SEQUENCE LISTING

<110> Givaudan SA

<120> Enzymes and Applications thereof

<130> 30578

<150> GB 1507207.7
<151> 2015-04-24

<160> 188

<170> PatentIn version 3.3

<210> 1
<211> 631
<212> PRT
<213> Alicyclobacillus acidocaldarius

<400> 1

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


Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
            20                  25                  30


Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
        35                  40                  45


Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
    50                  55                  60


Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65                  70                  75                  80


Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95


Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110


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

```
Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp Ala
            340                 345                 350
```

```
Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560
```

```
Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575


Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590


Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
        595                 600                 605


Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
    610                 615                 620


Lys Gln Ala Ile Glu Arg Arg
625                 630
```

<210> 2
<211> 725
<212> PRT
<213> Zymomonas mobilis

<400> 2

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Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1               5                   10                  15


Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
            20                  25                  30


Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
        35                  40                  45


Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
    50                  55                  60


Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65                  70                  75                  80


Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
                85                  90                  95


Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
            100                 105                 110
```

```
Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
```

```
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

```
Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720

Ile Asp Leu Asn Asn
                725
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<210> 3
<211> 658
<212> PRT
<213> Zymomonas mobilis

<400> 3

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Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1               5                  10                  15

Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
            20                  25                  30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
        35                  40                  45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
    50                  55                  60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Ile Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

Pro Val Ala Arg Asn Arg Arg Gly Ile Leu Val Asp Glu Leu Phe Val
        195                 200                 205
```

```
Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430
```

```
Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640
```

```
Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655


Gly Met
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<210> 4
<211> 684
<212> PRT
<213> Bradyrhizobium japonicum

<400> 4

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


Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
            20                  25                  30


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


Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
    50                  55                  60


Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65                  70                  75                  80


Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95


Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110


Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125


Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Tyr
    130                 135                 140


Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160
```

```
Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
```

```
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590
```

```
Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680
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<210> 5
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 5

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
            20                  25                  30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
        35                  40                  45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
    50                  55                  60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Ala Trp Ala Leu
65                  70                  75                  80
```

```
Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110

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

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
```

```
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510
```

```
Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
        595                 600                 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
    610                 615                 620

Lys Gln Ala Ile Glu Arg Arg
625                 630
```

<210> 6
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 6

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acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc    180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcgc gtgggccctg    240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat    300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag    360
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ggcgggatcg agtcgtcgcg cgtgttcacg cggatgtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

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ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 7

<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 7

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

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65 70 75 80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Val Glu Ala Tyr Val
85 90 95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
100 105 110

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

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
130 135 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145 150 155 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
165 170 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg

```
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400
```

```
Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
        595                 600                 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
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610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 8
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 8
atggctgagc agttggtgga agcgccggcc tacgcgcgga cgctggatcg cgcggtggag 60

tatctcctct cctgccaaaa ggacgaaggc tactggtggg ggccgcttct gagcaacgtc 120

acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

tacccgggtg ggccgccgga cctcgacacg accgtcgagg cgtacgtcgc gctcaagtat 300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgttcacg cggatgtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat 840

ccggcgttca tcaagggctg ggaaggtcta gagctgtacg gcgtggagct ggattacgga 900

ggatggatgt ttcaggcttc catctcgccg gtgtgggaca cgggcctcgc cgtgctcgcg 960

ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

gtggtgtggg cgctcaacac cctgcgcttg ccggacgagc gccgcaggcg ggacgccatg 1200

acgaagggat tccgctggat tgtcggcatg cagagctcga acggcggttg gggcgcctac 1260

gacgtcgaca acacgagcga tctcccgaac cacatcccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

ccggacggca gctggttcgg tcgttggggc gtcaattacc tctacggcac gggcgcggtg 1500

gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

ttcccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 9
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 9

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu

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65                  70                  75                  80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110

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

Leu Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285
```

```
Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
```

```
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
        595                 600                 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
    610                 615                 620

Lys Gln Ala Ile Glu Arg Arg
625                 630
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<210> 10
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 10

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atggctgagc agttggtgga agcgccggcc tacgcgcgga cgctggatcg cgcggtggag     60

tatctcctct cctgccaaaa ggacgaaggc tactggtggg ggccgcttct gagcaacgtc    120

acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc    180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg    240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat    300
```

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgctcacg cggatgtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat 840

ccggcgttca tcaagggctg ggaaggtcta gagctgtacg gcgtggagct ggattacgga 900

ggatggatgt ttcaggcttc catctcgccg gtgtgggaca cgggcctcgc cgtgctcgcg 960

ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

gtggtgtggg cgctcaacac cctgcgcttg ccggacgagc gccgcaggcg ggacgccatg 1200

acgaagggat tccgctggat tgtcggcatg cagagctcga acggcggttg gggcgcctac 1260

gacgtcgaca acacgagcga tctcccgaac cacatcccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

ccggacggca gctggttcgg tcgttggggc gtcaattacc tctacggcac gggcgcggtg 1500

gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

ttcccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 11
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 11

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65 70 75 80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
85 90 95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
100 105 110

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

Phe Thr Arg Arg Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
130 135 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145 150 155 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
165 170 175

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Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
```

385 390 395 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
405 410 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
420 425 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
435 440 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
450 455 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465 470 475 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
485 490 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
500 505 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
515 520 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
530 535 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545 550 555 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
565 570 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
580 585 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 12
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 12
atggctgagc agttggtgga agcgccggcc tacgcgcgga cgctggatcg cgcggtggag 60

tatctcctct cctgccaaaa ggacgaaggc tactggtggg ggccgcttct gagcaacgtc 120

acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat 300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgttcacg cggaggtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat 840

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ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

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gacgtcgaca acacgagcga tctcccgaac cacatcccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

ccggacggca gctggttcgg tcgttggggc gtcaattacc tctacggcac gggcgcggtg 1500

gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

ttcccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 13
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 13

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

