tct cca tac ggt       1056
```

```
Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser Pro Tyr Gly
            340                 345                 350

aga cca tac ttc aaa gct aag tct gat ttc gtc aaa gaa ccc att cca       1104
Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu Pro Ile Pro
        355                 360                 365

gtt ttg ggt tta aag ggt atg ttc aag aga atg atc gaa gag gat gcc       1152
Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu Glu Asp Ala
    370                 375                 380

tct ttc ttg att tgg aaa cca tac ggt ggt atg atg gct aga att cca       1200
Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala Arg Ile Pro
385                 390                 395                 400

gaa tcc gaa att cca ttt cca cac aga aac ggt act atc ttc aag atc       1248
Glu Ser Glu Ile Pro Phe Pro His Arg Asn Gly Thr Ile Phe Lys Ile
                405                 410                 415

cat tac ttc acc aag tgg tct gaa aac ggt tct tct tct gat gac aaa       1296
His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser Asp Asp Lys
            420                 425                 430

cac atg aag tgg atc agg gaa ctg tat tct tat atg acc cca tac gtt       1344
His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr Pro Tyr Val
        435                 440                 445

tct tct aac cca aga caa gct tac gtt aac tac aga gat ttg gac atc       1392
Ser Ser Asn Pro Arg Gln Ala Tyr Val Asn Tyr Arg Asp Leu Asp Ile
    450                 455                 460

ggt cag aac aag aag aat gac tct gaa gat aac ttt aga agg gct caa       1440
Gly Gln Asn Lys Lys Asn Asp Ser Glu Asp Asn Phe Arg Arg Ala Gln
465                 470                 475                 480

att tgg ggt gct aag tac ttt aag aac aac ttc aac agg ctg gtc aag       1488
Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Lys
                485                 490                 495

atc aag aca aaa gtt gat cca gaa aac ttg ttc agg cac gaa caa tct       1536
Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His Glu Gln Ser
            500                 505                 510

att cca cca tta cca att aga agg cag acc tct                          1569
Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser
        515                 520
```

<210> 109
<211> 523
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 109

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Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp Phe Ile Lys
1               5                  10                  15


Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp Lys Thr Phe
            20                  25                  30


Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val Leu Asn Thr
        35                  40                  45


Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro Lys Pro Glu
    50                  55                  60


Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala Ser Ile Ile
65                  70                  75                  80


Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser Gly Gly His
                85                  90                  95


Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr Pro Phe Val
            100                 105                 110


Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp Ile Glu Asp
        115                 120                 125


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


Arg Ile Ala Ala Lys Ser Lys Val His Gly Phe Pro Ala Gly Leu Cys
145                 150                 155                 160


Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly Tyr Gly Thr
                165                 170                 175


Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu Asp Ala Arg
            180                 185                 190


Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala Met Gly Glu
        195                 200                 205
```

```
Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly Val
    210                 215                 220

Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Leu Thr
225                 230                 235                 240

Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly Phe Lys Ile
                245                 250                 255

Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu Glu Leu Ser
            260                 265                 270

Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val Thr Thr Thr
        275                 280                 285

Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met Glu Val Met
    290                 295                 300

Lys Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp Cys Ile Glu
305                 310                 315                 320

Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe Thr Thr Arg
                325                 330                 335

Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser Pro Tyr Gly
            340                 345                 350

Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu Pro Ile Pro
        355                 360                 365

Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu Glu Asp Ala
    370                 375                 380

Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala Arg Ile Pro
385                 390                 395                 400

Glu Ser Glu Ile Pro Phe Pro His Arg Asn Gly Thr Ile Phe Lys Ile
                405                 410                 415
```

```
His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser Asp Asp Lys
            420                 425                 430

His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr Pro Tyr Val
        435                 440                 445

Ser Ser Asn Pro Arg Gln Ala Tyr Val Asn Tyr Arg Asp Leu Asp Ile
    450                 455                 460

Gly Gln Asn Lys Lys Asn Asp Ser Glu Asp Asn Phe Arg Arg Ala Gln
465                 470                 475                 480

Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Lys
                485                 490                 495

Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His Glu Gln Ser
            500                 505                 510

Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser
        515                 520
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<210>  110
<211>  1593
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS134-A0A1J3CT99-no signal peptide-strep Tag

<220>
<221>  CDS
<222>  (1)..(1593)

<400>  110

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atg aaa gaa cct acc tct tct acc tca ttg caa gat gat ttc atc aag         48
Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp Phe Ile Lys
1               5                   10                  15

tgc ttg cac aga aac acc aat gtt gat ttc cca ttg gac aag act ttc         96
Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp Lys Thr Phe
            20                  25                  30

ttc act cca caa aga aac tcc tcc aac ttc aaa gaa gtt ttg aac acc        144
Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val Leu Asn Thr
        35                  40                  45
```

```
acc gtc tgg aat caa aga tat atg act aag tct atg ccc aag cca gag        192
Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro Lys Pro Glu
    50                  55                  60

ttc att ttt aag cca gtt cat gaa tcc cat gtc caa gcc tct att att        240
Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala Ser Ile Ile
65                  70                  75                  80

tgc tct aag aag ttg aga atc cac ttc aga gtt aga tct ggt ggt cat        288
Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser Gly Gly His
                85                  90                  95

gat tat gag ggt ttg tct tac gtt tct caa atg gaa act cca ttc gtc        336
Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr Pro Phe Val
            100                 105                 110

ttg atc gat ttg tgg aag ttg aag caa atc aac gtc gac atc gaa gat        384
Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp Ile Glu Asp
        115                 120                 125

aat tct gct tgg gtt caa gct ggt gct act act ggt gag ttg tat tat        432
Asn Ser Ala Trp Val Gln Ala Gly Ala Thr Thr Gly Glu Leu Tyr Tyr
    130                 135                 140

aga att gct gcc aag tct aag gtt cat ggt ttt cca gct ggt ttg tgt        480
Arg Ile Ala Ala Lys Ser Lys Val His Gly Phe Pro Ala Gly Leu Cys
145                 150                 155                 160

tct act gtt ggt ata ggt ggt cat atc act ggt ggt ggt tat ggt act        528
Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly Tyr Gly Thr
                165                 170                 175

ttg atg aga aag tat ggt ttg tcc acc gat aac gtt ttg gat gct aga        576
Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu Asp Ala Arg
            180                 185                 190

atc gtt gat gct aat ggt cag ttg ttg aac aga act gct atg ggt gaa        624
Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala Met Gly Glu
        195                 200                 205

gat ttg ttc tgg gct att aga ggt ggt ggt ggc ggt tca ttt ggt gtt        672
Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly Val
    210                 215                 220

att ttg gct tgg aag atc aag ttg gtt cca gtt cca gaa act ttg acc        720
Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Leu Thr
225                 230                 235                 240

att ttc act att acc aag acc ttg gaa caa gat gcc ggt ttc aag att        768
Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly Phe Lys Ile
                245                 250                 255

ttg tct aag tgg caa aga atc gtc gac aag ttg gta gaa gaa ttg tcc        816
Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu Glu Leu Ser
```

```
            260                 265                 270

atc aga gtc ttg ttc aga aac act ggt aac aag act gtt act act acc        864
Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val Thr Thr Thr
        275                 280                 285

tac aga ggt gaa ttc ttg ggt gaa aaa ggt aca ttg atg gaa gtc atg        912
Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met Glu Val Met
    290                 295                 300

aag aag tgc ttt cca gaa ttg ggt ttg act caa gag gat tgc att gaa        960
Lys Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp Cys Ile Glu
305                 310                 315                 320

atg tct tgg atc gaa act gtt gtc aac aat gct ggt ttt act act aga       1008
Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe Thr Thr Arg
                325                 330                 335

cca cct cca cca ttg gaa att ttg ttg caa cca tct tct cca tac ggt       1056
Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser Pro Tyr Gly
            340                 345                 350

aga cca tac ttc aaa gct aag tct gat ttc gtc aaa gaa ccc att cca       1104
Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu Pro Ile Pro
        355                 360                 365

gtt ttg ggt tta aag ggt atg ttc aag aga atg atc gaa gag gat gcc       1152
Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu Glu Asp Ala
    370                 375                 380

tct ttc ttg att tgg aaa cca tac ggt ggt atg atg gct aga att cca       1200
Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala Arg Ile Pro
385                 390                 395                 400

gaa tcc gaa att cca ttt cca cac aga aac ggt act atc ttc aag atc       1248
Glu Ser Glu Ile Pro Phe Pro His Arg Asn Gly Thr Ile Phe Lys Ile
                405                 410                 415

cat tac ttc acc aag tgg tct gaa aac ggt tct tct tct gat gac aaa       1296
His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser Asp Asp Lys
            420                 425                 430

cac atg aag tgg atc agg gaa ctg tat tct tat atg acc cca tac gtt       1344
His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr Pro Tyr Val
        435                 440                 445

tct tct aac cca aga caa gct tac gtt aac tac aga gat ttg gac atc       1392
Ser Ser Asn Pro Arg Gln Ala Tyr Val Asn Tyr Arg Asp Leu Asp Ile
    450                 455                 460

ggt cag aac aag aag aat gac tct gaa gat aac ttt aga agg gct caa       1440
Gly Gln Asn Lys Lys Asn Asp Ser Glu Asp Asn Phe Arg Arg Ala Gln
465                 470                 475                 480
```

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att tgg ggt gct aag tac ttt aag aac aac ttc aac agg ctg gtc aag       1488
Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Lys
                485                 490                 495

atc aag aca aaa gtt gat cca gaa aac ttg ttc agg cac gaa caa tct       1536
Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His Glu Gln Ser
            500                 505                 510

att cca cca tta cca att aga agg cag acc tct tgg tca cat cca caa       1584
Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser Trp Ser His Pro Gln
        515                 520                 525

ttt gaa aag                                                           1593
Phe Glu Lys
    530
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<210> 111
<211> 531
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 111

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Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp Phe Ile Lys
1               5                   10                  15


Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp Lys Thr Phe
            20                  25                  30


Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val Leu Asn Thr
        35                  40                  45


Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro Lys Pro Glu
    50                  55                  60


Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala Ser Ile Ile
65                  70                  75                  80


Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser Gly Gly His
                85                  90                  95


Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr Pro Phe Val
            100                 105                 110
```

```
Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp Ile Glu Asp
        115                 120                 125

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

Arg Ile Ala Ala Lys Ser Lys Val His Gly Phe Pro Ala Gly Leu Cys
145                 150                 155                 160

Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly Tyr Gly Thr
                165                 170                 175

Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu Asp Ala Arg
            180                 185                 190

Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala Met Gly Glu
        195                 200                 205

Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser Phe Gly Val
    210                 215                 220

Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Leu Thr
225                 230                 235                 240

Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly Phe Lys Ile
                245                 250                 255

Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu Glu Leu Ser
            260                 265                 270

Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val Thr Thr Thr
        275                 280                 285

Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met Glu Val Met
    290                 295                 300

Lys Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp Cys Ile Glu
305                 310                 315                 320

Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe Thr Thr Arg
```

```
                325                 330                 335

Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser Pro Tyr Gly
            340                 345                 350

Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu Pro Ile Pro
        355                 360                 365

Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu Glu Asp Ala
    370                 375                 380

Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala Arg Ile Pro
385                 390                 395                 400

Glu Ser Glu Ile Pro Phe Pro His Arg Asn Gly Thr Ile Phe Lys Ile
                405                 410                 415

His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser Asp Asp Lys
            420                 425                 430

His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr Pro Tyr Val
        435                 440                 445

Ser Ser Asn Pro Arg Gln Ala Tyr Val Asn Tyr Arg Asp Leu Asp Ile
    450                 455                 460

Gly Gln Asn Lys Lys Asn Asp Ser Glu Asp Asn Phe Arg Arg Ala Gln
465                 470                 475                 480

Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Lys
                485                 490                 495

Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His Glu Gln Ser
            500                 505                 510

Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser Trp Ser His Pro Gln
        515                 520                 525

Phe Glu Lys
    530
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<210> 112
<211> 1650
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS134-A0A1J3CT99- truncated alpha factor - no signal peptide-strep Tag

<220>
<221> CDS
<222> (1)..(1650)

<400> 112

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atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca ctt gca atg aaa gaa cct acc tct tct acc tca ttg caa gat gat         96
Ala Leu Ala Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp
            20                  25                  30

ttc atc aag tgc ttg cac aga aac acc aat gtt gat ttc cca ttg gac        144
Phe Ile Lys Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp
        35                  40                  45

aag act ttc ttc act cca caa aga aac tcc tcc aac ttc aaa gaa gtt        192
Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val
    50                  55                  60

ttg aac acc acc gtc tgg aat caa aga tat atg act aag tct atg ccc        240
Leu Asn Thr Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro
65                  70                  75                  80

aag cca gag ttc att ttt aag cca gtt cat gaa tcc cat gtc caa gcc        288
Lys Pro Glu Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala
                85                  90                  95

tct att att tgc tct aag aag ttg aga atc cac ttc aga gtt aga tct        336
Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser
            100                 105                 110

ggt ggt cat gat tat gag ggt ttg tct tac gtt tct caa atg gaa act        384
Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr
        115                 120                 125

cca ttc gtc ttg atc gat ttg tgg aag ttg aag caa atc aac gtc gac        432
Pro Phe Val Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp
    130                 135                 140

atc gaa gat aat tct gct tgg gtt caa gct ggt gct act act ggt gag        480
Ile Glu Asp Asn Ser Ala Trp Val Gln Ala Gly Ala Thr Thr Gly Glu
```

```
145                 150                 155                 160

ttg tat tat aga att gct gcc aag tct aag gtt cat ggt ttt cca gct        528
Leu Tyr Tyr Arg Ile Ala Ala Lys Ser Lys Val His Gly Phe Pro Ala
                165                 170                 175

ggt ttg tgt tct act gtt ggt ata ggt ggt cat atc act ggt ggt ggt        576
Gly Leu Cys Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly
            180                 185                 190

tat ggt act ttg atg aga aag tat ggt ttg tcc acc gat aac gtt ttg        624
Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu
        195                 200                 205

gat gct aga atc gtt gat gct aat ggt cag ttg ttg aac aga act gct        672
Asp Ala Arg Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala
    210                 215                 220

atg ggt gaa gat ttg ttc tgg gct att aga ggt ggt ggt ggc ggt tca        720
Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Gly Ser
225                 230                 235                 240

ttt ggt gtt att ttg gct tgg aag atc aag ttg gtt cca gtt cca gaa        768
Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu
                245                 250                 255

act ttg acc att ttc act att acc aag acc ttg gaa caa gat gcc ggt        816
Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly
            260                 265                 270

ttc aag att ttg tct aag tgg caa aga atc gtc gac aag ttg gta gaa        864
Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu
        275                 280                 285

gaa ttg tcc atc aga gtc ttg ttc aga aac act ggt aac aag act gtt        912
Glu Leu Ser Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val
    290                 295                 300

act act acc tac aga ggt gaa ttc ttg ggt gaa aaa ggt aca ttg atg        960
Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met
305                 310                 315                 320

gaa gtc atg aag aag tgc ttt cca gaa ttg ggt ttg act caa gag gat       1008
Glu Val Met Lys Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp
                325                 330                 335

tgc att gaa atg tct tgg atc gaa act gtt gtc aac aat gct ggt ttt       1056
Cys Ile Glu Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe
            340                 345                 350

act act aga cca cct cca cca ttg gaa att ttg ttg caa cca tct tct       1104
Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser
        355                 360                 365
```

```
cca tac ggt aga cca tac ttc aaa gct aag tct gat ttc gtc aaa gaa       1152
Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu
    370                 375                 380

ccc att cca gtt ttg ggt tta aag ggt atg ttc aag aga atg atc gaa       1200
Pro Ile Pro Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu
385                 390                 395                 400

gag gat gcc tct ttc ttg att tgg aaa cca tac ggt ggt atg atg gct       1248
Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala
                405                 410                 415

aga att cca gaa tcc gaa att cca ttt cca cac aga aac ggt act atc       1296
Arg Ile Pro Glu Ser Glu Ile Pro Phe Pro His Arg Asn Gly Thr Ile
            420                 425                 430

ttc aag atc cat tac ttc acc aag tgg tct gaa aac ggt tct tct tct       1344
Phe Lys Ile His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser
        435                 440                 445

gat gac aaa cac atg aag tgg atc agg gaa ctg tat tct tat atg acc       1392
Asp Asp Lys His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr
    450                 455                 460

cca tac gtt tct tct aac cca aga caa gct tac gtt aac tac aga gat       1440
Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala Tyr Val Asn Tyr Arg Asp
465                 470                 475                 480

ttg gac atc ggt cag aac aag aag aat gac tct gaa gat aac ttt aga       1488
Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp Ser Glu Asp Asn Phe Arg
                485                 490                 495

agg gct caa att tgg ggt gct aag tac ttt aag aac aac ttc aac agg       1536
Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg
            500                 505                 510

ctg gtc aag atc aag aca aaa gtt gat cca gaa aac ttg ttc agg cac       1584
Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His
        515                 520                 525

gaa caa tct att cca cca tta cca att aga agg cag acc tct tgg tca       1632
Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser Trp Ser
    530                 535                 540

cat cca caa ttt gaa aag                                              1650
His Pro Gln Phe Glu Lys
545                 550
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<210> 113
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  113