```
Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65                  70                  75                  80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110

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

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

Gly Ala Lys Gly Gly Gly Gly Trp Ile Phe Asp Ala Leu Asp Arg Val
    210                 215                 220

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
```

```
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495
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Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
500 505 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
515 520 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
530 535 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545 550 555 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
565 570 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
580 585 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 14
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 14
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tatctcctct cctgccaaaa ggacgaaggc tactggtggg ggccgcttct gagcaacgtc 120

acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat 300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgttcacg cggatgtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg tgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat 840

ccggcgttca tcaagggctg ggaaggtcta gagctgtacg gcgtggagct ggattacgga 900

ggatggatgt ttcaggcttc catctcgccg gtgtgggaca cgggcctcgc cgtgctcgcg 960

ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

gtggtgtggg cgctcaacac cctgcgcttg ccggacgagc gccgcaggcg ggacgccatg 1200

acgaagggat tccgctggat tgtcggcatg cagagctcga acggcggttg gggcgcctac 1260

gacgtcgaca acacgagcga tctcccgaac cacatcccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

ccggacggca gctggttcgg tcgttggggc gtcaattacc tctacggcac gggcgcggtg 1500

gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

ttcccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 15
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 15

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65 70 75 80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
85 90 95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
100 105 110

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

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
130 135 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145 150 155 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala

```
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380
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Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Thr
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
```

595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 16
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 16
atggctgagc agttggtgga agcgccggcc tacgcgcgga cgctggatcg cgcggtggag 60

tatctcctct cctgccaaaa ggacgaaggc tactggtggg ggccgcttct gagcaacgtc 120

acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat 300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgttcacg cggatgtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat 840

ccggcgttca tcaagggctg ggaaggtcta gagctgtacg gcgtggagct ggattacgga 900

ggatggatgt ttcaggcttc catctcgccg gtgtgggaca cgggcctcgc cgtgctcgcg 960

ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

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acgaagggat tccgctggat tgtcggcatg cagagctcga acggcggttg gggcgcctac 1260

gacgtcgaca acacgagcga tctcccgaac cacaccccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

ccggacggca gctggttcgg tcgttggggc gtcaattacc tctacggcac gggcgcggtg 1500

gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

ttcccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 17
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 17

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile

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    50                  55                  60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65                  70                  75                  80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110

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

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270
```

```
Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
```

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               485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val His Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
        595                 600                 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
    610                 615                 620

Lys Gln Ala Ile Glu Arg Arg
625                 630


<210>  18
<211>  1896
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic AacSHC Derivative

<400>  18
atggctgagc agttggtgga agcgccggcc tacgcgcgga cgctggatcg cgcggtggag     60

tatctcctct cctgccaaaa ggacgaaggc tactggtggg ggccgcttct gagcaacgtc    120

acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc    180
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atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat 300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgttcacg cggatgtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

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ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

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gacgtcgaca acacgagcga tctcccgaac cacatcccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

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gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcattac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

ttcccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 19
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 19

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65 70 75 80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
85 90 95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
100 105 110

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

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
130 135 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145 150 155 160

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Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
```

```
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590
```

Glu Pro Tyr Tyr Thr Gly Thr Gly Tyr Pro Gly Asp Phe Tyr Leu Gly
595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 20
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 20
atggctgagc agttggtgga agcgccggcc tacgcgcgga cgctggatcg cgcggtggag 60

tatctcctct cctgccaaaa ggacgaaggc tactggtggg ggccgcttct gagcaacgtc 120

acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat 300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgttcacg cggatgtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat 840

ccggcgttca tcaagggctg ggaaggtcta gagctgtacg gcgtggagct ggattacgga 900

ggatggatgt ttcaggcttc catctcgccg gtgtgggaca cgggcctcgc cgtgctcgcg 960

ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

gtggtgtggg cgctcaacac cctgcgcttg ccggacgagc gccgcaggcg ggacgccatg 1200

acgaagggat tccgctggat tgtcggcatg cagagctcga acggcggttg gggcgcctac 1260

gacgtcgaca acacgagcga tctcccgaac cacatcccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

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atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

tacccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 21
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 21

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

```
Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
    50                  55                  60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65                  70                  75                  80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110

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

Phe Thr Arg Arg Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

Gly Ala Lys Gly Gly Gly Gly Trp Ile Phe Asp Ala Leu Asp Arg Val
    210                 215                 220

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
```

```
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Thr
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480
```

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
485 490 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
500 505 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
515 520 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
530 535 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545 550 555 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
565 570 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
580 585 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 22
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 22
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acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat 300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgttcacg cggaggtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg tgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

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ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

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gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

ttcccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 23
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 23

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65 70 75 80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
85 90 95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
100 105 110

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

Phe Thr Arg Arg Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
130 135 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro

```
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365
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Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Thr
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
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580 585 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 24
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 24
atggctgagc agttggtgga agctccggcc tacgcgcgga cgctggatcg cgcggtggag 60

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atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

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atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

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ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat 840

ccggcgttca tcaagggctg ggaaggtcta gagctgtacg gcgtggagct ggattacgga 900

ggatggatgt ttcaggcttc catctcgccg gtgtgggaca cgggcctcgc cgtgctcgcg 960

ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

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atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

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ttcccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 25
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 25

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu

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        35                  40                  45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
    50                  55                  60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65                  70                  75                  80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110

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

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255
```

```
Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
```

```
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Tyr Pro Gly Asp Phe Tyr Leu Gly
        595                 600                 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
    610                 615                 620

Lys Gln Ala Ile Glu Arg Arg
625                 630


<210>  26
<211>  1896
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic AacSHC Derivative

<400>  26
atggctgagc agttggtgga agcgccggcc tacgcgcgga cgctggatcg cgcggtggag     60
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acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

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ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

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atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

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ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

tacccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 27
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 27

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Ala Trp Ala Leu
65 70 75 80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Val Glu Ala Tyr Val
85 90 95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
100 105 110

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

Leu Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
130 135 140