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


Ala Leu Ala Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp
            20                  25                  30


Phe Ile Lys Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp
        35                  40                  45


Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val
    50                  55                  60


Leu Asn Thr Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro
65                  70                  75                  80


Lys Pro Glu Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala
                85                  90                  95


Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser
            100                 105                 110


Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr
        115                 120                 125


Pro Phe Val Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp
    130                 135                 140


Ile Glu Asp Asn Ser Ala Trp Val Gln Ala Gly Ala Thr Thr Gly Glu
145                 150                 155                 160


Leu Tyr Tyr Arg Ile Ala Ala Lys Ser Lys Val His Gly Phe Pro Ala
                165                 170                 175


Gly Leu Cys Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly
            180                 185                 190


Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu
```

```
        195                 200                 205

Asp Ala Arg Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala
    210                 215                 220

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

Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu
                245                 250                 255

Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly
            260                 265                 270

Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu
        275                 280                 285

Glu Leu Ser Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val
    290                 295                 300

Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met
305                 310                 315                 320

Glu Val Met Lys Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp
                325                 330                 335

Cys Ile Glu Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe
            340                 345                 350

Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser
        355                 360                 365

Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu
    370                 375                 380

Pro Ile Pro Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu
385                 390                 395                 400

Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala
                405                 410                 415
```

```
Arg Ile Pro Glu Ser Glu Ile Pro Phe Pro His Arg Asn Gly Thr Ile
            420                 425                 430

Phe Lys Ile His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser
        435                 440                 445

Asp Asp Lys His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr
    450                 455                 460

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

Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp Ser Glu Asp Asn Phe Arg
                485                 490                 495

Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg
            500                 505                 510

Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His
        515                 520                 525

Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser Trp Ser
    530                 535                 540

His Pro Gln Phe Glu Lys
545                 550
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<210>  114
<211>  1860
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS134-A0A1J3CT99-full alpha factor-no signal peptide-strep Tag

<220>
<221>  CDS
<222>  (1)..(1860)

<400>  114

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atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15
```

```
gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg aaa gaa cct acc tct tct        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Lys Glu Pro Thr Ser Ser
                85                  90                  95

acc tca ttg caa gat gat ttc atc aag tgc ttg cac aga aac acc aat        336
Thr Ser Leu Gln Asp Asp Phe Ile Lys Cys Leu His Arg Asn Thr Asn
            100                 105                 110

gtt gat ttc cca ttg gac aag act ttc ttc act cca caa aga aac tcc        384
Val Asp Phe Pro Leu Asp Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser
        115                 120                 125

tcc aac ttc aaa gaa gtt ttg aac acc acc gtc tgg aat caa aga tat        432
Ser Asn Phe Lys Glu Val Leu Asn Thr Thr Val Trp Asn Gln Arg Tyr
    130                 135                 140

atg act aag tct atg ccc aag cca gag ttc att ttt aag cca gtt cat        480
Met Thr Lys Ser Met Pro Lys Pro Glu Phe Ile Phe Lys Pro Val His
145                 150                 155                 160

gaa tcc cat gtc caa gcc tct att att tgc tct aag aag ttg aga atc        528
Glu Ser His Val Gln Ala Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile
                165                 170                 175

cac ttc aga gtt aga tct ggt ggt cat gat tat gag ggt ttg tct tac        576
His Phe Arg Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr
            180                 185                 190

gtt tct caa atg gaa act cca ttc gtc ttg atc gat ttg tgg aag ttg        624
Val Ser Gln Met Glu Thr Pro Phe Val Leu Ile Asp Leu Trp Lys Leu
        195                 200                 205

aag caa atc aac gtc gac atc gaa gat aat tct gct tgg gtt caa gct        672
Lys Gln Ile Asn Val Asp Ile Glu Asp Asn Ser Ala Trp Val Gln Ala
    210                 215                 220

ggt gct act act ggt gag ttg tat tat aga att gct gcc aag tct aag        720
```

```
Gly Ala Thr Thr Gly Glu Leu Tyr Tyr Arg Ile Ala Ala Lys Ser Lys
225                 230                 235                 240

gtt cat ggt ttt cca gct ggt ttg tgt tct act gtt ggt ata ggt ggt        768
Val His Gly Phe Pro Ala Gly Leu Cys Ser Thr Val Gly Ile Gly Gly
                245                 250                 255

cat atc act ggt ggt ggt tat ggt act ttg atg aga aag tat ggt ttg        816
His Ile Thr Gly Gly Gly Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu
            260                 265                 270

tcc acc gat aac gtt ttg gat gct aga atc gtt gat gct aat ggt cag        864
Ser Thr Asp Asn Val Leu Asp Ala Arg Ile Val Asp Ala Asn Gly Gln
        275                 280                 285

ttg ttg aac aga act gct atg ggt gaa gat ttg ttc tgg gct att aga        912
Leu Leu Asn Arg Thr Ala Met Gly Glu Asp Leu Phe Trp Ala Ile Arg
    290                 295                 300

ggt ggt ggt ggc ggt tca ttt ggt gtt att ttg gct tgg aag atc aag        960
Gly Gly Gly Gly Gly Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys
305                 310                 315                 320

ttg gtt cca gtt cca gaa act ttg acc att ttc act att acc aag acc       1008
Leu Val Pro Val Pro Glu Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr
                325                 330                 335

ttg gaa caa gat gcc ggt ttc aag att ttg tct aag tgg caa aga atc       1056
Leu Glu Gln Asp Ala Gly Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile
            340                 345                 350

gtc gac aag ttg gta gaa gaa ttg tcc atc aga gtc ttg ttc aga aac       1104
Val Asp Lys Leu Val Glu Glu Leu Ser Ile Arg Val Leu Phe Arg Asn
        355                 360                 365

act ggt aac aag act gtt act act acc tac aga ggt gaa ttc ttg ggt       1152
Thr Gly Asn Lys Thr Val Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly
    370                 375                 380

gaa aaa ggt aca ttg atg gaa gtc atg aag aag tgc ttt cca gaa ttg       1200
Glu Lys Gly Thr Leu Met Glu Val Met Lys Lys Cys Phe Pro Glu Leu
385                 390                 395                 400

ggt ttg act caa gag gat tgc att gaa atg tct tgg atc gaa act gtt       1248
Gly Leu Thr Gln Glu Asp Cys Ile Glu Met Ser Trp Ile Glu Thr Val
                405                 410                 415

gtc aac aat gct ggt ttt act act aga cca cct cca cca ttg gaa att       1296
Val Asn Asn Ala Gly Phe Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile
            420                 425                 430

ttg ttg caa cca tct tct cca tac ggt aga cca tac ttc aaa gct aag       1344
Leu Leu Gln Pro Ser Ser Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys
        435                 440                 445
```

```
tct gat ttc gtc aaa gaa ccc att cca gtt ttg ggt tta aag ggt atg       1392
Ser Asp Phe Val Lys Glu Pro Ile Pro Val Leu Gly Leu Lys Gly Met
    450                 455                 460

ttc aag aga atg atc gaa gag gat gcc tct ttc ttg att tgg aaa cca       1440
Phe Lys Arg Met Ile Glu Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro
465                 470                 475                 480

tac ggt ggt atg atg gct aga att cca gaa tcc gaa att cca ttt cca       1488
Tyr Gly Gly Met Met Ala Arg Ile Pro Glu Ser Glu Ile Pro Phe Pro
                485                 490                 495

cac aga aac ggt act atc ttc aag atc cat tac ttc acc aag tgg tct       1536
His Arg Asn Gly Thr Ile Phe Lys Ile His Tyr Phe Thr Lys Trp Ser
            500                 505                 510

gaa aac ggt tct tct tct gat gac aaa cac atg aag tgg atc agg gaa       1584
Glu Asn Gly Ser Ser Ser Asp Asp Lys His Met Lys Trp Ile Arg Glu
        515                 520                 525

ctg tat tct tat atg acc cca tac gtt tct tct aac cca aga caa gct       1632
Leu Tyr Ser Tyr Met Thr Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala
    530                 535                 540

tac gtt aac tac aga gat ttg gac atc ggt cag aac aag aag aat gac       1680
Tyr Val Asn Tyr Arg Asp Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp
545                 550                 555                 560

tct gaa gat aac ttt aga agg gct caa att tgg ggt gct aag tac ttt       1728
Ser Glu Asp Asn Phe Arg Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe
                565                 570                 575

aag aac aac ttc aac agg ctg gtc aag atc aag aca aaa gtt gat cca       1776
Lys Asn Asn Phe Asn Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro
            580                 585                 590

gaa aac ttg ttc agg cac gaa caa tct att cca cca tta cca att aga       1824
Glu Asn Leu Phe Arg His Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg
        595                 600                 605

agg cag acc tct tgg tca cat cca caa ttt gaa aag                       1860
Arg Gln Thr Ser Trp Ser His Pro Gln Phe Glu Lys
    610                 615                 620
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<210> 115
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 115

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

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

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

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Lys Glu Pro Thr Ser Ser
                85                  90                  95

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

Val Asp Phe Pro Leu Asp Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser
        115                 120                 125

Ser Asn Phe Lys Glu Val Leu Asn Thr Thr Val Trp Asn Gln Arg Tyr
    130                 135                 140

Met Thr Lys Ser Met Pro Lys Pro Glu Phe Ile Phe Lys Pro Val His
145                 150                 155                 160

Glu Ser His Val Gln Ala Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile
                165                 170                 175

His Phe Arg Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr
            180                 185                 190

Val Ser Gln Met Glu Thr Pro Phe Val Leu Ile Asp Leu Trp Lys Leu
        195                 200                 205
```

```
Lys Gln Ile Asn Val Asp Ile Glu Asp Asn Ser Ala Trp Val Gln Ala
    210                 215                 220

Gly Ala Thr Thr Gly Glu Leu Tyr Tyr Arg Ile Ala Ala Lys Ser Lys
225                 230                 235                 240

Val His Gly Phe Pro Ala Gly Leu Cys Ser Thr Val Gly Ile Gly Gly
                245                 250                 255

His Ile Thr Gly Gly Gly Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu
            260                 265                 270

Ser Thr Asp Asn Val Leu Asp Ala Arg Ile Val Asp Ala Asn Gly Gln
        275                 280                 285

Leu Leu Asn Arg Thr Ala Met Gly Glu Asp Leu Phe Trp Ala Ile Arg
    290                 295                 300

Gly Gly Gly Gly Gly Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys
305                 310                 315                 320

Leu Val Pro Val Pro Glu Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr
                325                 330                 335

Leu Glu Gln Asp Ala Gly Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile
            340                 345                 350

Val Asp Lys Leu Val Glu Glu Leu Ser Ile Arg Val Leu Phe Arg Asn
        355                 360                 365

Thr Gly Asn Lys Thr Val Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly
    370                 375                 380

Glu Lys Gly Thr Leu Met Glu Val Met Lys Lys Cys Phe Pro Glu Leu
385                 390                 395                 400

Gly Leu Thr Gln Glu Asp Cys Ile Glu Met Ser Trp Ile Glu Thr Val
                405                 410                 415

Val Asn Asn Ala Gly Phe Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile
            420                 425                 430
```

```
Leu Leu Gln Pro Ser Ser Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys
        435                 440                 445

Ser Asp Phe Val Lys Glu Pro Ile Pro Val Leu Gly Leu Lys Gly Met
    450                 455                 460

Phe Lys Arg Met Ile Glu Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro
465                 470                 475                 480

Tyr Gly Gly Met Met Ala Arg Ile Pro Glu Ser Glu Ile Pro Phe Pro
                485                 490                 495

His Arg Asn Gly Thr Ile Phe Lys Ile His Tyr Phe Thr Lys Trp Ser
            500                 505                 510

Glu Asn Gly Ser Ser Ser Asp Asp Lys His Met Lys Trp Ile Arg Glu
        515                 520                 525

Leu Tyr Ser Tyr Met Thr Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala
    530                 535                 540

Tyr Val Asn Tyr Arg Asp Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp
545                 550                 555                 560

Ser Glu Asp Asn Phe Arg Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe
                565                 570                 575

Lys Asn Asn Phe Asn Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro
            580                 585                 590

Glu Asn Leu Phe Arg His Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg
        595                 600                 605

Arg Gln Thr Ser Trp Ser His Pro Gln Phe Glu Lys
    610                 615                 620
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<210> 116
<211> 1638
<212> DNA
<213> Artificial Sequence

<220>
<223>  CBS146-A0A1J3J6A2


<220>
<221>  CDS
<222>  (1)..(1638)

<400>  116
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atg agg atc tct aag cca att cca gtc atc tcc tac att ttg ttc ttg         48
Met Arg Ile Ser Lys Pro Ile Pro Val Ile Ser Tyr Ile Leu Phe Leu
1               5                  10                  15

gcc caa tac ttc tca ttg cac aca aaa gaa cct acc tct tct acc tca         96
Ala Gln Tyr Phe Ser Leu His Thr Lys Glu Pro Thr Ser Ser Thr Ser
            20                  25                  30

ttg caa gat gat ttt gtt aag tgc ttg cac aga aac acc aac gtt gat        144
Leu Gln Asp Asp Phe Val Lys Cys Leu His Arg Asn Thr Asn Val Asp
        35                  40                  45

ttt cca ttg gac aag act ttc ttc acc cca caa aga aac tcc tcc aac        192
Phe Pro Leu Asp Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser Ser Asn
    50                  55                  60

ttc aaa gaa gtc ttg aac tct acc gtc tgg aat caa aga tat atg acc        240
Phe Lys Glu Val Leu Asn Ser Thr Val Trp Asn Gln Arg Tyr Met Thr
65                  70                  75                  80

aag tct atg cca aag cca gag ttc att ttt aag cca gtt cat gaa tcc        288
Lys Ser Met Pro Lys Pro Glu Phe Ile Phe Lys Pro Val His Glu Ser
                85                  90                  95

cat gtc caa gcc tct att att tgc tct aag aag ttg aga atc cac ttc        336
His Val Gln Ala Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile His Phe
            100                 105                 110

aga gtt aga tct ggt ggt cat gat tat gag ggt ttg tct tac gtt tct        384
Arg Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val Ser
        115                 120                 125

caa atg gaa act cca ttc gtc ttg atc gat ttg tgg aag ttg aag cag        432
Gln Met Glu Thr Pro Phe Val Leu Ile Asp Leu Trp Lys Leu Lys Gln
    130                 135                 140

att aac gtc gac atc gaa gat aat tct gct tgg gtt caa gct ggt gct        480
Ile Asn Val Asp Ile Glu Asp Asn Ser Ala Trp Val Gln Ala Gly Ala
145                 150                 155                 160

act act ggt gag ttg tat tat aga att gcc gag aag tct aag gtt cat        528
Thr Thr Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Val His
                165                 170                 175
```

```
ggt ttt cca gct ggt ttg tgt tct act gtt ggt ata ggt ggt cat atc        576
Gly Phe Pro Ala Gly Leu Cys Ser Thr Val Gly Ile Gly Gly His Ile
            180                 185                 190

act ggt ggt ggt tat ggt act ttg atg aga aag tat ggt ttg tcc acc        624
Thr Gly Gly Gly Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu Ser Thr
        195                 200                 205

gat aac gtt ttg gat gct aga atc gtt gat gct aat ggt cag ttg ttg        672
Asp Asn Val Leu Asp Ala Arg Ile Val Asp Ala Asn Gly Gln Leu Leu
    210                 215                 220

aac aga act gct atg ggt gaa gat ttg ttc tgg gct att tct ggt ggc        720
Asn Arg Thr Ala Met Gly Glu Asp Leu Phe Trp Ala Ile Ser Gly Gly
225                 230                 235                 240

ggt ggt ggt agt ttt ggt gtt att ttg gct tgg aag att aag ttg gtt        768
Gly Gly Gly Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val
                245                 250                 255

cca gtt cca gaa acc ttg acc att ttc act att acc aag acc ttg gaa        816
Pro Val Pro Glu Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr Leu Glu
            260                 265                 270

caa gat gcc ggt ttc aag att ttg tcc aaa tgg caa aga atc gtc gac        864
Gln Asp Ala Gly Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile Val Asp
        275                 280                 285

aag ttg gtt gaa gaa ttg tcc atc aga gtc ttg ttc aga aac act ggt        912
Lys Leu Val Glu Glu Leu Ser Ile Arg Val Leu Phe Arg Asn Thr Gly
    290                 295                 300

aac aag act gtt act act acc tac aga ggt gaa ttc ttg ggt gaa aaa        960
Asn Lys Thr Val Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly Glu Lys
305                 310                 315                 320

ggt aca ttg atg gaa gtc atg aac aag tgc ttt cca gaa ttg ggt ttg       1008
Gly Thr Leu Met Glu Val Met Asn Lys Cys Phe Pro Glu Leu Gly Leu
                325                 330                 335

act caa gag gat tgc att gaa atg tct tgg atc gaa act gtt gtc aac       1056
Thr Gln Glu Asp Cys Ile Glu Met Ser Trp Ile Glu Thr Val Val Asn
            340                 345                 350

aat gct ggt ttt act act aga cca cca cct cca ttg gaa att ttg ttg       1104
Asn Ala Gly Phe Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile Leu Leu
        355                 360                 365

caa cca tct tct cca tac ggt aga cca tac ttc aaa gct aag tct gat       1152
Gln Pro Ser Ser Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys Ser Asp
    370                 375                 380

ttc gtc aaa gaa ccc att cca gtt ttg ggt tta aag ggt atg ttc aag       1200
Phe Val Lys Glu Pro Ile Pro Val Leu Gly Leu Lys Gly Met Phe Lys
```

```
385                 390                 395                 400

aga atg atc gaa gag gat gcc tct ttc ttg att tgg aaa cca tac ggt       1248
Arg Met Ile Glu Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro Tyr Gly
                405                 410                 415

ggt atg atg gct aga att cca gaa tct gaa ttg cca ttt cca cac aga       1296
Gly Met Met Ala Arg Ile Pro Glu Ser Glu Leu Pro Phe Pro His Arg
            420                 425                 430

aac ggt act att ttc aag atc cat tac ttc acc aag tgg tcc gaa aat       1344
Asn Gly Thr Ile Phe Lys Ile His Tyr Phe Thr Lys Trp Ser Glu Asn
        435                 440                 445

ggt tct tct tct gat gac aaa cac atg aag tgg atc agg gaa ctg tat       1392
Gly Ser Ser Ser Asp Asp Lys His Met Lys Trp Ile Arg Glu Leu Tyr
    450                 455                 460

tct tat atg acc cca tac gtt tct tct aac cca aga caa gct tac gtt       1440
Ser Tyr Met Thr Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala Tyr Val
465                 470                 475                 480

aac tac aga gat ttg gac atc ggt cag aac aag aag aac gat tct gaa       1488
Asn Tyr Arg Asp Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp Ser Glu
                485                 490                 495

aac aat ttc aga agg gct caa att tgg ggt gct aag tac ttt aag aac       1536
Asn Asn Phe Arg Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe Lys Asn
            500                 505                 510

aac ttc aac agg ctg gtc aag atc aag aca aaa gtt gat cca gaa aac       1584
Asn Phe Asn Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn
        515                 520                 525

ttg ttc agg cac gaa caa tct att cca cca ttg cca att aga agg caa       1632
Leu Phe Arg His Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg Arg Gln
    530                 535                 540

acc tct                                                              1638
Thr Ser
545
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<210> 117
<211> 546
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 117

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Met Arg Ile Ser Lys Pro Ile Pro Val Ile Ser Tyr Ile Leu Phe Leu
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```
1               5                   10                  15

Ala Gln Tyr Phe Ser Leu His Thr Lys Glu Pro Thr Ser Ser Thr Ser
            20                  25                  30

Leu Gln Asp Asp Phe Val Lys Cys Leu His Arg Asn Thr Asn Val Asp
        35                  40                  45

Phe Pro Leu Asp Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser Ser Asn
    50                  55                  60

Phe Lys Glu Val Leu Asn Ser Thr Val Trp Asn Gln Arg Tyr Met Thr
65                  70                  75                  80

Lys Ser Met Pro Lys Pro Glu Phe Ile Phe Lys Pro Val His Glu Ser
                85                  90                  95

His Val Gln Ala Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile His Phe
            100                 105                 110

Arg Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val Ser
        115                 120                 125

Gln Met Glu Thr Pro Phe Val Leu Ile Asp Leu Trp Lys Leu Lys Gln
    130                 135                 140

Ile Asn Val Asp Ile Glu Asp Asn Ser Ala Trp Val Gln Ala Gly Ala
145                 150                 155                 160

Thr Thr Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Val His
                165                 170                 175

Gly Phe Pro Ala Gly Leu Cys Ser Thr Val Gly Ile Gly Gly His Ile
            180                 185                 190

Thr Gly Gly Gly Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu Ser Thr
        195                 200                 205

Asp Asn Val Leu Asp Ala Arg Ile Val Asp Ala Asn Gly Gln Leu Leu
    210                 215                 220
```

```
Asn Arg Thr Ala Met Gly Glu Asp Leu Phe Trp Ala Ile Ser Gly Gly
225                 230                 235                 240


Gly Gly Gly Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val
                245                 250                 255


Pro Val Pro Glu Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr Leu Glu
            260                 265                 270


Gln Asp Ala Gly Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile Val Asp
        275                 280                 285


Lys Leu Val Glu Glu Leu Ser Ile Arg Val Leu Phe Arg Asn Thr Gly
    290                 295                 300


Asn Lys Thr Val Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly Glu Lys
305                 310                 315                 320


Gly Thr Leu Met Glu Val Met Asn Lys Cys Phe Pro Glu Leu Gly Leu
                325                 330                 335


Thr Gln Glu Asp Cys Ile Glu Met Ser Trp Ile Glu Thr Val Val Asn
            340                 345                 350


Asn Ala Gly Phe Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile Leu Leu
        355                 360                 365


Gln Pro Ser Ser Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys Ser Asp
    370                 375                 380


Phe Val Lys Glu Pro Ile Pro Val Leu Gly Leu Lys Gly Met Phe Lys
385                 390                 395                 400


Arg Met Ile Glu Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro Tyr Gly
                405                 410                 415


Gly Met Met Ala Arg Ile Pro Glu Ser Glu Leu Pro Phe Pro His Arg
            420                 425                 430


Asn Gly Thr Ile Phe Lys Ile His Tyr Phe Thr Lys Trp Ser Glu Asn
```

```
        435                 440                 445

Gly Ser Ser Ser Asp Asp Lys His Met Lys Trp Ile Arg Glu Leu Tyr
    450                 455                 460

Ser Tyr Met Thr Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala Tyr Val
465                 470                 475                 480

Asn Tyr Arg Asp Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp Ser Glu
                485                 490                 495

Asn Asn Phe Arg Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe Lys Asn
            500                 505                 510

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

Leu Phe Arg His Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg Arg Gln
    530                 535                 540

Thr Ser
545


<210>  118
<211>  1569
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS146-A0A1J3J6A2-no signal peptide


<220>
<221>  CDS
<222>  (1)..(1569)

<400>  118
atg aaa gaa cct acc tct tct acc tca ttg caa gat gat ttt gtt aag         48
Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp Phe Val Lys
1               5                   10                  15

tgc ttg cac aga aac acc aac gtt gat ttt cca ttg gac aag act ttc         96
Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp Lys Thr Phe
            20                  25                  30

ttc acc cca caa aga aac tcc tcc aac ttc aaa gaa gtc ttg aac tct        144
```

```
Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val Leu Asn Ser
        35                  40                  45

acc gtc tgg aat caa aga tat atg acc aag tct atg cca aag cca gag        192
Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro Lys Pro Glu
    50                  55                  60

ttc att ttt aag cca gtt cat gaa tcc cat gtc caa gcc tct att att        240
Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala Ser Ile Ile
65                  70                  75                  80

tgc tct aag aag ttg aga atc cac ttc aga gtt aga tct ggt ggt cat        288
Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser Gly Gly His
                85                  90                  95

gat tat gag ggt ttg tct tac gtt tct caa atg gaa act cca ttc gtc        336
Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr Pro Phe Val
            100                 105                 110

ttg atc gat ttg tgg aag ttg aag cag att aac gtc gac atc gaa gat        384
Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp Ile Glu Asp
        115                 120                 125

aat tct gct tgg gtt caa gct ggt gct act act ggt gag ttg tat tat        432
Asn Ser Ala Trp Val Gln Ala Gly Ala Thr Thr Gly Glu Leu Tyr Tyr
    130                 135                 140

aga att gcc gag aag tct aag gtt cat ggt ttt cca gct ggt ttg tgt        480
Arg Ile Ala Glu Lys Ser Lys Val His Gly Phe Pro Ala Gly Leu Cys
145                 150                 155                 160

tct act gtt ggt ata ggt ggt cat atc act ggt ggt ggt tat ggt act        528
Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly Tyr Gly Thr
                165                 170                 175

ttg atg aga aag tat ggt ttg tcc acc gat aac gtt ttg gat gct aga        576
Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu Asp Ala Arg
            180                 185                 190

atc gtt gat gct aat ggt cag ttg ttg aac aga act gct atg ggt gaa        624
Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala Met Gly Glu
        195                 200                 205

gat ttg ttc tgg gct att tct ggt ggc ggt ggt ggt agt ttt ggt gtt        672
Asp Leu Phe Trp Ala Ile Ser Gly Gly Gly Gly Gly Ser Phe Gly Val
    210                 215                 220

att ttg gct tgg aag att aag ttg gtt cca gtt cca gaa acc ttg acc        720
Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Leu Thr
225                 230                 235                 240

att ttc act att acc aag acc ttg gaa caa gat gcc ggt ttc aag att        768
Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly Phe Lys Ile
                245                 250                 255
```

```
ttg tcc aaa tgg caa aga atc gtc gac aag ttg gtt gaa gaa ttg tcc        816
Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu Glu Leu Ser
            260                 265                 270

atc aga gtc ttg ttc aga aac act ggt aac aag act gtt act act acc        864
Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val Thr Thr Thr
        275                 280                 285

tac aga ggt gaa ttc ttg ggt gaa aaa ggt aca ttg atg gaa gtc atg        912
Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met Glu Val Met
    290                 295                 300

aac aag tgc ttt cca gaa ttg ggt ttg act caa gag gat tgc att gaa        960
Asn Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp Cys Ile Glu
305                 310                 315                 320

atg tct tgg atc gaa act gtt gtc aac aat gct ggt ttt act act aga       1008
Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe Thr Thr Arg
                325                 330                 335

cca cca cct cca ttg gaa att ttg ttg caa cca tct tct cca tac ggt       1056
Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser Pro Tyr Gly
            340                 345                 350

aga cca tac ttc aaa gct aag tct gat ttc gtc aaa gaa ccc att cca       1104
Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu Pro Ile Pro
        355                 360                 365

gtt ttg ggt tta aag ggt atg ttc aag aga atg atc gaa gag gat gcc       1152
Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu Glu Asp Ala
    370                 375                 380

tct ttc ttg att tgg aaa cca tac ggt ggt atg atg gct aga att cca       1200
Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala Arg Ile Pro
385                 390                 395                 400

gaa tct gaa ttg cca ttt cca cac aga aac ggt act att ttc aag atc       1248
Glu Ser Glu Leu Pro Phe Pro His Arg Asn Gly Thr Ile Phe Lys Ile
                405                 410                 415

cat tac ttc acc aag tgg tcc gaa aat ggt tct tct tct gat gac aaa       1296
His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser Asp Asp Lys
            420                 425                 430

cac atg aag tgg atc agg gaa ctg tat tct tat atg acc cca tac gtt       1344
His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr Pro Tyr Val
        435                 440                 445

tct tct aac cca aga caa gct tac gtt aac tac aga gat ttg gac atc       1392
Ser Ser Asn Pro Arg Gln Ala Tyr Val Asn Tyr Arg Asp Leu Asp Ile
    450                 455                 460

ggt cag aac aag aag aac gat tct gaa aac aat ttc aga agg gct caa       1440
```

```
Gly Gln Asn Lys Lys Asn Asp Ser Glu Asn Asn Phe Arg Arg Ala Gln
465                 470                 475                 480

att tgg ggt gct aag tac ttt aag aac aac ttc aac agg ctg gtc aag       1488
Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Lys
                485                 490                 495

atc aag aca aaa gtt gat cca gaa aac ttg ttc agg cac gaa caa tct       1536
Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His Glu Gln Ser
            500                 505                 510

att cca cca ttg cca att aga agg caa acc tct                           1569
Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser
        515                 520
```

<210> 119
<211> 523
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 119

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Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp Phe Val Lys
1               5                   10                  15

Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp Lys Thr Phe
            20                  25                  30

Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val Leu Asn Ser
        35                  40                  45

Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro Lys Pro Glu
    50                  55                  60

Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala Ser Ile Ile
65                  70                  75                  80

Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser Gly Gly His
                85                  90                  95

Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr Pro Phe Val
            100                 105                 110
```

```
Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp Ile Glu Asp
        115                 120                 125

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

Arg Ile Ala Glu Lys Ser Lys Val His Gly Phe Pro Ala Gly Leu Cys
145                 150                 155                 160

Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly Tyr Gly Thr
                165                 170                 175

Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu Asp Ala Arg
            180                 185                 190

Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala Met Gly Glu
        195                 200                 205

Asp Leu Phe Trp Ala Ile Ser Gly Gly Gly Gly Gly Ser Phe Gly Val
    210                 215                 220

Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Leu Thr
225                 230                 235                 240

Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly Phe Lys Ile
                245                 250                 255

Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu Glu Leu Ser
            260                 265                 270

Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val Thr Thr Thr
        275                 280                 285

Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met Glu Val Met
    290                 295                 300

Asn Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp Cys Ile Glu
305                 310                 315                 320

Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe Thr Thr Arg
                325                 330                 335
```

```
Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser Pro Tyr Gly
            340                 345                 350

Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu Pro Ile Pro
        355                 360                 365

Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu Glu Asp Ala
    370                 375                 380

Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala Arg Ile Pro
385                 390                 395                 400

Glu Ser Glu Leu Pro Phe Pro His Arg Asn Gly Thr Ile Phe Lys Ile
                405                 410                 415

His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser Asp Asp Lys
            420                 425                 430

His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr Pro Tyr Val
        435                 440                 445

Ser Ser Asn Pro Arg Gln Ala Tyr Val Asn Tyr Arg Asp Leu Asp Ile
    450                 455                 460

Gly Gln Asn Lys Lys Asn Asp Ser Glu Asn Asn Phe Arg Arg Ala Gln
465                 470                 475                 480

Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Lys
                485                 490                 495

Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His Glu Gln Ser
            500                 505                 510

Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser
        515                 520
```

<210> 120
<211> 1593
<212> DNA
<213> Artificial Sequence

<220>
<223>  CBS146-A0A1J3J6A2- no signal peptide-strep Tag

<220>
<221>  CDS
<222>  (1)..(1593)

<400>  120
atg aaa gaa cct acc tct tct acc tca ttg caa gat gat ttt gtt aag  48
Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp Phe Val Lys
1               5                   10                  15

tgc ttg cac aga aac acc aac gtt gat ttt cca ttg gac aag act ttc  96
Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp Lys Thr Phe
            20                  25                  30

ttc acc cca caa aga aac tcc tcc aac ttc aaa gaa gtc ttg aac tct 144
Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val Leu Asn Ser
        35                  40                  45

acc gtc tgg aat caa aga tat atg acc aag tct atg cca aag cca gag 192
Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro Lys Pro Glu
    50                  55                  60

ttc att ttt aag cca gtt cat gaa tcc cat gtc caa gcc tct att att 240
Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala Ser Ile Ile
65                  70                  75                  80

tgc tct aag aag ttg aga atc cac ttc aga gtt aga tct ggt ggt cat 288
Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser Gly Gly His
                85                  90                  95

gat tat gag ggt ttg tct tac gtt tct caa atg gaa act cca ttc gtc 336
Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr Pro Phe Val
            100                 105                 110

ttg atc gat ttg tgg aag ttg aag cag att aac gtc gac atc gaa gat 384
Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp Ile Glu Asp
        115                 120                 125

aat tct gct tgg gtt caa gct ggt gct act act ggt gag ttg tat tat 432
Asn Ser Ala Trp Val Gln Ala Gly Ala Thr Thr Gly Glu Leu Tyr Tyr
    130                 135                 140

aga att gcc gag aag tct aag gtt cat ggt ttt cca gct ggt ttg tgt 480
Arg Ile Ala Glu Lys Ser Lys Val His Gly Phe Pro Ala Gly Leu Cys
145                 150                 155                 160

tct act gtt ggt ata ggt ggt cat atc act ggt ggt ggt tat ggt act 528
Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly Tyr Gly Thr
                165                 170                 175

```
ttg atg aga aag tat ggt ttg tcc acc gat aac gtt ttg gat gct aga        576
Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu Asp Ala Arg
            180                 185                 190

atc gtt gat gct aat ggt cag ttg ttg aac aga act gct atg ggt gaa        624
Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala Met Gly Glu
        195                 200                 205

gat ttg ttc tgg gct att tct ggt ggc ggt ggt ggt agt ttt ggt gtt        672
Asp Leu Phe Trp Ala Ile Ser Gly Gly Gly Gly Gly Ser Phe Gly Val
    210                 215                 220

att ttg gct tgg aag att aag ttg gtt cca gtt cca gaa acc ttg acc        720
Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Leu Thr
225                 230                 235                 240

att ttc act att acc aag acc ttg gaa caa gat gcc ggt ttc aag att        768
Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly Phe Lys Ile
                245                 250                 255

ttg tcc aaa tgg caa aga atc gtc gac aag ttg gtt gaa gaa ttg tcc        816
Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu Glu Leu Ser
            260                 265                 270

atc aga gtc ttg ttc aga aac act ggt aac aag act gtt act act acc        864
Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val Thr Thr Thr
        275                 280                 285

tac aga ggt gaa ttc ttg ggt gaa aaa ggt aca ttg atg gaa gtc atg        912
Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met Glu Val Met
    290                 295                 300

aac aag tgc ttt cca gaa ttg ggt ttg act caa gag gat tgc att gaa        960
Asn Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp Cys Ile Glu
305                 310                 315                 320

atg tct tgg atc gaa act gtt gtc aac aat gct ggt ttt act act aga       1008
Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe Thr Thr Arg
                325                 330                 335

cca cca cct cca ttg gaa att ttg ttg caa cca tct tct cca tac ggt       1056
Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser Pro Tyr Gly
            340                 345                 350

aga cca tac ttc aaa gct aag tct gat ttc gtc aaa gaa ccc att cca       1104
Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu Pro Ile Pro
        355                 360                 365

gtt ttg ggt tta aag ggt atg ttc aag aga atg atc gaa gag gat gcc       1152
Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu Glu Asp Ala
    370                 375                 380

tct ttc ttg att tgg aaa cca tac ggt ggt atg atg gct aga att cca       1200
Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala Arg Ile Pro
```

```
385                 390                 395                 400

gaa tct gaa ttg cca ttt cca cac aga aac ggt act att ttc aag atc       1248
Glu Ser Glu Leu Pro Phe Pro His Arg Asn Gly Thr Ile Phe Lys Ile
                405                 410                 415

cat tac ttc acc aag tgg tcc gaa aat ggt tct tct tct gat gac aaa       1296
His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser Asp Asp Lys
            420                 425                 430

cac atg aag tgg atc agg gaa ctg tat tct tat atg acc cca tac gtt       1344
His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr Pro Tyr Val
        435                 440                 445

tct tct aac cca aga caa gct tac gtt aac tac aga gat ttg gac atc       1392
Ser Ser Asn Pro Arg Gln Ala Tyr Val Asn Tyr Arg Asp Leu Asp Ile
    450                 455                 460

ggt cag aac aag aag aac gat tct gaa aac aat ttc aga agg gct caa       1440
Gly Gln Asn Lys Lys Asn Asp Ser Glu Asn Asn Phe Arg Arg Ala Gln
465                 470                 475                 480

att tgg ggt gct aag tac ttt aag aac aac ttc aac agg ctg gtc aag       1488
Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Lys
                485                 490                 495

atc aag aca aaa gtt gat cca gaa aac ttg ttc agg cac gaa caa tct       1536
Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His Glu Gln Ser
            500                 505                 510

att cca cca ttg cca att aga agg caa acc tct tgg tca cat cca caa       1584
Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser Trp Ser His Pro Gln
        515                 520                 525

ttt gaa aag                                                           1593
Phe Glu Lys
    530
```