```
Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
```

```
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575
```

```
Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
        595                 600                 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
    610                 615                 620

Lys Gln Ala Ile Glu Arg Arg
625                 630
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<210> 28
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 28

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acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc    180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcgc gtgggccctg    240

tacccgggtg ggccgccgga cctcgacacg accgtcgagg cgtacgtcgc gctcaagtat    300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag    360

ggcgggatcg agtcgtcgcg cgtgctcacg cggatgtggc tggcgctggt gggagaatat    420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg    480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg    540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag    600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg    660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc    720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg    780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat    840
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ccggcgttca tcaagggctg ggaaggtcta gagctgtacg gcgtggagct ggattacgga 900

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ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

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ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

gtggtgtggg cgctcaacac cctgcgcttg ccggacgagc gccgcaggcg ggacgccatg 1200

acgaagggat tccgctggat tgtcggcatg cagagctcga acggcggttg gggcgcctac 1260

gacgtcgaca acacgagcga tctcccgaac cacatcccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

ccggacggca gctggttcgg tcgttggggc gtcaattacc tctacggcac gggcgcggtg 1500

gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

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ttcccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 29
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 29

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

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Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
        35                  40                  45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
    50                  55                  60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65                  70                  75                  80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110

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

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
```

```
               245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460
```

```
Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val His Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Tyr Pro Gly Asp Phe Tyr Leu Gly
        595                 600                 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
    610                 615                 620

Lys Gln Ala Ile Glu Arg Arg
625                 630
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<210> 30
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 30

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tatctcctct cctgccaaaa ggacgaaggc tactggtggg ggccgcttct gagcaacgtc 120

acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat 300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgttcacg cggatgtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat 840

ccggcgttca tcaagggctg ggaaggtcta gagctgtacg gcgtggagct ggattacgga 900

ggatggatgt ttcaggcttc catctcgccg gtgtgggaca cgggcctcgc cgtgctcgcg 960

ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

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gacgtcgaca acacgagcga tctcccgaac cacatcccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

ccggacggca gctggttcgg tcgttggggc gtcaattacc tctacggcac gggcgcggtg 1500

gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcattac 1740

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tacccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 31
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 31

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65 70 75 80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
85 90 95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
100 105 110

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

Leu Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys

```
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp Ala
            340                 345                 350
```

```
Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
```

565 570 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
580 585 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 32
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 32
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accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

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ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 33
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 33

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp

```
            20                  25                  30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
        35                  40                  45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
    50                  55                  60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65                  70                  75                  80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110

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

Leu Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240
```

```
Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
```

```
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Tyr Pro Gly Asp Phe Tyr Leu Gly
        595                 600                 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
    610                 615                 620

Lys Gln Ala Ile Glu Arg Arg
625                 630
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<210> 34
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 34
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acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat 300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgctcacg cggatgtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat 840

ccggcgttca tcaagggctg ggaaggtcta gagctgtacg gcgtggagct ggattacgga 900

ggatggatgt ttcaggcttc catctcgccg gtgtgggaca cgggcctcgc cgtgctcgcg 960

ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

gtggtgtggg cgctcaacac cctgcgcttg ccggacgagc gccgcaggcg ggacgccatg 1200

acgaagggat tccgctggat tgtcggcatg cagagctcga acggcggttg gggcgcctac 1260

gacgtcgaca acacgagcga tctcccgaac cacatcccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

ccggacggca gctggttcgg tcgttggggc gtcaattacc tctacggcac gggcgcggtg 1500

gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

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ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 35
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 35

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65 70 75 80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
85 90 95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
100 105 110

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

```
Leu Thr Arg Arg Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp Ala
```

```
            340                 345                 350

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Thr
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560
```

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
565 570 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
580 585 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 36
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 36
atggctgagc agttggtgga agcgccggcc tacgcgcgga cgctggatcg cgcggtggag 60

tatctcctct cctgccaaaa ggacgaaggc tactggtggg ggccgcttct gagcaacgtc 120

acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat 300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgctcacg cggaggtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat 840

ccggcgttca tcaagggctg ggaaggtcta gagctgtacg gcgtggagct ggattacgga 900

ggatggatgt ttcaggcttc catctcgccg gtgtgggaca cgggcctcgc cgtgctcgcg 960

ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

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gacgtcgaca acacgagcga tctcccgaac cacaccccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

ccggacggca gctggttcgg tcgttggggc gtcaattacc tctacggcac gggcgcggtg 1500

gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

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ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 37
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 37

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

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Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
            20                  25                  30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
        35                  40                  45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
    50                  55                  60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65                  70                  75                  80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110

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

Phe Thr Arg Arg Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
```

225 230 235 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
245 250 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
260 265 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
275 280 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
290 295 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305 310 315 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
325 330 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
355 360 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
370 375 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385 390 395 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
405 410 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Thr
420 425 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
435 440 445

```
Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Tyr Pro Gly Asp Phe Tyr Leu Gly
        595                 600                 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
    610                 615                 620

Lys Gln Ala Ile Glu Arg Arg
625                 630
```

<210> 38
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 38
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acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

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atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

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ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

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atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

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ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

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gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

tacccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 39
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 39

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65 70 75 80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
85 90 95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
100 105 110

Ala Leu Arg Phe Ile Gln Ser Gln Gly Gly Ile Glu Ser Ser Arg Val

```
        115                 120                 125

Leu Thr Arg Arg Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335
```

```
Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp Ala
            340                 345                 350

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Thr
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
```

545 550 555 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
565 570 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
580 585 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Tyr Pro Gly Asp Phe Tyr Leu Gly
595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 40
<211> 1896
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic AacSHC Derivative