<210>  121
<211>  531
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  121

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Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp Phe Val Lys
1               5                   10                  15

Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp Lys Thr Phe
```

```
            20                  25                  30

Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val Leu Asn Ser
        35                  40                  45

Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro Lys Pro Glu
    50                  55                  60

Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala Ser Ile Ile
65                  70                  75                  80

Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser Gly Gly His
                85                  90                  95

Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr Pro Phe Val
            100                 105                 110

Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp Ile Glu Asp
        115                 120                 125

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

Arg Ile Ala Glu Lys Ser Lys Val His Gly Phe Pro Ala Gly Leu Cys
145                 150                 155                 160

Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly Tyr Gly Thr
                165                 170                 175

Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu Asp Ala Arg
            180                 185                 190

Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala Met Gly Glu
        195                 200                 205

Asp Leu Phe Trp Ala Ile Ser Gly Gly Gly Gly Gly Ser Phe Gly Val
    210                 215                 220

Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu Thr Leu Thr
225                 230                 235                 240
```

```
Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly Phe Lys Ile
                245                 250                 255

Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu Glu Leu Ser
            260                 265                 270

Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val Thr Thr Thr
        275                 280                 285

Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met Glu Val Met
    290                 295                 300

Asn Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp Cys Ile Glu
305                 310                 315                 320

Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe Thr Thr Arg
                325                 330                 335

Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser Pro Tyr Gly
            340                 345                 350

Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu Pro Ile Pro
        355                 360                 365

Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu Glu Asp Ala
    370                 375                 380

Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala Arg Ile Pro
385                 390                 395                 400

Glu Ser Glu Leu Pro Phe Pro His Arg Asn Gly Thr Ile Phe Lys Ile
                405                 410                 415

His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser Asp Asp Lys
            420                 425                 430

His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr Pro Tyr Val
        435                 440                 445

Ser Ser Asn Pro Arg Gln Ala Tyr Val Asn Tyr Arg Asp Leu Asp Ile
```

```
    450                 455                 460

Gly Gln Asn Lys Lys Asn Asp Ser Glu Asn Asn Phe Arg Arg Ala Gln
465                 470                 475                 480

Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg Leu Val Lys
                485                 490                 495

Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His Glu Gln Ser
            500                 505                 510

Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser Trp Ser His Pro Gln
        515                 520                 525

Phe Glu Lys
    530
```

<210> 122
<211> 1650
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS146-A0A1J3J6A2-truncated alpha factor - no signal peptide-strep Tag

<220>
<221> CDS
<222> (1)..(1650)

<400> 122

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atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca ctt gca atg aaa gaa cct acc tct tct acc tca ttg caa gat gat         96
Ala Leu Ala Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp
            20                  25                  30

ttt gtt aag tgc ttg cac aga aac acc aac gtt gat ttt cca ttg gac        144
Phe Val Lys Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp
        35                  40                  45

aag act ttc ttc acc cca caa aga aac tcc tcc aac ttc aaa gaa gtc        192
Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val
    50                  55                  60
```

```
ttg aac tct acc gtc tgg aat caa aga tat atg acc aag tct atg cca        240
Leu Asn Ser Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro
65                  70                  75                  80

aag cca gag ttc att ttt aag cca gtt cat gaa tcc cat gtc caa gcc        288
Lys Pro Glu Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala
                85                  90                  95

tct att att tgc tct aag aag ttg aga atc cac ttc aga gtt aga tct        336
Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser
            100                 105                 110

ggt ggt cat gat tat gag ggt ttg tct tac gtt tct caa atg gaa act        384
Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr
        115                 120                 125

cca ttc gtc ttg atc gat ttg tgg aag ttg aag cag att aac gtc gac        432
Pro Phe Val Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp
    130                 135                 140

atc gaa gat aat tct gct tgg gtt caa gct ggt gct act act ggt gag        480
Ile Glu Asp Asn Ser Ala Trp Val Gln Ala Gly Ala Thr Thr Gly Glu
145                 150                 155                 160

ttg tat tat aga att gcc gag aag tct aag gtt cat ggt ttt cca gct        528
Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Val His Gly Phe Pro Ala
                165                 170                 175

ggt ttg tgt tct act gtt ggt ata ggt ggt cat atc act ggt ggt ggt        576
Gly Leu Cys Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly
            180                 185                 190

tat ggt act ttg atg aga aag tat ggt ttg tcc acc gat aac gtt ttg        624
Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu
        195                 200                 205

gat gct aga atc gtt gat gct aat ggt cag ttg ttg aac aga act gct        672
Asp Ala Arg Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala
    210                 215                 220

atg ggt gaa gat ttg ttc tgg gct att tct ggt ggc ggt ggt ggt agt        720
Met Gly Glu Asp Leu Phe Trp Ala Ile Ser Gly Gly Gly Gly Gly Ser
225                 230                 235                 240

ttt ggt gtt att ttg gct tgg aag att aag ttg gtt cca gtt cca gaa        768
Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu
                245                 250                 255

acc ttg acc att ttc act att acc aag acc ttg gaa caa gat gcc ggt        816
Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly
            260                 265                 270

ttc aag att ttg tcc aaa tgg caa aga atc gtc gac aag ttg gtt gaa        864
Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu
```

```
        275                 280                 285

gaa ttg tcc atc aga gtc ttg ttc aga aac act ggt aac aag act gtt        912
Glu Leu Ser Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val
    290                 295                 300

act act acc tac aga ggt gaa ttc ttg ggt gaa aaa ggt aca ttg atg        960
Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met
305                 310                 315                 320

gaa gtc atg aac aag tgc ttt cca gaa ttg ggt ttg act caa gag gat       1008
Glu Val Met Asn Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp
                325                 330                 335

tgc att gaa atg tct tgg atc gaa act gtt gtc aac aat gct ggt ttt       1056
Cys Ile Glu Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe
            340                 345                 350

act act aga cca cca cct cca ttg gaa att ttg ttg caa cca tct tct       1104
Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser
        355                 360                 365

cca tac ggt aga cca tac ttc aaa gct aag tct gat ttc gtc aaa gaa       1152
Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu
    370                 375                 380

ccc att cca gtt ttg ggt tta aag ggt atg ttc aag aga atg atc gaa       1200
Pro Ile Pro Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu
385                 390                 395                 400

gag gat gcc tct ttc ttg att tgg aaa cca tac ggt ggt atg atg gct       1248
Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala
                405                 410                 415

aga att cca gaa tct gaa ttg cca ttt cca cac aga aac ggt act att       1296
Arg Ile Pro Glu Ser Glu Leu Pro Phe Pro His Arg Asn Gly Thr Ile
            420                 425                 430

ttc aag atc cat tac ttc acc aag tgg tcc gaa aat ggt tct tct tct       1344
Phe Lys Ile His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser
        435                 440                 445

gat gac aaa cac atg aag tgg atc agg gaa ctg tat tct tat atg acc       1392
Asp Asp Lys His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr
    450                 455                 460

cca tac gtt tct tct aac cca aga caa gct tac gtt aac tac aga gat       1440
Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala Tyr Val Asn Tyr Arg Asp
465                 470                 475                 480

ttg gac atc ggt cag aac aag aag aac gat tct gaa aac aat ttc aga       1488
Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp Ser Glu Asn Asn Phe Arg
                485                 490                 495
```

```
agg gct caa att tgg ggt gct aag tac ttt aag aac aac ttc aac agg       1536
Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg
            500                 505                 510

ctg gtc aag atc aag aca aaa gtt gat cca gaa aac ttg ttc agg cac       1584
Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His
        515                 520                 525

gaa caa tct att cca cca ttg cca att aga agg caa acc tct tgg tca       1632
Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser Trp Ser
    530                 535                 540

cat cca caa ttt gaa aag                                              1650
His Pro Gln Phe Glu Lys
545                 550
```

<210> 123
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 123

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


Ala Leu Ala Met Lys Glu Pro Thr Ser Ser Thr Ser Leu Gln Asp Asp
            20                  25                  30


Phe Val Lys Cys Leu His Arg Asn Thr Asn Val Asp Phe Pro Leu Asp
        35                  40                  45


Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser Ser Asn Phe Lys Glu Val
    50                  55                  60


Leu Asn Ser Thr Val Trp Asn Gln Arg Tyr Met Thr Lys Ser Met Pro
65                  70                  75                  80


Lys Pro Glu Phe Ile Phe Lys Pro Val His Glu Ser His Val Gln Ala
                85                  90                  95


Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile His Phe Arg Val Arg Ser
            100                 105                 110
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Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val Ser Gln Met Glu Thr
        115                 120                 125

Pro Phe Val Leu Ile Asp Leu Trp Lys Leu Lys Gln Ile Asn Val Asp
    130                 135                 140

Ile Glu Asp Asn Ser Ala Trp Val Gln Ala Gly Ala Thr Thr Gly Glu
145                 150                 155                 160

Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Val His Gly Phe Pro Ala
                165                 170                 175

Gly Leu Cys Ser Thr Val Gly Ile Gly Gly His Ile Thr Gly Gly Gly
            180                 185                 190

Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu Ser Thr Asp Asn Val Leu
        195                 200                 205

Asp Ala Arg Ile Val Asp Ala Asn Gly Gln Leu Leu Asn Arg Thr Ala
    210                 215                 220

Met Gly Glu Asp Leu Phe Trp Ala Ile Ser Gly Gly Gly Gly Gly Ser
225                 230                 235                 240

Phe Gly Val Ile Leu Ala Trp Lys Ile Lys Leu Val Pro Val Pro Glu
                245                 250                 255

Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr Leu Glu Gln Asp Ala Gly
            260                 265                 270

Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile Val Asp Lys Leu Val Glu
        275                 280                 285

Glu Leu Ser Ile Arg Val Leu Phe Arg Asn Thr Gly Asn Lys Thr Val
    290                 295                 300

Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly Glu Lys Gly Thr Leu Met
305                 310                 315                 320

Glu Val Met Asn Lys Cys Phe Pro Glu Leu Gly Leu Thr Gln Glu Asp
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                325                 330                 335

Cys Ile Glu Met Ser Trp Ile Glu Thr Val Val Asn Asn Ala Gly Phe
            340                 345                 350

Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile Leu Leu Gln Pro Ser Ser
        355                 360                 365

Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys Ser Asp Phe Val Lys Glu
    370                 375                 380

Pro Ile Pro Val Leu Gly Leu Lys Gly Met Phe Lys Arg Met Ile Glu
385                 390                 395                 400

Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro Tyr Gly Gly Met Met Ala
                405                 410                 415

Arg Ile Pro Glu Ser Glu Leu Pro Phe Pro His Arg Asn Gly Thr Ile
            420                 425                 430

Phe Lys Ile His Tyr Phe Thr Lys Trp Ser Glu Asn Gly Ser Ser Ser
        435                 440                 445

Asp Asp Lys His Met Lys Trp Ile Arg Glu Leu Tyr Ser Tyr Met Thr
    450                 455                 460

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

Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp Ser Glu Asn Asn Phe Arg
                485                 490                 495

Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe Lys Asn Asn Phe Asn Arg
            500                 505                 510

Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn Leu Phe Arg His
        515                 520                 525

Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg Arg Gln Thr Ser Trp Ser
    530                 535                 540
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His Pro Gln Phe Glu Lys
545                 550


<210>  124
<211>  1860
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS146-A0A1J3J6A2- full alpha factor -no signal peptide-strep Tag


<220>
<221>  CDS
<222>  (1)..(1860)

<400>  124
atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg aaa gaa cct acc tct tct        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Lys Glu Pro Thr Ser Ser
                85                  90                  95

acc tca ttg caa gat gat ttt gtt aag tgc ttg cac aga aac acc aac        336
Thr Ser Leu Gln Asp Asp Phe Val Lys Cys Leu His Arg Asn Thr Asn
            100                 105                 110

gtt gat ttt cca ttg gac aag act ttc ttc acc cca caa aga aac tcc        384
Val Asp Phe Pro Leu Asp Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser
        115                 120                 125