<400> 40
atggctgagc agttggtgga agcgccggcc tacgcgcgga cgctggatcg cgcggtggag 60

tatctcctct cctgccaaaa ggacgaaggc tactggtggg ggccgcttct gagcaacgtc 120

acgatggaag cggagtacgt cctcttgtgc cacattctcg atcgcgtcga tcgggatcgc 180

atggagaaga tccggcggta cctgttgcac gagcagcgcg aggacggcac gtgggccctg 240

tacccgggtg ggccgccgga cctcgacacg accatcgagg cgtacgtcgc gctcaagtat 300

atcggcatgt cgcgcgacga ggagccgatg cagaaggcgc tccggttcat tcagagccag 360

ggcgggatcg agtcgtcgcg cgtgctcacg cggaggtggc tggcgctggt gggagaatat 420

ccgtgggaga aggtgcccat ggtcccgccg gagatcatgt tcctcggcaa gcgcatgccg 480

ctcaacatct acgagtttgg ctcgtgggct cgggcgaccg tcgtggcgct ctcgattgtg 540

atgagccgcc agccggtgtt cccgctgccc gagcgggcgc gcgtgcccga gctgtacgag 600

accgacgtgc ctccgcgccg gcgcggtgcc aagggagggg gtgggtggat cttcgacgcg 660

ctcgaccggg cgctgcacgg gtatcagaag ctgtcggtgc acccgttccg ccgcgcggcc 720

gagatccgcg ccttggactg gttgctcgag cgccaggccg gagacggcag ctggggcggg 780

attcagccgc cttggtttta cgcgctcatc gcgctcaaga ttctcgacat gacgcagcat 840

ccggcgttca tcaagggctg ggaaggtcta gagctgtacg gcgtggagct ggattacgga 900

ggatggatgt ttcaggcttc catctcgccg gtgtgggaca cgggcctcgc cgtgctcgcg 960

ctgcgcgctg cggggcttcc ggccgatcac gaccgcttgg tcaaggcggg cgagtggctg 1020

ttggaccggc agatcacggt tccgggcgac tgggcggtga agcgcccgaa cctcaagccg 1080

ggcgggttcg cgttccagtt cgacaacgtg tactacccgg acgtggacga cacggccgtc 1140

gtggtgtggg cgctcaacac cctgcgcttg ccggacgagc gccgcaggcg ggacgccatg 1200

acgaagggat tccgctggat tgtcggcatg cagagctcga acggcggttg gggcgcctac 1260

gacgtcgaca acacgagcga tctcccgaac cacaccccgt tctgcgactt cggcgaagtg 1320

accgatccgc cgtcagagga cgtcaccgcc cacgtgctcg agtgtttcgg cagcttcggg 1380

tacgatgacg cctggaaggt catccggcgc gcggtggaat atctcaagcg ggagcagaag 1440

ccggacggca gctggttcgg tcgttggggc gtcaattacc tctacggcac gggcgcggtg 1500

gtgtcggcgc tgaaggcggt cgggatcgac acgcgcgagc cgtacattca aaaggcgctc 1560

gactgggtcg agcagcatca gaacccggac ggcggctggg gcgaggactg ccgctcgtac 1620

gaggatccgg cgtacgcggg taagggcgcg agcaccccgt cgcagacggc ctgggcgctg 1680

atggcgctca tcgcgggcgg cagggcggag tccgaggccg cgcgccgcgg cgtgcaatac 1740

ctcgtggaga cgcagcgccc ggacggcggc tgggatgagc cgtactacac cggcacgggc 1800

tacccagggg atttctacct cggctacacc atgtaccgcc acgtgtttcc gacgctcgcg 1860

ctcggccgct acaagcaagc catcgagcgc aggtga 1896

<210> 41
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 41

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys

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1               5                   10                  15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
            20                  25                  30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
        35                  40                  45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
    50                  55                  60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65                  70                  75                  80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
                85                  90                  95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
            100                 105                 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125

Ala Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

Pro Asp Asn Phe Val Phe Ser Ile Tyr Asn Phe Ala Gln Trp Ala Arg
    210                 215                 220
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Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
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        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655
```

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660   665   670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675   680   685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690   695   700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705   710   715   720

Ile Asp Leu Asn Asn
                725

<210> 42
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<220>
<221> misc_feature
<222> (387)..(387)
<223> n is a, c, g, or t

<400> 42
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gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga   120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg   180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc   240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg   300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt   360

ttggaaatgc agcgggaaga tggcgcntgg ggagtctatt tcggcgctgg aaatggcgat   420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat   480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt   540

gtctttaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 43
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 43

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
115 120 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
130 135 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145 150 155 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu

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                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380
```

```
Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
```

595 600 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
610 615 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625 630 635 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
645 650 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
660 665 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
675 680 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
690 695 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705 710 715 720

Ile Asp Leu Asn Asn
725

<210> 44
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 44
atgggtattg acagaatgaa tagcttaagt cgcttgttaa tgaagaagat tttcggggct 60

gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga 120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

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catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 45
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 45

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
115 120 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr

```
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

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

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350
```

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Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
```

```
               565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
               645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720

Ile Asp Leu Asn Asn
               725
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<210> 46
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<220>
<221> misc_feature

<222> (544)..(546)
<223> ntn is ttr or ctn

<400> 46
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ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtcntnaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 47
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 47

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

```
Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
                85                  90                  95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
            100                 105                 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Arg Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
```

```
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510
```

```
Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720

Ile Asp Leu Asn Asn
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725

<210> 48
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<220>
<221> misc_feature
<222> (553)..(555)
<223> ngn is agr or cgn

<400> 48
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ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gtngntggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 49
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 49

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile

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            20                  25                  30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
        35                  40                  45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
    50                  55                  60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65                  70                  75                  80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
                85                  90                  95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
            100                 105                 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240
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Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Val Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
```

```
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670
```

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
675 680 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
690 695 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705 710 715 720

Ile Asp Leu Asn Asn
725

<210> 50
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<220>
<221> misc_feature
<222> (846)..(846)
<223> n is a, c, g, or t

<400> 50
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gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga 120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtgtnttac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

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ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 51

<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 51

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
115 120 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
130 135 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145 150 155 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
165 170 175

Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu

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            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400
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```
Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Thr Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
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610 615 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625 630 635 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
645 650 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
660 665 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
675 680 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
690 695 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705 710 715 720

Ile Asp Leu Asn Asn
725

<210> 52
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<220>
<221> misc_feature
<222> (1494)..(1494)
<223> n is a, c, g, or t

<400> 52
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gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga 120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aacnccttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 53
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 53

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
115 120 125

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Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
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            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560
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```
Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720

Ile Asp Leu Asn Asn
                725
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<210> 54
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 54

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gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga 120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 55
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 55

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

```
Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
            100                 105                 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
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305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525
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Arg Asp Met Pro Val Ile Gln Lys Ala Ile Asp Tyr Val Arg Ser Glu
    530                 535                 540

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Tyr Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720

Ile Asp Leu Asn Asn
                725
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<210> 56

<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 56
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gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga 120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg ataycccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 57
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 57

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

```
Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65                  70                  75                  80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
                85                  90                  95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
            100                 105                 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Arg Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Val Leu His Trp Val Gln Ser
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        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495
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Lys Thr Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
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705 710 715 720

Ile Asp Leu Asn Asn
725

<210> 58
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<220>
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<222> (553)..(555)
<223> ngn is agr or cgn

<220>
<221> misc_feature
<222> (846)..(846)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1494)..(1494)
<223> n is a, c, g, or t

<400> 58
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ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gtngntggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtgtnttac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

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gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

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ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aacnccttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

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tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

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gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 59

<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 59

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
115 120 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
130 135 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145 150 155 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
165 170 175

Lys Asn Ile Arg Val Phe Thr Arg Arg Trp Leu Ala Leu Ile Gly Glu

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            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400
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Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Thr Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
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610 615 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625 630 635 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
645 650 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
660 665 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
675 680 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
690 695 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705 710 715 720

Ile Asp Leu Asn Asn
725

<210> 60
<211> 2178
<212> DNA
<213> Artificial sequence

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<220>
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<222> (553)..(555)
<223> ngn is agr or cgn

<220>
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<222> (1494)..(1494)
<223> n is a, c, g, or t

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gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga 120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gtngntggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

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tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

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gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 61
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 61

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
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Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

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Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320
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Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

Arg Asp Met Pro Val Ile Gln Lys Ala Ile Asp Tyr Val Arg Ser Glu
    530                 535                 540
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Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560


Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575


Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590


Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605


Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620


Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640


Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655


Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Tyr Pro Gly Tyr Gly
            660                 665                 670


Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685


Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700


Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720


Ile Asp Leu Asn Asn
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<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

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ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

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ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

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ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg ataycccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

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<212> PRT
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<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 63

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

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Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
                85                  90                  95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
            100                 105                 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125

Ala Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

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

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285
```

```
Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510
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Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720
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Ile Asp Leu Asn Asn
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<210> 64
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

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<222> (387)..(387)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (544)..(546)
<223> ntn is ttr or ctn

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ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggcgcntgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtcntnaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

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ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

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gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

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gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

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attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

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<210> 65
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 65

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Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
            20                  25                  30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
        35                  40                  45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
    50                  55                  60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65                  70                  75                  80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
                85                  90                  95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
            100                 105                 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430
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Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
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645 650 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Tyr Pro Gly Tyr Gly
660 665 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
675 680 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
690 695 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705 710 715 720

Ile Asp Leu Asn Asn
725

<210> 66
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

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ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

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ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

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tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

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tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

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<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 67

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
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Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
115 120 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
130 135 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145 150 155 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
165 170 175

Lys Asn Ile Arg Val Leu Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu

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            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400
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Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
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    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720

Ile Asp Leu Asn Asn
                725


<210>  68
<211>  2178
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic ZmoSHC1 Derivative


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<222>  (544)..(546)
<223>  ntn is ttr or ctn

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ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg    180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc    240
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gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtcntnaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

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gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

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tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 69
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 69

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
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Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
115 120 125

```
Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

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

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
```

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            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560
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Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Tyr Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720

Ile Asp Leu Asn Asn
                725
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<210> 70
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<220>
<221> misc_feature
<222> (544)..(546)
<223> ntn is ttr or ctn

<400> 70
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gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga   120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg   180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc   240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg   300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt   360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat   420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat   480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt   540

gtcntnaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac   600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc   660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc   720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat   780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac   840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct   900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga   960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat   1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga   1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg   1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc   1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat   1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat   1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa   1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt   1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg ataycccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 71
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 71

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro

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65                  70                  75                  80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
                85                  90                  95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
            100                 105                 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Leu Thr Arg Arg Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285
```

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Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Thr Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
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            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720
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Ile Asp Leu Asn Asn
725

<210> 72
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<220>
<221> misc_feature
<222> (544)..(546)
<223> ntn is ttr or ctn

<220>
<221> misc_feature
<222> (553)..(555)
<223> ngn is agr or cgn

<220>
<221> misc_feature
<222> (1494)..(1494)
<223> n is a, c, g, or t

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ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtcntnaccc gtngntggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aacnccttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 73
<211> 725
<212> PRT

<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 73

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Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
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Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
            20                  25                  30


Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
        35                  40                  45


Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
    50                  55                  60


Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65                  70                  75                  80


Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
                85                  90                  95


Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
            100                 105                 110


Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125


Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140


Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160


Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175


Lys Asn Ile Arg Val Phe Thr Arg Arg Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190
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Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
```

```
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Thr Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620
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Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640


Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655


Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Tyr Pro Gly Tyr Gly
            660                 665                 670


Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685


Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700


Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720


Ile Asp Leu Asn Asn
                725


<210>  74
<211>  2178
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic ZmoSHC1 Derivative


<220>
<221>  misc_feature
<222>  (553)..(555)
<223>  ngn is agr or cgn

<220>
<221>  misc_feature
<222>  (1494)..(1494)
<223>  n is a, c, g, or t

<400>  74
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gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga    120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg    180
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aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gtngntggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aacnccttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg ataycccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 75
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 75

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