tcc aac ttc aaa gaa gtc ttg aac tct acc gtc tgg aat caa aga tat        432
Ser Asn Phe Lys Glu Val Leu Asn Ser Thr Val Trp Asn Gln Arg Tyr
    130                 135                 140
```

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atg acc aag tct atg cca aag cca gag ttc att ttt aag cca gtt cat        480
Met Thr Lys Ser Met Pro Lys Pro Glu Phe Ile Phe Lys Pro Val His
145                 150                 155                 160

gaa tcc cat gtc caa gcc tct att att tgc tct aag aag ttg aga atc        528
Glu Ser His Val Gln Ala Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile
                165                 170                 175

cac ttc aga gtt aga tct ggt ggt cat gat tat gag ggt ttg tct tac        576
His Phe Arg Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr
            180                 185                 190

gtt tct caa atg gaa act cca ttc gtc ttg atc gat ttg tgg aag ttg        624
Val Ser Gln Met Glu Thr Pro Phe Val Leu Ile Asp Leu Trp Lys Leu
        195                 200                 205

aag cag att aac gtc gac atc gaa gat aat tct gct tgg gtt caa gct        672
Lys Gln Ile Asn Val Asp Ile Glu Asp Asn Ser Ala Trp Val Gln Ala
    210                 215                 220

ggt gct act act ggt gag ttg tat tat aga att gcc gag aag tct aag        720
Gly Ala Thr Thr Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys
225                 230                 235                 240

gtt cat ggt ttt cca gct ggt ttg tgt tct act gtt ggt ata ggt ggt        768
Val His Gly Phe Pro Ala Gly Leu Cys Ser Thr Val Gly Ile Gly Gly
                245                 250                 255

cat atc act ggt ggt ggt tat ggt act ttg atg aga aag tat ggt ttg        816
His Ile Thr Gly Gly Gly Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu
            260                 265                 270

tcc acc gat aac gtt ttg gat gct aga atc gtt gat gct aat ggt cag        864
Ser Thr Asp Asn Val Leu Asp Ala Arg Ile Val Asp Ala Asn Gly Gln
        275                 280                 285

ttg ttg aac aga act gct atg ggt gaa gat ttg ttc tgg gct att tct        912
Leu Leu Asn Arg Thr Ala Met Gly Glu Asp Leu Phe Trp Ala Ile Ser
    290                 295                 300

ggt ggc ggt ggt ggt agt ttt ggt gtt att ttg gct tgg aag att aag        960
Gly Gly Gly Gly Gly Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys
305                 310                 315                 320

ttg gtt cca gtt cca gaa acc ttg acc att ttc act att acc aag acc       1008
Leu Val Pro Val Pro Glu Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr
                325                 330                 335

ttg gaa caa gat gcc ggt ttc aag att ttg tcc aaa tgg caa aga atc       1056
Leu Glu Gln Asp Ala Gly Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile
            340                 345                 350

gtc gac aag ttg gtt gaa gaa ttg tcc atc aga gtc ttg ttc aga aac       1104
```

```
Val Asp Lys Leu Val Glu Glu Leu Ser Ile Arg Val Leu Phe Arg Asn
        355                 360                 365

act ggt aac aag act gtt act act acc tac aga ggt gaa ttc ttg ggt       1152
Thr Gly Asn Lys Thr Val Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly
    370                 375                 380

gaa aaa ggt aca ttg atg gaa gtc atg aac aag tgc ttt cca gaa ttg       1200
Glu Lys Gly Thr Leu Met Glu Val Met Asn Lys Cys Phe Pro Glu Leu
385                 390                 395                 400

ggt ttg act caa gag gat tgc att gaa atg tct tgg atc gaa act gtt       1248
Gly Leu Thr Gln Glu Asp Cys Ile Glu Met Ser Trp Ile Glu Thr Val
                405                 410                 415

gtc aac aat gct ggt ttt act act aga cca cca cct cca ttg gaa att       1296
Val Asn Asn Ala Gly Phe Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile
            420                 425                 430

ttg ttg caa cca tct tct cca tac ggt aga cca tac ttc aaa gct aag       1344
Leu Leu Gln Pro Ser Ser Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys
        435                 440                 445

tct gat ttc gtc aaa gaa ccc att cca gtt ttg ggt tta aag ggt atg       1392
Ser Asp Phe Val Lys Glu Pro Ile Pro Val Leu Gly Leu Lys Gly Met
    450                 455                 460

ttc aag aga atg atc gaa gag gat gcc tct ttc ttg att tgg aaa cca       1440
Phe Lys Arg Met Ile Glu Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro
465                 470                 475                 480

tac ggt ggt atg atg gct aga att cca gaa tct gaa ttg cca ttt cca       1488
Tyr Gly Gly Met Met Ala Arg Ile Pro Glu Ser Glu Leu Pro Phe Pro
                485                 490                 495

cac aga aac ggt act att ttc aag atc cat tac ttc acc aag tgg tcc       1536
His Arg Asn Gly Thr Ile Phe Lys Ile His Tyr Phe Thr Lys Trp Ser
            500                 505                 510

gaa aat ggt tct tct tct gat gac aaa cac atg aag tgg atc agg gaa       1584
Glu Asn Gly Ser Ser Ser Asp Asp Lys His Met Lys Trp Ile Arg Glu
        515                 520                 525

ctg tat tct tat atg acc cca tac gtt tct tct aac cca aga caa gct       1632
Leu Tyr Ser Tyr Met Thr Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala
    530                 535                 540

tac gtt aac tac aga gat ttg gac atc ggt cag aac aag aag aac gat       1680
Tyr Val Asn Tyr Arg Asp Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp
545                 550                 555                 560

tct gaa aac aat ttc aga agg gct caa att tgg ggt gct aag tac ttt       1728
Ser Glu Asn Asn Phe Arg Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe
                565                 570                 575
```

```
aag aac aac ttc aac agg ctg gtc aag atc aag aca aaa gtt gat cca       1776
Lys Asn Asn Phe Asn Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro
            580                 585                 590

gaa aac ttg ttc agg cac gaa caa tct att cca cca ttg cca att aga       1824
Glu Asn Leu Phe Arg His Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg
        595                 600                 605

agg caa acc tct tgg tca cat cca caa ttt gaa aag                       1860
Arg Gln Thr Ser Trp Ser His Pro Gln Phe Glu Lys
    610                 615                 620
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<210> 125
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 125

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


Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30


Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45


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


Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80


Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Lys Glu Pro Thr Ser Ser
                85                  90                  95


Thr Ser Leu Gln Asp Asp Phe Val Lys Cys Leu His Arg Asn Thr Asn
            100                 105                 110


Val Asp Phe Pro Leu Asp Lys Thr Phe Phe Thr Pro Gln Arg Asn Ser
        115                 120                 125
```

```
Ser Asn Phe Lys Glu Val Leu Asn Ser Thr Val Trp Asn Gln Arg Tyr
    130                 135                 140

Met Thr Lys Ser Met Pro Lys Pro Glu Phe Ile Phe Lys Pro Val His
145                 150                 155                 160

Glu Ser His Val Gln Ala Ser Ile Ile Cys Ser Lys Lys Leu Arg Ile
                165                 170                 175

His Phe Arg Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr
            180                 185                 190

Val Ser Gln Met Glu Thr Pro Phe Val Leu Ile Asp Leu Trp Lys Leu
        195                 200                 205

Lys Gln Ile Asn Val Asp Ile Glu Asp Asn Ser Ala Trp Val Gln Ala
    210                 215                 220

Gly Ala Thr Thr Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys
225                 230                 235                 240

Val His Gly Phe Pro Ala Gly Leu Cys Ser Thr Val Gly Ile Gly Gly
                245                 250                 255

His Ile Thr Gly Gly Gly Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu
            260                 265                 270

Ser Thr Asp Asn Val Leu Asp Ala Arg Ile Val Asp Ala Asn Gly Gln
        275                 280                 285

Leu Leu Asn Arg Thr Ala Met Gly Glu Asp Leu Phe Trp Ala Ile Ser
    290                 295                 300

Gly Gly Gly Gly Gly Ser Phe Gly Val Ile Leu Ala Trp Lys Ile Lys
305                 310                 315                 320

Leu Val Pro Val Pro Glu Thr Leu Thr Ile Phe Thr Ile Thr Lys Thr
                325                 330                 335
```

```
Leu Glu Gln Asp Ala Gly Phe Lys Ile Leu Ser Lys Trp Gln Arg Ile
            340                 345                 350

Val Asp Lys Leu Val Glu Glu Leu Ser Ile Arg Val Leu Phe Arg Asn
        355                 360                 365

Thr Gly Asn Lys Thr Val Thr Thr Thr Tyr Arg Gly Glu Phe Leu Gly
    370                 375                 380

Glu Lys Gly Thr Leu Met Glu Val Met Asn Lys Cys Phe Pro Glu Leu
385                 390                 395                 400

Gly Leu Thr Gln Glu Asp Cys Ile Glu Met Ser Trp Ile Glu Thr Val
                405                 410                 415

Val Asn Asn Ala Gly Phe Thr Thr Arg Pro Pro Pro Pro Leu Glu Ile
            420                 425                 430

Leu Leu Gln Pro Ser Ser Pro Tyr Gly Arg Pro Tyr Phe Lys Ala Lys
        435                 440                 445

Ser Asp Phe Val Lys Glu Pro Ile Pro Val Leu Gly Leu Lys Gly Met
    450                 455                 460

Phe Lys Arg Met Ile Glu Glu Asp Ala Ser Phe Leu Ile Trp Lys Pro
465                 470                 475                 480

Tyr Gly Gly Met Met Ala Arg Ile Pro Glu Ser Glu Leu Pro Phe Pro
                485                 490                 495

His Arg Asn Gly Thr Ile Phe Lys Ile His Tyr Phe Thr Lys Trp Ser
            500                 505                 510

Glu Asn Gly Ser Ser Ser Asp Asp Lys His Met Lys Trp Ile Arg Glu
        515                 520                 525

Leu Tyr Ser Tyr Met Thr Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala
    530                 535                 540

Tyr Val Asn Tyr Arg Asp Leu Asp Ile Gly Gln Asn Lys Lys Asn Asp
545                 550                 555                 560
```

```
Ser Glu Asn Asn Phe Arg Arg Ala Gln Ile Trp Gly Ala Lys Tyr Phe
                565                 570                 575


Lys Asn Asn Phe Asn Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro
            580                 585                 590


Glu Asn Leu Phe Arg His Glu Gln Ser Ile Pro Pro Leu Pro Ile Arg
        595                 600                 605


Arg Gln Thr Ser Trp Ser His Pro Gln Phe Glu Lys
    610                 615                 620


<210>  126
<211>  1629
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS152-A0A1S3BE31


<220>
<221>  CDS
<222>  (1)..(1629)

<400>  126
atg aag tcc ttg atc acc tct ttc ttg cac atc ttc atc gtt ttg tct         48
Met Lys Ser Leu Ile Thr Ser Phe Leu His Ile Phe Ile Val Leu Ser
1               5                   10                  15

ttt gct tgg gct gct tct gct cat aat cat gaa tct ttc tta cac tgc         96
Phe Ala Trp Ala Ala Ser Ala His Asn His Glu Ser Phe Leu His Cys
            20                  25                  30

ttg tcc cat cat tct cca aac acc tct tct atc tcc aag att atc tac        144
Leu Ser His His Ser Pro Asn Thr Ser Ser Ile Ser Lys Ile Ile Tyr
        35                  40                  45

act cca act aac ccc tct tac tcc tct gtt ttg aac ttc tcc att cac        192
Thr Pro Thr Asn Pro Ser Tyr Ser Ser Val Leu Asn Phe Ser Ile His
    50                  55                  60

aac ttg aga ttc acc tct cca aaa act cca aag cca cat att atc gtt        240
Asn Leu Arg Phe Thr Ser Pro Lys Thr Pro Lys Pro His Ile Ile Val
65                  70                  75                  80

acc cca ttc ttg gtg tct caa att caa gcc tct att atc tgc gct aaa        288
Thr Pro Phe Leu Val Ser Gln Ile Gln Ala Ser Ile Ile Cys Ala Lys
```

```
                85                  90                  95

aag acc ggt ttc caa atc aga act aga tct ggt ggt cat gat tac gaa        336
Lys Thr Gly Phe Gln Ile Arg Thr Arg Ser Gly Gly His Asp Tyr Glu
            100                 105                 110

ggt ttg tct tac gtt tcc gat gtt tcc ttc gtt gtt gtt gac ttg att        384
Gly Leu Ser Tyr Val Ser Asp Val Ser Phe Val Val Val Asp Leu Ile
        115                 120                 125

aac ctg aga tcc att tct gtt gat gcc gaa aac aat gtt gct tgg gtt        432
Asn Leu Arg Ser Ile Ser Val Asp Ala Glu Asn Asn Val Ala Trp Val
    130                 135                 140

caa tct ggt gct act att ggt gag ttg tac tac aga att gcc gaa aag        480
Gln Ser Gly Ala Thr Ile Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys
145                 150                 155                 160

tct aag acc ttg ggt ttt cca gct ggt gtt tgt cca act gtt ggt gtt        528
Ser Lys Thr Leu Gly Phe Pro Ala Gly Val Cys Pro Thr Val Gly Val
                165                 170                 175

ggt ggt cac ttt tct ggt ggt ggt tat ggt ttg atg ttg aga aaa ttt        576
Gly Gly His Phe Ser Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe
            180                 185                 190

ggt ttg gcc gct gat aac gtc att gat gct tac ttc att gat gtc aac        624
Gly Leu Ala Ala Asp Asn Val Ile Asp Ala Tyr Phe Ile Asp Val Asn
        195                 200                 205

ggt aag ctg cat gac aga aaa tct atg ggt gaa gat gtt ttc tgg gct        672
Gly Lys Leu His Asp Arg Lys Ser Met Gly Glu Asp Val Phe Trp Ala
    210                 215                 220

att aga ggt ggt ggt ggc gct tct ttt ggt ata gtt ttg gct tgg aag        720
Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Ile Val Leu Ala Trp Lys
225                 230                 235                 240

atc aag ttg ttg cca gtt cca tct atc gtt act gtt ttc act att acc        768
Ile Lys Leu Leu Pro Val Pro Ser Ile Val Thr Val Phe Thr Ile Thr
                245                 250                 255

aga acc ttg gaa caa aac gcc acc gat ttg att cat aga tgg caa tac        816
Arg Thr Leu Glu Gln Asn Ala Thr Asp Leu Ile His Arg Trp Gln Tyr
            260                 265                 270

gtt tct tct aag cag gat gac aag ttg ttc atc aga att atc ttg acc        864
Val Ser Ser Lys Gln Asp Asp Lys Leu Phe Ile Arg Ile Ile Leu Thr
        275                 280                 285

ggt atc aac acc acc aat tca caa cat ggt aac aag aga act att gaa        912
Gly Ile Asn Thr Thr Asn Ser Gln His Gly Asn Lys Arg Thr Ile Glu
    290                 295                 300
```

```
gct gcc ttc aac tct ttg ttc ttg ggt aag att gaa gag ttg gtc cca        960
Ala Ala Phe Asn Ser Leu Phe Leu Gly Lys Ile Glu Glu Leu Val Pro
305                 310                 315                 320

att atg gaa aag act ttc cca gaa ttg ggt ttg acc aaa gaa gat tgc       1008
Ile Met Glu Lys Thr Phe Pro Glu Leu Gly Leu Thr Lys Glu Asp Cys
                325                 330                 335

att gag atg tcc tgg att gag tct gtc ttg tac ttt gct ggt ttt tct       1056
Ile Glu Met Ser Trp Ile Glu Ser Val Leu Tyr Phe Ala Gly Phe Ser
            340                 345                 350

aga ggt caa cca ttg aac gtt ttg ttg gat aga agg cca ttg act cca       1104
Arg Gly Gln Pro Leu Asn Val Leu Leu Asp Arg Arg Pro Leu Thr Pro
        355                 360                 365

aag aga ttt ttc aag gct aag tcc gat tac gtc aac gaa cct att cca       1152
Lys Arg Phe Phe Lys Ala Lys Ser Asp Tyr Val Asn Glu Pro Ile Pro
    370                 375                 380

aaa gct ggt ttg gaa ggt att tgg gag ttg ttc gat gaa gaa gaa gct       1200
Lys Ala Gly Leu Glu Gly Ile Trp Glu Leu Phe Asp Glu Glu Glu Ala
385                 390                 395                 400

gaa gct gct gtt ttg att ttg tct cca tac ggt ggt atc atg gac aag       1248
Glu Ala Ala Val Leu Ile Leu Ser Pro Tyr Gly Gly Ile Met Asp Lys
                405                 410                 415

att tcc gaa tcc gaa att cca ttt cca cat aga gct ggc aac ctg tac       1296
Ile Ser Glu Ser Glu Ile Pro Phe Pro His Arg Ala Gly Asn Leu Tyr
            420                 425                 430

aaa atc caa cat ttg gtt tac tgg gac gaa gaa ggt gaa gat att gct       1344
Lys Ile Gln His Leu Val Tyr Trp Asp Glu Glu Gly Glu Asp Ile Ala
        435                 440                 445

aag aga cat atc aac tgg atc aga aag ctg tac tct tac atg gct cca       1392
Lys Arg His Ile Asn Trp Ile Arg Lys Leu Tyr Ser Tyr Met Ala Pro
    450                 455                 460

ttc gtt tct aaa aat cca aga gct gcc tac atc aac tac aga gat ttg       1440
Phe Val Ser Lys Asn Pro Arg Ala Ala Tyr Ile Asn Tyr Arg Asp Leu
465                 470                 475                 480

gat att ggc acc aac gaa aag aac ggt aga aac act tct tac aac gaa       1488
Asp Ile Gly Thr Asn Glu Lys Asn Gly Arg Asn Thr Ser Tyr Asn Glu
                485                 490                 495

gct tct gtt tgg ggt gtt aag tac ttt aag ggt aac ttc aag agg ctg       1536
Ala Ser Val Trp Gly Val Lys Tyr Phe Lys Gly Asn Phe Lys Arg Leu
            500                 505                 510

gtt tct gtt aag aca aag gtt gac cca tcc aat ttc ttc aag aac gaa       1584
Val Ser Val Lys Thr Lys Val Asp Pro Ser Asn Phe Phe Lys Asn Glu
```

```
        515                 520                 525

caa tcc att cca tcc ttg aaa cca tgg tgg aac aag aga ggt tat          1629
Gln Ser Ile Pro Ser Leu Lys Pro Trp Trp Asn Lys Arg Gly Tyr
    530                 535                 540


<210>  127
<211>  543
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  127

Met Lys Ser Leu Ile Thr Ser Phe Leu His Ile Phe Ile Val Leu Ser
1               5                   10                  15


Phe Ala Trp Ala Ala Ser Ala His Asn His Glu Ser Phe Leu His Cys
            20                  25                  30


Leu Ser His His Ser Pro Asn Thr Ser Ser Ile Ser Lys Ile Ile Tyr
        35                  40                  45


Thr Pro Thr Asn Pro Ser Tyr Ser Ser Val Leu Asn Phe Ser Ile His
    50                  55                  60


Asn Leu Arg Phe Thr Ser Pro Lys Thr Pro Lys Pro His Ile Ile Val
65                  70                  75                  80


Thr Pro Phe Leu Val Ser Gln Ile Gln Ala Ser Ile Ile Cys Ala Lys
                85                  90                  95


Lys Thr Gly Phe Gln Ile Arg Thr Arg Ser Gly Gly His Asp Tyr Glu
            100                 105                 110


Gly Leu Ser Tyr Val Ser Asp Val Ser Phe Val Val Val Asp Leu Ile
        115                 120                 125


Asn Leu Arg Ser Ile Ser Val Asp Ala Glu Asn Asn Val Ala Trp Val
    130                 135                 140


Gln Ser Gly Ala Thr Ile Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys
```

```
145                 150                 155                 160

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

Gly Gly His Phe Ser Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe
            180                 185                 190

Gly Leu Ala Ala Asp Asn Val Ile Asp Ala Tyr Phe Ile Asp Val Asn
        195                 200                 205

Gly Lys Leu His Asp Arg Lys Ser Met Gly Glu Asp Val Phe Trp Ala
    210                 215                 220

Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Ile Val Leu Ala Trp Lys
225                 230                 235                 240

Ile Lys Leu Leu Pro Val Pro Ser Ile Val Thr Val Phe Thr Ile Thr
                245                 250                 255

Arg Thr Leu Glu Gln Asn Ala Thr Asp Leu Ile His Arg Trp Gln Tyr
            260                 265                 270

Val Ser Ser Lys Gln Asp Asp Lys Leu Phe Ile Arg Ile Ile Leu Thr
        275                 280                 285

Gly Ile Asn Thr Thr Asn Ser Gln His Gly Asn Lys Arg Thr Ile Glu
    290                 295                 300

Ala Ala Phe Asn Ser Leu Phe Leu Gly Lys Ile Glu Glu Leu Val Pro
305                 310                 315                 320

Ile Met Glu Lys Thr Phe Pro Glu Leu Gly Leu Thr Lys Glu Asp Cys
                325                 330                 335

Ile Glu Met Ser Trp Ile Glu Ser Val Leu Tyr Phe Ala Gly Phe Ser
            340                 345                 350

Arg Gly Gln Pro Leu Asn Val Leu Leu Asp Arg Arg Pro Leu Thr Pro
        355                 360                 365
```

```
Lys Arg Phe Phe Lys Ala Lys Ser Asp Tyr Val Asn Glu Pro Ile Pro
    370                 375                 380

Lys Ala Gly Leu Glu Gly Ile Trp Glu Leu Phe Asp Glu Glu Glu Ala
385                 390                 395                 400

Glu Ala Ala Val Leu Ile Leu Ser Pro Tyr Gly Gly Ile Met Asp Lys
                405                 410                 415

Ile Ser Glu Ser Glu Ile Pro Phe Pro His Arg Ala Gly Asn Leu Tyr
            420                 425                 430

Lys Ile Gln His Leu Val Tyr Trp Asp Glu Glu Gly Glu Asp Ile Ala
        435                 440                 445

Lys Arg His Ile Asn Trp Ile Arg Lys Leu Tyr Ser Tyr Met Ala Pro
    450                 455                 460

Phe Val Ser Lys Asn Pro Arg Ala Ala Tyr Ile Asn Tyr Arg Asp Leu
465                 470                 475                 480

Asp Ile Gly Thr Asn Glu Lys Asn Gly Arg Asn Thr Ser Tyr Asn Glu
                485                 490                 495

Ala Ser Val Trp Gly Val Lys Tyr Phe Lys Gly Asn Phe Lys Arg Leu
            500                 505                 510

Val Ser Val Lys Thr Lys Val Asp Pro Ser Asn Phe Phe Lys Asn Glu
        515                 520                 525

Gln Ser Ile Pro Ser Leu Lys Pro Trp Trp Asn Lys Arg Gly Tyr
    530                 535                 540
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<210>  128
<211>  1566
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS152-A0A1S3BE31- no signal peptide

<220>
<221> CDS
<222> (1)..(1566)

<400> 128
atg gct cat aat cat gaa tct ttc tta cac tgc ttg tcc cat cat tct 48
Met Ala His Asn His Glu Ser Phe Leu His Cys Leu Ser His His Ser
1 5 10 15

cca aac acc tct tct atc tcc aag att atc tac act cca act aac ccc 96
Pro Asn Thr Ser Ser Ile Ser Lys Ile Ile Tyr Thr Pro Thr Asn Pro
20 25 30

tct tac tcc tct gtt ttg aac ttc tcc att cac aac ttg aga ttc acc 144
Ser Tyr Ser Ser Val Leu Asn Phe Ser Ile His Asn Leu Arg Phe Thr
35 40 45

tct cca aaa act cca aag cca cat att atc gtt acc cca ttc ttg gtg 192
Ser Pro Lys Thr Pro Lys Pro His Ile Ile Val Thr Pro Phe Leu Val
50 55 60

tct caa att caa gcc tct att atc tgc gct aaa aag acc ggt ttc caa 240
Ser Gln Ile Gln Ala Ser Ile Ile Cys Ala Lys Lys Thr Gly Phe Gln
65 70 75 80

atc aga act aga tct ggt ggt cat gat tac gaa ggt ttg tct tac gtt 288
Ile Arg Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val
85 90 95

tcc gat gtt tcc ttc gtt gtt gtt gac ttg att aac ctg aga tcc att 336
Ser Asp Val Ser Phe Val Val Val Asp Leu Ile Asn Leu Arg Ser Ile
100 105 110

tct gtt gat gcc gaa aac aat gtt gct tgg gtt caa tct ggt gct act 384
Ser Val Asp Ala Glu Asn Asn Val Ala Trp Val Gln Ser Gly Ala Thr
115 120 125

att ggt gag ttg tac tac aga att gcc gaa aag tct aag acc ttg ggt 432
Ile Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Thr Leu Gly
130 135 140

ttt cca gct ggt gtt tgt cca act gtt ggt gtt ggt ggt cac ttt tct 480
Phe Pro Ala Gly Val Cys Pro Thr Val Gly Val Gly Gly His Phe Ser
145 150 155 160

ggt ggt ggt tat ggt ttg atg ttg aga aaa ttt ggt ttg gcc gct gat 528
Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe Gly Leu Ala Ala Asp
165 170 175

aac gtc att gat gct tac ttc att gat gtc aac ggt aag ctg cat gac 576
Asn Val Ile Asp Ala Tyr Phe Ile Asp Val Asn Gly Lys Leu His Asp
180 185 190

aga aaa tct atg ggt gaa gat gtt ttc tgg gct att aga ggt ggt ggt 624

```
Arg Lys Ser Met Gly Glu Asp Val Phe Trp Ala Ile Arg Gly Gly Gly
        195                 200                 205

ggc gct tct ttt ggt ata gtt ttg gct tgg aag atc aag ttg ttg cca        672
Gly Ala Ser Phe Gly Ile Val Leu Ala Trp Lys Ile Lys Leu Leu Pro
    210                 215                 220

gtt cca tct atc gtt act gtt ttc act att acc aga acc ttg gaa caa        720
Val Pro Ser Ile Val Thr Val Phe Thr Ile Thr Arg Thr Leu Glu Gln
225                 230                 235                 240

aac gcc acc gat ttg att cat aga tgg caa tac gtt tct tct aag cag        768
Asn Ala Thr Asp Leu Ile His Arg Trp Gln Tyr Val Ser Ser Lys Gln
                245                 250                 255

gat gac aag ttg ttc atc aga att atc ttg acc ggt atc aac acc acc        816
Asp Asp Lys Leu Phe Ile Arg Ile Ile Leu Thr Gly Ile Asn Thr Thr
            260                 265                 270

aat tca caa cat ggt aac aag aga act att gaa gct gcc ttc aac tct        864
Asn Ser Gln His Gly Asn Lys Arg Thr Ile Glu Ala Ala Phe Asn Ser
        275                 280                 285

ttg ttc ttg ggt aag att gaa gag ttg gtc cca att atg gaa aag act        912
Leu Phe Leu Gly Lys Ile Glu Glu Leu Val Pro Ile Met Glu Lys Thr
    290                 295                 300

ttc cca gaa ttg ggt ttg acc aaa gaa gat tgc att gag atg tcc tgg        960
Phe Pro Glu Leu Gly Leu Thr Lys Glu Asp Cys Ile Glu Met Ser Trp
305                 310                 315                 320

att gag tct gtc ttg tac ttt gct ggt ttt tct aga ggt caa cca ttg       1008
Ile Glu Ser Val Leu Tyr Phe Ala Gly Phe Ser Arg Gly Gln Pro Leu
                325                 330                 335

aac gtt ttg ttg gat aga agg cca ttg act cca aag aga ttt ttc aag       1056
Asn Val Leu Leu Asp Arg Arg Pro Leu Thr Pro Lys Arg Phe Phe Lys
            340                 345                 350

gct aag tcc gat tac gtc aac gaa cct att cca aaa gct ggt ttg gaa       1104
Ala Lys Ser Asp Tyr Val Asn Glu Pro Ile Pro Lys Ala Gly Leu Glu
        355                 360                 365

ggt att tgg gag ttg ttc gat gaa gaa gaa gct gaa gct gct gtt ttg       1152
Gly Ile Trp Glu Leu Phe Asp Glu Glu Glu Ala Glu Ala Ala Val Leu
    370                 375                 380

att ttg tct cca tac ggt ggt atc atg gac aag att tcc gaa tcc gaa       1200
Ile Leu Ser Pro Tyr Gly Gly Ile Met Asp Lys Ile Ser Glu Ser Glu
385                 390                 395                 400

att cca ttt cca cat aga gct ggc aac ctg tac aaa atc caa cat ttg       1248
Ile Pro Phe Pro His Arg Ala Gly Asn Leu Tyr Lys Ile Gln His Leu
                405                 410                 415
```

```
gtt tac tgg gac gaa gaa ggt gaa gat att gct aag aga cat atc aac       1296
Val Tyr Trp Asp Glu Glu Gly Glu Asp Ile Ala Lys Arg His Ile Asn
            420                 425                 430

tgg atc aga aag ctg tac tct tac atg gct cca ttc gtt tct aaa aat       1344
Trp Ile Arg Lys Leu Tyr Ser Tyr Met Ala Pro Phe Val Ser Lys Asn
        435                 440                 445

cca aga gct gcc tac atc aac tac aga gat ttg gat att ggc acc aac       1392
Pro Arg Ala Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile Gly Thr Asn
    450                 455                 460

gaa aag aac ggt aga aac act tct tac aac gaa gct tct gtt tgg ggt       1440
Glu Lys Asn Gly Arg Asn Thr Ser Tyr Asn Glu Ala Ser Val Trp Gly
465                 470                 475                 480

gtt aag tac ttt aag ggt aac ttc aag agg ctg gtt tct gtt aag aca       1488
Val Lys Tyr Phe Lys Gly Asn Phe Lys Arg Leu Val Ser Val Lys Thr
                485                 490                 495

aag gtt gac cca tcc aat ttc ttc aag aac gaa caa tcc att cca tcc       1536
Lys Val Asp Pro Ser Asn Phe Phe Lys Asn Glu Gln Ser Ile Pro Ser
            500                 505                 510

ttg aaa cca tgg tgg aac aag aga ggt tat                              1566
Leu Lys Pro Trp Trp Asn Lys Arg Gly Tyr
        515                 520
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<210> 129
<211> 522
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 129

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Met Ala His Asn His Glu Ser Phe Leu His Cys Leu Ser His His Ser
1               5                   10                  15


Pro Asn Thr Ser Ser Ile Ser Lys Ile Ile Tyr Thr Pro Thr Asn Pro
            20                  25                  30


Ser Tyr Ser Ser Val Leu Asn Phe Ser Ile His Asn Leu Arg Phe Thr
        35                  40                  45


Ser Pro Lys Thr Pro Lys Pro His Ile Ile Val Thr Pro Phe Leu Val
    50                  55                  60
```

```
Ser Gln Ile Gln Ala Ser Ile Ile Cys Ala Lys Lys Thr Gly Phe Gln
65                  70                  75                  80

Ile Arg Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val
                85                  90                  95

Ser Asp Val Ser Phe Val Val Val Asp Leu Ile Asn Leu Arg Ser Ile
            100                 105                 110

Ser Val Asp Ala Glu Asn Asn Val Ala Trp Val Gln Ser Gly Ala Thr
        115                 120                 125

Ile Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Thr Leu Gly
    130                 135                 140

Phe Pro Ala Gly Val Cys Pro Thr Val Gly Val Gly Gly His Phe Ser
145                 150                 155                 160

Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe Gly Leu Ala Ala Asp
                165                 170                 175

Asn Val Ile Asp Ala Tyr Phe Ile Asp Val Asn Gly Lys Leu His Asp
            180                 185                 190

Arg Lys Ser Met Gly Glu Asp Val Phe Trp Ala Ile Arg Gly Gly Gly
        195                 200                 205

Gly Ala Ser Phe Gly Ile Val Leu Ala Trp Lys Ile Lys Leu Leu Pro
    210                 215                 220

Val Pro Ser Ile Val Thr Val Phe Thr Ile Thr Arg Thr Leu Glu Gln
225                 230                 235                 240

Asn Ala Thr Asp Leu Ile His Arg Trp Gln Tyr Val Ser Ser Lys Gln
                245                 250                 255

Asp Asp Lys Leu Phe Ile Arg Ile Ile Leu Thr Gly Ile Asn Thr Thr
            260                 265                 270
```

```
Asn Ser Gln His Gly Asn Lys Arg Thr Ile Glu Ala Ala Phe Asn Ser
        275                 280                 285

Leu Phe Leu Gly Lys Ile Glu Glu Leu Val Pro Ile Met Glu Lys Thr
    290                 295                 300

Phe Pro Glu Leu Gly Leu Thr Lys Glu Asp Cys Ile Glu Met Ser Trp
305                 310                 315                 320

Ile Glu Ser Val Leu Tyr Phe Ala Gly Phe Ser Arg Gly Gln Pro Leu
                325                 330                 335

Asn Val Leu Leu Asp Arg Arg Pro Leu Thr Pro Lys Arg Phe Phe Lys
            340                 345                 350

Ala Lys Ser Asp Tyr Val Asn Glu Pro Ile Pro Lys Ala Gly Leu Glu
        355                 360                 365

Gly Ile Trp Glu Leu Phe Asp Glu Glu Glu Ala Glu Ala Ala Val Leu
    370                 375                 380

Ile Leu Ser Pro Tyr Gly Gly Ile Met Asp Lys Ile Ser Glu Ser Glu
385                 390                 395                 400

Ile Pro Phe Pro His Arg Ala Gly Asn Leu Tyr Lys Ile Gln His Leu
                405                 410                 415

Val Tyr Trp Asp Glu Glu Gly Glu Asp Ile Ala Lys Arg His Ile Asn
            420                 425                 430

Trp Ile Arg Lys Leu Tyr Ser Tyr Met Ala Pro Phe Val Ser Lys Asn
        435                 440                 445

Pro Arg Ala Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile Gly Thr Asn
    450                 455                 460

Glu Lys Asn Gly Arg Asn Thr Ser Tyr Asn Glu Ala Ser Val Trp Gly
465                 470                 475                 480

Val Lys Tyr Phe Lys Gly Asn Phe Lys Arg Leu Val Ser Val Lys Thr
                485                 490                 495
```

```
Lys Val Asp Pro Ser Asn Phe Phe Lys Asn Glu Gln Ser Ile Pro Ser
            500                 505                 510


Leu Lys Pro Trp Trp Asn Lys Arg Gly Tyr
        515                 520


<210>  130
<211>  1590
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS152-A0A1S3BE31- no signal peptide-strep Tag


<220>
<221>  CDS
<222>  (1)..(1590)

<400>  130
atg gct cat aat cat gaa tct ttc tta cac tgc ttg tcc cat cat tct         48
Met Ala His Asn His Glu Ser Phe Leu His Cys Leu Ser His His Ser
1               5                   10                  15

cca aac acc tct tct atc tcc aag att atc tac act cca act aac ccc         96
Pro Asn Thr Ser Ser Ile Ser Lys Ile Ile Tyr Thr Pro Thr Asn Pro
            20                  25                  30

tct tac tcc tct gtt ttg aac ttc tcc att cac aac ttg aga ttc acc        144
Ser Tyr Ser Ser Val Leu Asn Phe Ser Ile His Asn Leu Arg Phe Thr
        35                  40                  45

tct cca aaa act cca aag cca cat att atc gtt acc cca ttc ttg gtg        192
Ser Pro Lys Thr Pro Lys Pro His Ile Ile Val Thr Pro Phe Leu Val
    50                  55                  60

tct caa att caa gcc tct att atc tgc gct aaa aag acc ggt ttc caa        240
Ser Gln Ile Gln Ala Ser Ile Ile Cys Ala Lys Lys Thr Gly Phe Gln
65                  70                  75                  80

atc aga act aga tct ggt ggt cat gat tac gaa ggt ttg tct tac gtt        288
Ile Arg Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val
                85                  90                  95

tcc gat gtt tcc ttc gtt gtt gtt gac ttg att aac ctg aga tcc att        336
Ser Asp Val Ser Phe Val Val Val Asp Leu Ile Asn Leu Arg Ser Ile
            100                 105                 110

tct gtt gat gcc gaa aac aat gtt gct tgg gtt caa tct ggt gct act        384
Ser Val Asp Ala Glu Asn Asn Val Ala Trp Val Gln Ser Gly Ala Thr
```