```
Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Leu Thr Arg Arg Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335
```

```
Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Thr Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

```
Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560


Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575


Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590


Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605


Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620


Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640


Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655


Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Tyr Pro Gly Tyr Gly
            660                 665                 670


Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685


Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700


Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720


Ile Asp Leu Asn Asn
                725


<210>  76
<211>  2178
<212>  DNA
<213>  Artificial sequence

<220>
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<223> Synthetic ZmoSHC1 Derivative

<220>
<221> misc_feature
<222> (544)..(546)
<223> ntn is ttr or ctn

<220>
<221> misc_feature
<222> (553)..(555)
<223> ngn is agr or cgn

<220>
<221> misc_feature
<222> (1494)..(1494)
<223> n is a, c, g, or t

<400> 76
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gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga 120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtcntnaccc gtngntggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aacncctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg ataycccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 77
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 77

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1 5 10 15

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Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
            20                  25                  30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
        35                  40                  45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
    50                  55                  60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Ala Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Ile Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240
```

```
Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445
```

```
Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
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<210> 78
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<220>
<221> misc_feature
<222> (255)..(255)
<223> n is a, c, g, or t

<400> 78
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attatccaaa aggccacccg tgccttgctt gagaagcagc agcaggatgg ccattgggtt 120

tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcgcntggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtctt tacacgtatt 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

ttgaatggtg aagacgggtt gggtgctatt tatccggcga ttgccaatag cgtcatgatg 840

tatgatgcct tgggatatcc cgaaaaccat ccagaaagag ccattgcccg tcgggctgtc 900

gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

ccttgtttat ccccgatttg ggataccgct ttggttgccc atgccatgtt ggaagtcgga 1020

ggcgatgagg ctgaaaaatc ggctatttct gccttgagct ggttaaagcc gcaacaaatt 1080

ttggatgtaa agggcgattg ggcatggcgg cggcctgatc tcagacccgg gggatgggcc 1140

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gccatggaat ggaccattgg gatgcaaagc gataatggcg gttggggcgc tttcgatgcc 1320

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gattatagcg gatacgagcc gatggattcg acggcttccc aaacagcatg ggctttattg 1740

ggcttgatgg ctgttgggga agctaattcc gaggccgtga caaagggtat aaactggttg 1800

gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggtttt 1860

ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 79
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 79

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1 5 10 15

Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
50 55 60

```
Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Ile Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270
```

```
Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495
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Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
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<210> 80
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 80
atgactgtat cgacttcctc ggcttttcat catagcccgt tgtctgatga tgttgagccg 60

attatccaaa aggccacccg tgccttgctt gagaagcagc agcaggatgg ccattgggtt 120

tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcggatggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtctt tacacgtatt 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

ttgaatggtg aagacgggtt gggtgctatt tatccggcga ttgccaatag cgtcatgatg 840

tatgatgcct tgggatatcc cgaaaaccat ccagaaagag ccattgcccg tcgggctgtc 900

gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

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gcattgaatg tggccgcttt accccatgat catttagctg ttcagaaagc tgtggcttgg 1620

ctgaaaacta ttcaaaatga agatggtggt tggggtgaaa attgcgatag ctatgccctt 1680

gattatagcg gatacgagcc gatggattcg acggcttccc aaacagcatg ggctttattg 1740

ggcttgatgg ctgttgggga agctaattcc gaggccgtga caaagggtat aaactggttg 1800

gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggtttt 1860

ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 81
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 81

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1 5 10 15

Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
50 55 60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65 70 75 80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
85 90 95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
100 105 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
115 120 125

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Gly Gly Ala Met Arg Ala Asn Val Leu Thr Arg Ile Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335
```

```
Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560
```

```
Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575


Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590


Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605


Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620


Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640


Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655


Gly Met
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<210> 82
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<220>
<221> misc_feature
<222> (409)..(411)
<223> ntn is ttr or ctn

<400> 82
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tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcggatggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtcnt nacacgtatt 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

ttgaatggtg aagacgggtt gggtgctatt tatccggcga ttgccaatag cgtcatgatg 840

tatgatgcct tgggatatcc cgaaaaccat ccagaaagag ccattgcccg tcgggctgtc 900

gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

ccttgtttat ccccgatttg ggataccgct ttggttgccc atgccatgtt ggaagtcgga 1020

ggcgatgagg ctgaaaaatc ggctatttct gccttgagct ggttaaagcc gcaacaaatt 1080

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gccatggaat ggaccattgg gatgcaaagc gataatggcg gttggggcgc tttcgatgcc 1320

aataacagct atacttatct gaataatatt ccctttgctg atcatggcgc gttacttgat 1380

ccgccaacgg tcgatgtctc ggcacgctgc gtttcaatga tggcgcaagc cggtatctcg 1440

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ctgaaaacta ttcaaaatga agatggtggt tggggtgaaa attgcgatag ctatgccctt 1680

gattatagcg gatacgagcc gatggattcg acggcttccc aaacagcatg ggctttattg 1740

ggcttgatgg ctgttgggga agctaattcc gaggccgtga caaagggtat aaactggttg 1800

gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggtttt 1860

ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 83
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 83