```
        115                 120                 125

att ggt gag ttg tac tac aga att gcc gaa aag tct aag acc ttg ggt        432
Ile Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Thr Leu Gly
    130                 135                 140

ttt cca gct ggt gtt tgt cca act gtt ggt gtt ggt ggt cac ttt tct        480
Phe Pro Ala Gly Val Cys Pro Thr Val Gly Val Gly Gly His Phe Ser
145                 150                 155                 160

ggt ggt ggt tat ggt ttg atg ttg aga aaa ttt ggt ttg gcc gct gat        528
Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe Gly Leu Ala Ala Asp
                165                 170                 175

aac gtc att gat gct tac ttc att gat gtc aac ggt aag ctg cat gac        576
Asn Val Ile Asp Ala Tyr Phe Ile Asp Val Asn Gly Lys Leu His Asp
            180                 185                 190

aga aaa tct atg ggt gaa gat gtt ttc tgg gct att aga ggt ggt ggt        624
Arg Lys Ser Met Gly Glu Asp Val Phe Trp Ala Ile Arg Gly Gly Gly
        195                 200                 205

ggc gct tct ttt ggt ata gtt ttg gct tgg aag atc aag ttg ttg cca        672
Gly Ala Ser Phe Gly Ile Val Leu Ala Trp Lys Ile Lys Leu Leu Pro
    210                 215                 220

gtt cca tct atc gtt act gtt ttc act att acc aga acc ttg gaa caa        720
Val Pro Ser Ile Val Thr Val Phe Thr Ile Thr Arg Thr Leu Glu Gln
225                 230                 235                 240

aac gcc acc gat ttg att cat aga tgg caa tac gtt tct tct aag cag        768
Asn Ala Thr Asp Leu Ile His Arg Trp Gln Tyr Val Ser Ser Lys Gln
                245                 250                 255

gat gac aag ttg ttc atc aga att atc ttg acc ggt atc aac acc acc        816
Asp Asp Lys Leu Phe Ile Arg Ile Ile Leu Thr Gly Ile Asn Thr Thr
            260                 265                 270

aat tca caa cat ggt aac aag aga act att gaa gct gcc ttc aac tct        864
Asn Ser Gln His Gly Asn Lys Arg Thr Ile Glu Ala Ala Phe Asn Ser
        275                 280                 285

ttg ttc ttg ggt aag att gaa gag ttg gtc cca att atg gaa aag act        912
Leu Phe Leu Gly Lys Ile Glu Glu Leu Val Pro Ile Met Glu Lys Thr
    290                 295                 300

ttc cca gaa ttg ggt ttg acc aaa gaa gat tgc att gag atg tcc tgg        960
Phe Pro Glu Leu Gly Leu Thr Lys Glu Asp Cys Ile Glu Met Ser Trp
305                 310                 315                 320

att gag tct gtc ttg tac ttt gct ggt ttt tct aga ggt caa cca ttg       1008
Ile Glu Ser Val Leu Tyr Phe Ala Gly Phe Ser Arg Gly Gln Pro Leu
                325                 330                 335
```

```
aac gtt ttg ttg gat aga agg cca ttg act cca aag aga ttt ttc aag       1056
Asn Val Leu Leu Asp Arg Arg Pro Leu Thr Pro Lys Arg Phe Phe Lys
            340                 345                 350

gct aag tcc gat tac gtc aac gaa cct att cca aaa gct ggt ttg gaa       1104
Ala Lys Ser Asp Tyr Val Asn Glu Pro Ile Pro Lys Ala Gly Leu Glu
        355                 360                 365

ggt att tgg gag ttg ttc gat gaa gaa gaa gct gaa gct gct gtt ttg       1152
Gly Ile Trp Glu Leu Phe Asp Glu Glu Glu Ala Glu Ala Ala Val Leu
    370                 375                 380

att ttg tct cca tac ggt ggt atc atg gac aag att tcc gaa tcc gaa       1200
Ile Leu Ser Pro Tyr Gly Gly Ile Met Asp Lys Ile Ser Glu Ser Glu
385                 390                 395                 400

att cca ttt cca cat aga gct ggc aac ctg tac aaa atc caa cat ttg       1248
Ile Pro Phe Pro His Arg Ala Gly Asn Leu Tyr Lys Ile Gln His Leu
                405                 410                 415

gtt tac tgg gac gaa gaa ggt gaa gat att gct aag aga cat atc aac       1296
Val Tyr Trp Asp Glu Glu Gly Glu Asp Ile Ala Lys Arg His Ile Asn
            420                 425                 430

tgg atc aga aag ctg tac tct tac atg gct cca ttc gtt tct aaa aat       1344
Trp Ile Arg Lys Leu Tyr Ser Tyr Met Ala Pro Phe Val Ser Lys Asn
        435                 440                 445

cca aga gct gcc tac atc aac tac aga gat ttg gat att ggc acc aac       1392
Pro Arg Ala Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile Gly Thr Asn
    450                 455                 460

gaa aag aac ggt aga aac act tct tac aac gaa gct tct gtt tgg ggt       1440
Glu Lys Asn Gly Arg Asn Thr Ser Tyr Asn Glu Ala Ser Val Trp Gly
465                 470                 475                 480

gtt aag tac ttt aag ggt aac ttc aag agg ctg gtt tct gtt aag aca       1488
Val Lys Tyr Phe Lys Gly Asn Phe Lys Arg Leu Val Ser Val Lys Thr
                485                 490                 495

aag gtt gac cca tcc aat ttc ttc aag aac gaa caa tcc att cca tcc       1536
Lys Val Asp Pro Ser Asn Phe Phe Lys Asn Glu Gln Ser Ile Pro Ser
            500                 505                 510

ttg aaa cca tgg tgg aac aag aga ggt tat tgg tca cat cca caa ttt       1584
Leu Lys Pro Trp Trp Asn Lys Arg Gly Tyr Trp Ser His Pro Gln Phe
        515                 520                 525

gaa aag                                                               1590
Glu Lys
    530
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<210>  131

<211> 530
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 131

Met Ala His Asn His Glu Ser Phe Leu His Cys Leu Ser His His Ser
1 5 10 15

Pro Asn Thr Ser Ser Ile Ser Lys Ile Ile Tyr Thr Pro Thr Asn Pro
20 25 30

Ser Tyr Ser Ser Val Leu Asn Phe Ser Ile His Asn Leu Arg Phe Thr
35 40 45

Ser Pro Lys Thr Pro Lys Pro His Ile Ile Val Thr Pro Phe Leu Val
50 55 60

Ser Gln Ile Gln Ala Ser Ile Ile Cys Ala Lys Lys Thr Gly Phe Gln
65 70 75 80

Ile Arg Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val
85 90 95

Ser Asp Val Ser Phe Val Val Val Asp Leu Ile Asn Leu Arg Ser Ile
100 105 110

Ser Val Asp Ala Glu Asn Asn Val Ala Trp Val Gln Ser Gly Ala Thr
115 120 125

Ile Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Thr Leu Gly
130 135 140

Phe Pro Ala Gly Val Cys Pro Thr Val Gly Val Gly Gly His Phe Ser
145 150 155 160

Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe Gly Leu Ala Ala Asp
165 170 175

Asn Val Ile Asp Ala Tyr Phe Ile Asp Val Asn Gly Lys Leu His Asp

```
            180                 185                 190

Arg Lys Ser Met Gly Glu Asp Val Phe Trp Ala Ile Arg Gly Gly Gly
        195                 200                 205

Gly Ala Ser Phe Gly Ile Val Leu Ala Trp Lys Ile Lys Leu Leu Pro
    210                 215                 220

Val Pro Ser Ile Val Thr Val Phe Thr Ile Thr Arg Thr Leu Glu Gln
225                 230                 235                 240

Asn Ala Thr Asp Leu Ile His Arg Trp Gln Tyr Val Ser Ser Lys Gln
                245                 250                 255

Asp Asp Lys Leu Phe Ile Arg Ile Ile Leu Thr Gly Ile Asn Thr Thr
            260                 265                 270

Asn Ser Gln His Gly Asn Lys Arg Thr Ile Glu Ala Ala Phe Asn Ser
        275                 280                 285

Leu Phe Leu Gly Lys Ile Glu Glu Leu Val Pro Ile Met Glu Lys Thr
    290                 295                 300

Phe Pro Glu Leu Gly Leu Thr Lys Glu Asp Cys Ile Glu Met Ser Trp
305                 310                 315                 320

Ile Glu Ser Val Leu Tyr Phe Ala Gly Phe Ser Arg Gly Gln Pro Leu
                325                 330                 335

Asn Val Leu Leu Asp Arg Arg Pro Leu Thr Pro Lys Arg Phe Phe Lys
            340                 345                 350

Ala Lys Ser Asp Tyr Val Asn Glu Pro Ile Pro Lys Ala Gly Leu Glu
        355                 360                 365

Gly Ile Trp Glu Leu Phe Asp Glu Glu Glu Ala Glu Ala Ala Val Leu
    370                 375                 380

Ile Leu Ser Pro Tyr Gly Gly Ile Met Asp Lys Ile Ser Glu Ser Glu
385                 390                 395                 400
```

```
Ile Pro Phe Pro His Arg Ala Gly Asn Leu Tyr Lys Ile Gln His Leu
                405                 410                 415

Val Tyr Trp Asp Glu Glu Gly Glu Asp Ile Ala Lys Arg His Ile Asn
            420                 425                 430

Trp Ile Arg Lys Leu Tyr Ser Tyr Met Ala Pro Phe Val Ser Lys Asn
        435                 440                 445

Pro Arg Ala Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile Gly Thr Asn
    450                 455                 460

Glu Lys Asn Gly Arg Asn Thr Ser Tyr Asn Glu Ala Ser Val Trp Gly
465                 470                 475                 480

Val Lys Tyr Phe Lys Gly Asn Phe Lys Arg Leu Val Ser Val Lys Thr
                485                 490                 495

Lys Val Asp Pro Ser Asn Phe Phe Lys Asn Glu Gln Ser Ile Pro Ser
            500                 505                 510

Leu Lys Pro Trp Trp Asn Lys Arg Gly Tyr Trp Ser His Pro Gln Phe
        515                 520                 525

Glu Lys
    530
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<210>  132
<211>  1647
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CBS152-A0A1S3BE31- no signal peptide-truncated alpha factor-strep Tag

<220>
<221>  CDS
<222>  (1)..(1647)

<400>  132

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atg aga ttt cct tcc atc ttc acg gct gtg cta ttt gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
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```
1               5                   10                  15

gca ctt gca atg gct cat aat cat gaa tct ttc tta cac tgc ttg tcc         96
Ala Leu Ala Met Ala His Asn His Glu Ser Phe Leu His Cys Leu Ser
            20                  25                  30

cat cat tct cca aac acc tct tct atc tcc aag att atc tac act cca        144
His His Ser Pro Asn Thr Ser Ser Ile Ser Lys Ile Ile Tyr Thr Pro
        35                  40                  45

act aac ccc tct tac tcc tct gtt ttg aac ttc tcc att cac aac ttg        192
Thr Asn Pro Ser Tyr Ser Ser Val Leu Asn Phe Ser Ile His Asn Leu
    50                  55                  60

aga ttc acc tct cca aaa act cca aag cca cat att atc gtt acc cca        240
Arg Phe Thr Ser Pro Lys Thr Pro Lys Pro His Ile Ile Val Thr Pro
65                  70                  75                  80

ttc ttg gtg tct caa att caa gcc tct att atc tgc gct aaa aag acc        288
Phe Leu Val Ser Gln Ile Gln Ala Ser Ile Ile Cys Ala Lys Lys Thr
                85                  90                  95

ggt ttc caa atc aga act aga tct ggt ggt cat gat tac gaa ggt ttg        336
Gly Phe Gln Ile Arg Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu
            100                 105                 110

tct tac gtt tcc gat gtt tcc ttc gtt gtt gtt gac ttg att aac ctg        384
Ser Tyr Val Ser Asp Val Ser Phe Val Val Val Asp Leu Ile Asn Leu
        115                 120                 125

aga tcc att tct gtt gat gcc gaa aac aat gtt gct tgg gtt caa tct        432
Arg Ser Ile Ser Val Asp Ala Glu Asn Asn Val Ala Trp Val Gln Ser
    130                 135                 140

ggt gct act att ggt gag ttg tac tac aga att gcc gaa aag tct aag        480
Gly Ala Thr Ile Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys
145                 150                 155                 160

acc ttg ggt ttt cca gct ggt gtt tgt cca act gtt ggt gtt ggt ggt        528
Thr Leu Gly Phe Pro Ala Gly Val Cys Pro Thr Val Gly Val Gly Gly
                165                 170                 175

cac ttt tct ggt ggt ggt tat ggt ttg atg ttg aga aaa ttt ggt ttg        576
His Phe Ser Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe Gly Leu
            180                 185                 190

gcc gct gat aac gtc att gat gct tac ttc att gat gtc aac ggt aag        624
Ala Ala Asp Asn Val Ile Asp Ala Tyr Phe Ile Asp Val Asn Gly Lys
        195                 200                 205

ctg cat gac aga aaa tct atg ggt gaa gat gtt ttc tgg gct att aga        672
Leu His Asp Arg Lys Ser Met Gly Glu Asp Val Phe Trp Ala Ile Arg
    210                 215                 220
```

```
ggt ggt ggt ggc gct tct ttt ggt ata gtt ttg gct tgg aag atc aag        720
Gly Gly Gly Gly Ala Ser Phe Gly Ile Val Leu Ala Trp Lys Ile Lys
225                 230                 235                 240

ttg ttg cca gtt cca tct atc gtt act gtt ttc act att acc aga acc        768
Leu Leu Pro Val Pro Ser Ile Val Thr Val Phe Thr Ile Thr Arg Thr
                245                 250                 255

ttg gaa caa aac gcc acc gat ttg att cat aga tgg caa tac gtt tct        816
Leu Glu Gln Asn Ala Thr Asp Leu Ile His Arg Trp Gln Tyr Val Ser
            260                 265                 270

tct aag cag gat gac aag ttg ttc atc aga att atc ttg acc ggt atc        864
Ser Lys Gln Asp Asp Lys Leu Phe Ile Arg Ile Ile Leu Thr Gly Ile
        275                 280                 285

aac acc acc aat tca caa cat ggt aac aag aga act att gaa gct gcc        912
Asn Thr Thr Asn Ser Gln His Gly Asn Lys Arg Thr Ile Glu Ala Ala
    290                 295                 300

ttc aac tct ttg ttc ttg ggt aag att gaa gag ttg gtc cca att atg        960
Phe Asn Ser Leu Phe Leu Gly Lys Ile Glu Glu Leu Val Pro Ile Met
305                 310                 315                 320

gaa aag act ttc cca gaa ttg ggt ttg acc aaa gaa gat tgc att gag       1008
Glu Lys Thr Phe Pro Glu Leu Gly Leu Thr Lys Glu Asp Cys Ile Glu
                325                 330                 335

atg tcc tgg att gag tct gtc ttg tac ttt gct ggt ttt tct aga ggt       1056
Met Ser Trp Ile Glu Ser Val Leu Tyr Phe Ala Gly Phe Ser Arg Gly
            340                 345                 350

caa cca ttg aac gtt ttg ttg gat aga agg cca ttg act cca aag aga       1104
Gln Pro Leu Asn Val Leu Leu Asp Arg Arg Pro Leu Thr Pro Lys Arg
        355                 360                 365

ttt ttc aag gct aag tcc gat tac gtc aac gaa cct att cca aaa gct       1152
Phe Phe Lys Ala Lys Ser Asp Tyr Val Asn Glu Pro Ile Pro Lys Ala
    370                 375                 380

ggt ttg gaa ggt att tgg gag ttg ttc gat gaa gaa gaa gct gaa gct       1200
Gly Leu Glu Gly Ile Trp Glu Leu Phe Asp Glu Glu Glu Ala Glu Ala
385                 390                 395                 400

gct gtt ttg att ttg tct cca tac ggt ggt atc atg gac aag att tcc       1248
Ala Val Leu Ile Leu Ser Pro Tyr Gly Gly Ile Met Asp Lys Ile Ser
                405                 410                 415

gaa tcc gaa att cca ttt cca cat aga gct ggc aac ctg tac aaa atc       1296
Glu Ser Glu Ile Pro Phe Pro His Arg Ala Gly Asn Leu Tyr Lys Ile
            420                 425                 430

caa cat ttg gtt tac tgg gac gaa gaa ggt gaa gat att gct aag aga       1344
Gln His Leu Val Tyr Trp Asp Glu Glu Gly Glu Asp Ile Ala Lys Arg
```

```
        435                 440                 445

cat atc aac tgg atc aga aag ctg tac tct tac atg gct cca ttc gtt       1392
His Ile Asn Trp Ile Arg Lys Leu Tyr Ser Tyr Met Ala Pro Phe Val
    450                 455                 460

tct aaa aat cca aga gct gcc tac atc aac tac aga gat ttg gat att       1440
Ser Lys Asn Pro Arg Ala Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile
465                 470                 475                 480

ggc acc aac gaa aag aac ggt aga aac act tct tac aac gaa gct tct       1488
Gly Thr Asn Glu Lys Asn Gly Arg Asn Thr Ser Tyr Asn Glu Ala Ser
                485                 490                 495

gtt tgg ggt gtt aag tac ttt aag ggt aac ttc aag agg ctg gtt tct       1536
Val Trp Gly Val Lys Tyr Phe Lys Gly Asn Phe Lys Arg Leu Val Ser
            500                 505                 510

gtt aag aca aag gtt gac cca tcc aat ttc ttc aag aac gaa caa tcc       1584
Val Lys Thr Lys Val Asp Pro Ser Asn Phe Phe Lys Asn Glu Gln Ser
        515                 520                 525

att cca tcc ttg aaa cca tgg tgg aac aag aga ggt tat tgg tca cat       1632
Ile Pro Ser Leu Lys Pro Trp Trp Asn Lys Arg Gly Tyr Trp Ser His
    530                 535                 540

cca caa ttt gaa aag                                                  1647
Pro Gln Phe Glu Lys
545
```