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
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Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
50 55 60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65 70 75 80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
85 90 95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
100 105 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
115 120 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Arg Gln Leu Ala Leu
130 135 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145 150 155 160

```
Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380
```

```
Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590
```

```
Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
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<210> 84
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<220>
<221> misc_feature
<222> (418)..(420)
<223> ngn is agr or cgn

<400> 84
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tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcggatggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtctt tacacgtngn 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

ttgaatggtg aagacgggtt gggtgctatt tatccggcga ttgccaatag cgtcatgatg 840

tatgatgcct tgggatatcc cgaaaaccat ccagaaagag ccattgcccg tcgggctgtc 900

gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

ccttgtttat ccccgatttg ggataccgct ttggttgccc atgccatgtt ggaagtcgga 1020

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gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggtttt 1860

ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 85
<211> 658
<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic ZmoSHC2 Derivative

<400> 85

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Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
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Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
            20                  25                  30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
        35                  40                  45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
    50                  55                  60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Ile Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

Pro Val Ala Arg Asn Arg Arg Gly Ile Leu Val Asp Glu Leu Phe Val
        195                 200                 205
```

```
Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415
```

```
Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640
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Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
645 650 655

Gly Met

<210> 86
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 86
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tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcggatggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtctt tacacgtatt 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

ttgaatggtg aagacgggtt gggtgctatt tatccggcga ttgccaatag cgtcatgatg 840

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gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggtttt 1860

ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

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<210> 87
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 87

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
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Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

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Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
    50                  55                  60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Ile Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270
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Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Thr Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480
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Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
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<210> 88
<211> 1977
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic ZmoSHC2 Derivative

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<223> n is a, c, g, or t

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tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcggatggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtctt tacacgtatt 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

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gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggtttt 1860

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gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 89
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 89

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1 5 10 15

Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
50 55 60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65 70 75 80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
85 90 95

```
Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Ile Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300
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Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525
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His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile His Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
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<210> 90
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 90
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gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtctt tacacgtatt 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

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ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 91
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 91

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
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Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
50 55 60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65 70 75 80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
85 90 95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
100 105 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
115 120 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Ile Gln Leu Ala Leu
130 135 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145 150 155 160

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Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365
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Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590
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Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Tyr Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
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<210> 92
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 92

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gattatagcg gatacgagcc gatggattcg acggcttccc aaacagcatg ggctttattg 1740

ggcttgatgg ctgttgggga agctaattcc gaggccgtga caaagggtat aaactggttg 1800

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<210> 93
<211> 658
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<400> 93

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Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
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Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
        35                  40                  45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
    50                  55                  60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
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Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Arg Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

Pro Val Ala Arg Asn Arg Arg Gly Ile Leu Val Asp Glu Leu Phe Val
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Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
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Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
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Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430
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Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Thr Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655
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Gly Met

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<211> 1977
<212> DNA
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<220>
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<222> (418)..(420)
<223> ngn is agr or cgn

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cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

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gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

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Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1 5 10 15

Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys

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            20                  25                  30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
        35                  40                  45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
    50                  55                  60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Arg Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240
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Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Thr Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
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    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
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Gly Met
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<210> 96
<211> 1977
<212> DNA
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caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

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ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

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<400> 97

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Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

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Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
    50                  55                  60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Ile Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255
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Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480
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Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Tyr Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
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gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggttay 1860

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<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 99

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
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Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
50 55 60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65 70 75 80

Gly Glu His Gly Ala Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
85 90 95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
100 105 110

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Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Leu Thr Arg Ile Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320
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Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540
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Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560


Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575


Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590


Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605


Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620


Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
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Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655


Gly Met
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<210> 100
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

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<222> (255)..(255)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (409)..(411)
<223> ntn is ttr or ctn

<400> 100

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tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcgcntggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

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gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtcnt nacacgtatt 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

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gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

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ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 101
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 101

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1 5 10 15

Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
50 55 60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65 70 75 80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
85 90 95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
100 105 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
115 120 125

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Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Ile Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
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            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560
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Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
565 570 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
580 585 590

Val Thr Lys Gly Ile His Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
595 600 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Tyr Pro Arg Val Phe
610 615 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625 630 635 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
645 650 655

Gly Met

<210> 102
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 102
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tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcggatggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtctt tacacgtatt 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

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gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

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gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggttay 1860

ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

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<210> 103
<211> 658
<212> PRT

<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 103

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
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Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
50 55 60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65 70 75 80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
85 90 95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
100 105 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
115 120 125

Gly Gly Ala Met Arg Ala Asn Val Leu Thr Arg Ile Gln Leu Ala Leu
130 135 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145 150 155 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
165 170 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
180 185 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
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               405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620
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Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
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Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
645 650 655

Gly Met

<210> 104
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<220>
<221> misc_feature
<222> (409)..(411)
<223> ntn is ttr or ctn

<400> 104
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gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

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ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 105
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 105