<210> 133
<211> 549
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 133

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


Ala Leu Ala Met Ala His Asn His Glu Ser Phe Leu His Cys Leu Ser
            20                  25                  30


His His Ser Pro Asn Thr Ser Ser Ile Ser Lys Ile Ile Tyr Thr Pro
        35                  40                  45


Thr Asn Pro Ser Tyr Ser Ser Val Leu Asn Phe Ser Ile His Asn Leu
```

```
    50                  55                  60

Arg Phe Thr Ser Pro Lys Thr Pro Lys Pro His Ile Ile Val Thr Pro
65                  70                  75                  80

Phe Leu Val Ser Gln Ile Gln Ala Ser Ile Ile Cys Ala Lys Lys Thr
                85                  90                  95

Gly Phe Gln Ile Arg Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu
            100                 105                 110

Ser Tyr Val Ser Asp Val Ser Phe Val Val Val Asp Leu Ile Asn Leu
        115                 120                 125

Arg Ser Ile Ser Val Asp Ala Glu Asn Asn Val Ala Trp Val Gln Ser
    130                 135                 140

Gly Ala Thr Ile Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys
145                 150                 155                 160

Thr Leu Gly Phe Pro Ala Gly Val Cys Pro Thr Val Gly Val Gly Gly
                165                 170                 175

His Phe Ser Gly Gly Gly Tyr Gly Leu Met Leu Arg Lys Phe Gly Leu
            180                 185                 190

Ala Ala Asp Asn Val Ile Asp Ala Tyr Phe Ile Asp Val Asn Gly Lys
        195                 200                 205

Leu His Asp Arg Lys Ser Met Gly Glu Asp Val Phe Trp Ala Ile Arg
    210                 215                 220

Gly Gly Gly Gly Ala Ser Phe Gly Ile Val Leu Ala Trp Lys Ile Lys
225                 230                 235                 240

Leu Leu Pro Val Pro Ser Ile Val Thr Val Phe Thr Ile Thr Arg Thr
                245                 250                 255

Leu Glu Gln Asn Ala Thr Asp Leu Ile His Arg Trp Gln Tyr Val Ser
            260                 265                 270
```

```
Ser Lys Gln Asp Asp Lys Leu Phe Ile Arg Ile Ile Leu Thr Gly Ile
        275                 280                 285

Asn Thr Thr Asn Ser Gln His Gly Asn Lys Arg Thr Ile Glu Ala Ala
    290                 295                 300

Phe Asn Ser Leu Phe Leu Gly Lys Ile Glu Glu Leu Val Pro Ile Met
305                 310                 315                 320

Glu Lys Thr Phe Pro Glu Leu Gly Leu Thr Lys Glu Asp Cys Ile Glu
                325                 330                 335

Met Ser Trp Ile Glu Ser Val Leu Tyr Phe Ala Gly Phe Ser Arg Gly
            340                 345                 350

Gln Pro Leu Asn Val Leu Leu Asp Arg Arg Pro Leu Thr Pro Lys Arg
        355                 360                 365

Phe Phe Lys Ala Lys Ser Asp Tyr Val Asn Glu Pro Ile Pro Lys Ala
    370                 375                 380

Gly Leu Glu Gly Ile Trp Glu Leu Phe Asp Glu Glu Glu Ala Glu Ala
385                 390                 395                 400

Ala Val Leu Ile Leu Ser Pro Tyr Gly Gly Ile Met Asp Lys Ile Ser
                405                 410                 415

Glu Ser Glu Ile Pro Phe Pro His Arg Ala Gly Asn Leu Tyr Lys Ile
            420                 425                 430

Gln His Leu Val Tyr Trp Asp Glu Glu Gly Glu Asp Ile Ala Lys Arg
        435                 440                 445

His Ile Asn Trp Ile Arg Lys Leu Tyr Ser Tyr Met Ala Pro Phe Val
    450                 455                 460

Ser Lys Asn Pro Arg Ala Ala Tyr Ile Asn Tyr Arg Asp Leu Asp Ile
465                 470                 475                 480

Gly Thr Asn Glu Lys Asn Gly Arg Asn Thr Ser Tyr Asn Glu Ala Ser
```

```
               485                 490                 495

Val Trp Gly Val Lys Tyr Phe Lys Gly Asn Phe Lys Arg Leu Val Ser
            500                 505                 510

Val Lys Thr Lys Val Asp Pro Ser Asn Phe Phe Lys Asn Glu Gln Ser
        515                 520                 525

Ile Pro Ser Leu Lys Pro Trp Trp Asn Lys Arg Gly Tyr Trp Ser His
    530                 535                 540

Pro Gln Phe Glu Lys
545
```

<210> 134
<211> 1857
<212> DNA
<213> Artificial Sequence

<220>
<223> CBS152-A0A1S3BE31- no signal peptide-full alpha factor -strep Tag

<220>
<221> CDS
<222> (1)..(1857)

<400> 134

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atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc         48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa         96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct atg gct cat aat cat gaa tct        288
```

```
Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ala His Asn His Glu Ser
                85                  90                  95

ttc tta cac tgc ttg tcc cat cat tct cca aac acc tct tct atc tcc        336
Phe Leu His Cys Leu Ser His His Ser Pro Asn Thr Ser Ser Ile Ser
            100                 105                 110

aag att atc tac act cca act aac ccc tct tac tcc tct gtt ttg aac        384
Lys Ile Ile Tyr Thr Pro Thr Asn Pro Ser Tyr Ser Ser Val Leu Asn
        115                 120                 125

ttc tcc att cac aac ttg aga ttc acc tct cca aaa act cca aag cca        432
Phe Ser Ile His Asn Leu Arg Phe Thr Ser Pro Lys Thr Pro Lys Pro
    130                 135                 140

cat att atc gtt acc cca ttc ttg gtg tct caa att caa gcc tct att        480
His Ile Ile Val Thr Pro Phe Leu Val Ser Gln Ile Gln Ala Ser Ile
145                 150                 155                 160

atc tgc gct aaa aag acc ggt ttc caa atc aga act aga tct ggt ggt        528
Ile Cys Ala Lys Lys Thr Gly Phe Gln Ile Arg Thr Arg Ser Gly Gly
                165                 170                 175

cat gat tac gaa ggt ttg tct tac gtt tcc gat gtt tcc ttc gtt gtt        576
His Asp Tyr Glu Gly Leu Ser Tyr Val Ser Asp Val Ser Phe Val Val
            180                 185                 190

gtt gac ttg att aac ctg aga tcc att tct gtt gat gcc gaa aac aat        624
Val Asp Leu Ile Asn Leu Arg Ser Ile Ser Val Asp Ala Glu Asn Asn
        195                 200                 205

gtt gct tgg gtt caa tct ggt gct act att ggt gag ttg tac tac aga        672
Val Ala Trp Val Gln Ser Gly Ala Thr Ile Gly Glu Leu Tyr Tyr Arg
    210                 215                 220

att gcc gaa aag tct aag acc ttg ggt ttt cca gct ggt gtt tgt cca        720
Ile Ala Glu Lys Ser Lys Thr Leu Gly Phe Pro Ala Gly Val Cys Pro
225                 230                 235                 240

act gtt ggt gtt ggt ggt cac ttt tct ggt ggt ggt tat ggt ttg atg        768
Thr Val Gly Val Gly Gly His Phe Ser Gly Gly Gly Tyr Gly Leu Met
                245                 250                 255

ttg aga aaa ttt ggt ttg gcc gct gat aac gtc att gat gct tac ttc        816
Leu Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Ile Asp Ala Tyr Phe
            260                 265                 270

att gat gtc aac ggt aag ctg cat gac aga aaa tct atg ggt gaa gat        864
Ile Asp Val Asn Gly Lys Leu His Asp Arg Lys Ser Met Gly Glu Asp
        275                 280                 285

gtt ttc tgg gct att aga ggt ggt ggt ggc gct tct ttt ggt ata gtt        912
Val Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Ile Val
    290                 295                 300
```

```
ttg gct tgg aag atc aag ttg ttg cca gtt cca tct atc gtt act gtt        960
Leu Ala Trp Lys Ile Lys Leu Leu Pro Val Pro Ser Ile Val Thr Val
305                 310                 315                 320

ttc act att acc aga acc ttg gaa caa aac gcc acc gat ttg att cat       1008
Phe Thr Ile Thr Arg Thr Leu Glu Gln Asn Ala Thr Asp Leu Ile His
                325                 330                 335

aga tgg caa tac gtt tct tct aag cag gat gac aag ttg ttc atc aga       1056
Arg Trp Gln Tyr Val Ser Ser Lys Gln Asp Asp Lys Leu Phe Ile Arg
            340                 345                 350

att atc ttg acc ggt atc aac acc acc aat tca caa cat ggt aac aag       1104
Ile Ile Leu Thr Gly Ile Asn Thr Thr Asn Ser Gln His Gly Asn Lys
        355                 360                 365

aga act att gaa gct gcc ttc aac tct ttg ttc ttg ggt aag att gaa       1152
Arg Thr Ile Glu Ala Ala Phe Asn Ser Leu Phe Leu Gly Lys Ile Glu
    370                 375                 380

gag ttg gtc cca att atg gaa aag act ttc cca gaa ttg ggt ttg acc       1200
Glu Leu Val Pro Ile Met Glu Lys Thr Phe Pro Glu Leu Gly Leu Thr
385                 390                 395                 400

aaa gaa gat tgc att gag atg tcc tgg att gag tct gtc ttg tac ttt       1248
Lys Glu Asp Cys Ile Glu Met Ser Trp Ile Glu Ser Val Leu Tyr Phe
                405                 410                 415

gct ggt ttt tct aga ggt caa cca ttg aac gtt ttg ttg gat aga agg       1296
Ala Gly Phe Ser Arg Gly Gln Pro Leu Asn Val Leu Leu Asp Arg Arg
            420                 425                 430

cca ttg act cca aag aga ttt ttc aag gct aag tcc gat tac gtc aac       1344
Pro Leu Thr Pro Lys Arg Phe Phe Lys Ala Lys Ser Asp Tyr Val Asn
        435                 440                 445

gaa cct att cca aaa gct ggt ttg gaa ggt att tgg gag ttg ttc gat       1392
Glu Pro Ile Pro Lys Ala Gly Leu Glu Gly Ile Trp Glu Leu Phe Asp
    450                 455                 460

gaa gaa gaa gct gaa gct gct gtt ttg att ttg tct cca tac ggt ggt       1440
Glu Glu Glu Ala Glu Ala Ala Val Leu Ile Leu Ser Pro Tyr Gly Gly
465                 470                 475                 480

atc atg gac aag att tcc gaa tcc gaa att cca ttt cca cat aga gct       1488
Ile Met Asp Lys Ile Ser Glu Ser Glu Ile Pro Phe Pro His Arg Ala
                485                 490                 495

ggc aac ctg tac aaa atc caa cat ttg gtt tac tgg gac gaa gaa ggt       1536
Gly Asn Leu Tyr Lys Ile Gln His Leu Val Tyr Trp Asp Glu Glu Gly
            500                 505                 510

gaa gat att gct aag aga cat atc aac tgg atc aga aag ctg tac tct       1584
```

```
Glu Asp Ile Ala Lys Arg His Ile Asn Trp Ile Arg Lys Leu Tyr Ser
        515                 520                 525

tac atg gct cca ttc gtt tct aaa aat cca aga gct gcc tac atc aac       1632
Tyr Met Ala Pro Phe Val Ser Lys Asn Pro Arg Ala Ala Tyr Ile Asn
    530                 535                 540

tac aga gat ttg gat att ggc acc aac gaa aag aac ggt aga aac act       1680
Tyr Arg Asp Leu Asp Ile Gly Thr Asn Glu Lys Asn Gly Arg Asn Thr
545                 550                 555                 560

tct tac aac gaa gct tct gtt tgg ggt gtt aag tac ttt aag ggt aac       1728
Ser Tyr Asn Glu Ala Ser Val Trp Gly Val Lys Tyr Phe Lys Gly Asn
                565                 570                 575

ttc aag agg ctg gtt tct gtt aag aca aag gtt gac cca tcc aat ttc       1776
Phe Lys Arg Leu Val Ser Val Lys Thr Lys Val Asp Pro Ser Asn Phe
            580                 585                 590

ttc aag aac gaa caa tcc att cca tcc ttg aaa cca tgg tgg aac aag       1824
Phe Lys Asn Glu Gln Ser Ile Pro Ser Leu Lys Pro Trp Trp Asn Lys
        595                 600                 605

aga ggt tat tgg tca cat cca caa ttt gaa aag                           1857
Arg Gly Tyr Trp Ser His Pro Gln Phe Glu Lys
    610                 615
```

<210> 135
<211> 619
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 135

```
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

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

```
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Met Ala His Asn His Glu Ser
                85                  90                  95

Phe Leu His Cys Leu Ser His His Ser Pro Asn Thr Ser Ser Ile Ser
            100                 105                 110

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

Phe Ser Ile His Asn Leu Arg Phe Thr Ser Pro Lys Thr Pro Lys Pro
    130                 135                 140

His Ile Ile Val Thr Pro Phe Leu Val Ser Gln Ile Gln Ala Ser Ile
145                 150                 155                 160

Ile Cys Ala Lys Lys Thr Gly Phe Gln Ile Arg Thr Arg Ser Gly Gly
                165                 170                 175

His Asp Tyr Glu Gly Leu Ser Tyr Val Ser Asp Val Ser Phe Val Val
            180                 185                 190

Val Asp Leu Ile Asn Leu Arg Ser Ile Ser Val Asp Ala Glu Asn Asn
        195                 200                 205

Val Ala Trp Val Gln Ser Gly Ala Thr Ile Gly Glu Leu Tyr Tyr Arg
    210                 215                 220

Ile Ala Glu Lys Ser Lys Thr Leu Gly Phe Pro Ala Gly Val Cys Pro
225                 230                 235                 240

Thr Val Gly Val Gly Gly His Phe Ser Gly Gly Gly Tyr Gly Leu Met
                245                 250                 255

Leu Arg Lys Phe Gly Leu Ala Ala Asp Asn Val Ile Asp Ala Tyr Phe
            260                 265                 270

Ile Asp Val Asn Gly Lys Leu His Asp Arg Lys Ser Met Gly Glu Asp
        275                 280                 285
```

```
Val Phe Trp Ala Ile Arg Gly Gly Gly Gly Ala Ser Phe Gly Ile Val
    290                 295                 300

Leu Ala Trp Lys Ile Lys Leu Leu Pro Val Pro Ser Ile Val Thr Val
305                 310                 315                 320

Phe Thr Ile Thr Arg Thr Leu Glu Gln Asn Ala Thr Asp Leu Ile His
                325                 330                 335

Arg Trp Gln Tyr Val Ser Ser Lys Gln Asp Asp Lys Leu Phe Ile Arg
            340                 345                 350

Ile Ile Leu Thr Gly Ile Asn Thr Thr Asn Ser Gln His Gly Asn Lys
        355                 360                 365

Arg Thr Ile Glu Ala Ala Phe Asn Ser Leu Phe Leu Gly Lys Ile Glu
    370                 375                 380

Glu Leu Val Pro Ile Met Glu Lys Thr Phe Pro Glu Leu Gly Leu Thr
385                 390                 395                 400

Lys Glu Asp Cys Ile Glu Met Ser Trp Ile Glu Ser Val Leu Tyr Phe
                405                 410                 415

Ala Gly Phe Ser Arg Gly Gln Pro Leu Asn Val Leu Leu Asp Arg Arg
            420                 425                 430

Pro Leu Thr Pro Lys Arg Phe Phe Lys Ala Lys Ser Asp Tyr Val Asn
        435                 440                 445

Glu Pro Ile Pro Lys Ala Gly Leu Glu Gly Ile Trp Glu Leu Phe Asp
    450                 455                 460

Glu Glu Glu Ala Glu Ala Ala Val Leu Ile Leu Ser Pro Tyr Gly Gly
465                 470                 475                 480

Ile Met Asp Lys Ile Ser Glu Ser Glu Ile Pro Phe Pro His Arg Ala
                485                 490                 495
```

```
Gly Asn Leu Tyr Lys Ile Gln His Leu Val Tyr Trp Asp Glu Glu Gly
            500                 505                 510

Glu Asp Ile Ala Lys Arg His Ile Asn Trp Ile Arg Lys Leu Tyr Ser
        515                 520                 525

Tyr Met Ala Pro Phe Val Ser Lys Asn Pro Arg Ala Ala Tyr Ile Asn
    530                 535                 540

Tyr Arg Asp Leu Asp Ile Gly Thr Asn Glu Lys Asn Gly Arg Asn Thr
545                 550                 555                 560

Ser Tyr Asn Glu Ala Ser Val Trp Gly Val Lys Tyr Phe Lys Gly Asn
                565                 570                 575

Phe Lys Arg Leu Val Ser Val Lys Thr Lys Val Asp Pro Ser Asn Phe
            580                 585                 590

Phe Lys Asn Glu Gln Ser Ile Pro Ser Leu Lys Pro Trp Trp Asn Lys
        595                 600                 605

Arg Gly Tyr Trp Ser His Pro Gln Phe Glu Lys
    610                 615
```