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
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Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
            20                  25                  30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
        35                  40                  45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
    50                  55                  60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Leu Thr Arg Ile Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
```

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225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445
```

```
Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Tyr Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
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<210> 106
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<220>
<221> misc_feature
<222> (409)..(411)
<223> ntn is ttr or ctn

<400> 106
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attatccaaa aggccacccg tgccttgctt gagaagcagc agcaggatgg ccattgggtt 120

tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcggatggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtcnt nacacgtatt 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

ttgaatggtg aagacgggtt gggtgctatt tatccggcga ttgccaatag cgtcatgatg 840

tatgatgcct tgggatatcc cgaaaaccat ccagaaagag ccattgcccg tcgggctgtc 900

gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

ccttgtttat ccccgatttg ggataccgct ttggttgccc atgccatgtt ggaagtcgga 1020

ggcgatgagg ctgaaaaatc ggctatttct gccttgagct ggttaaagcc gcaacaaatt 1080

ttggatgtaa agggcgattg ggcatggcgg cggcctgatc tcagacccgg gggatgggcc 1140

tttcaatata gaaatgacta ttatcccgat gtcgatgata cggctgttgt gactatggcg 1200

atggatcgag ccgcaaaatt gtcggatctt cacgatgatt ttgaggaatc taaagcgcgt 1260

gccatggaat ggaccattgg gatgcaaagc gataatggcg gttggggcgc tttcgatgcc 1320

aataacagct atacttatct gaataatatt ccctttgctg atcatggcgc gttacttgat 1380

ccgccaacgg tcgatgtctc ggcacgctgc gtttcaatga tggcgcaagc cggtatctcg 1440

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ggtagctggt tcgggcgttg gggtgtcaat tacatatatg gcacatggtc ggccttatgt 1560

gcattgaatg tggccgcttt accccatgat catttagctg ttcagaaagc tgtggcttgg 1620

ctgaaaacta ttcaaaatga agatggtggt tggggtgaaa attgcgatag ctatgccctt 1680

gattatagcg gatacgagcc gatggattcg acggcttccc aaacagcatg ggctttattg 1740

ggcttgatgg ctgttgggga agctaattcc gaggccgtga caaagggtat aaactggttg 1800

gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggttay 1860

ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 107
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 107

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1 5 10 15

Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu

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    50                  55                  60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Leu Thr Arg Arg Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270
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```
Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Thr Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
```

```
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
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<210> 108
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<220>
<221> misc_feature
<222> (409)..(411)
<223> ntn is ttr or ctn

<220>
<221> misc_feature
<222> (418)..(420)
<223> ngn is agr or cgn

<220>
<221> misc_feature
<222> (1350)..(1350)
<223> n is a, c, g, or t

<400> 108
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attatccaaa aggccacccg tgccttgctt gagaagcagc agcaggatgg ccattgggtt 120

tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcggatggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtcnt nacacgtngn 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

ttgaatggtg aagacgggtt gggtgctatt tatccggcga ttgccaatag cgtcatgatg 840

tatgatgcct tgggatatcc cgaaaaccat ccagaaagag ccattgcccg tcgggctgtc 900

gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

ccttgtttat ccccgatttg ggataccgct ttggttgccc atgccatgtt ggaagtcgga 1020

ggcgatgagg ctgaaaaatc ggctatttct gccttgagct ggttaaagcc gcaacaaatt 1080

ttggatgtaa agggcgattg ggcatggcgg cggcctgatc tcagacccgg gggatgggcc 1140

tttcaatata gaaatgacta ttatcccgat gtcgatgata cggctgttgt gactatggcg 1200

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gccatggaat ggaccattgg gatgcaaagc gataatggcg gttggggcgc tttcgatgcc 1320

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gcattgaatg tggccgcttt accccatgat catttagctg ttcagaaagc tgtggcttgg 1620

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gattatagcg gatacgagcc gatggattcg acggcttccc aaacagcatg ggctttattg 1740

ggcttgatgg ctgttgggga agctaattcc gaggccgtga caaagggtat aaactggttg 1800

gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggtttt 1860

ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 109
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 109

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1 5 10 15

Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu

```
    50                  55                  60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Arg Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270
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Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Thr Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
```

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                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Tyr Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
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<210> 110
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<220>
<221> misc_feature
<222> (418)..(420)
<223> ngn is agr or cgn

<220>
<221> misc_feature
<222> (1350)..(1350)
<223> n is a, c, g, or t

<400> 110
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attatccaaa aggccacccg tgccttgctt gagaagcagc agcaggatgg ccattgggtt 120

tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcggatggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtctt tacacgtngn 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

ttgaatggtg aagacgggtt gggtgctatt tatccggcga ttgccaatag cgtcatgatg 840

tatgatgcct tgggatatcc cgaaaaccat ccagaaagag ccattgcccg tcgggctgtc 900

gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

ccttgtttat ccccgatttg ggataccgct ttggttgccc atgccatgtt ggaagtcgga 1020

ggcgatgagg ctgaaaaatc ggctatttct gccttgagct ggttaaagcc gcaacaaatt 1080

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gcattgaatg tggccgcttt accccatgat catttagctg ttcagaaagc tgtggcttgg 1620

ctgaaaacta ttcaaaatga agatggtggt tggggtgaaa attgcgatag ctatgccctt 1680

gattatagcg gatacgagcc gatggattcg acggcttccc aaacagcatg ggctttattg 1740

ggcttgatgg ctgttgggga agctaattcc gaggccgtga caaagggtat aaactggttg 1800

gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggttay 1860

ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 111
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 111

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1 5 10 15

Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
50 55 60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65 70 75 80

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Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Leu Thr Arg Arg Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285
```

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Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Thr Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510
```

```
Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Tyr Pro Arg Val Phe
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
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<210> 112
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<220>
<221> misc_feature
<222> (409)..(411)

<223> ntn is ttr or ctn

<220>
<221> misc_feature
<222> (418)..(420)
<223> ngn is agr or cgn

<220>
<221> misc_feature
<222> (1350)..(1350)
<223> n is a, c, g, or t

<400> 112
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attatccaaa aggccacccg tgccttgctt gagaagcagc agcaggatgg ccattgggtt 120

tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg 180

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcggatggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtcnt nacacgtngn 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

ttgaatggtg aagacgggtt gggtgctatt tatccggcga ttgccaatag cgtcatgatg 840

tatgatgcct tgggatatcc cgaaaaccat ccagaaagag ccattgcccg tcgggctgtc 900

gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

ccttgtttat ccccgatttg ggataccgct ttggttgccc atgccatgtt ggaagtcgga 1020

ggcgatgagg ctgaaaaatc ggctatttct gccttgagct ggttaaagcc gcaacaaatt 1080

ttggatgtaa agggcgattg ggcatggcgg cggcctgatc tcagacccgg gggatgggcc 1140

tttcaatata gaaatgacta ttatcccgat gtcgatgata cggctgttgt gactatggcg 1200

atggatcgag ccgcaaaatt gtcggatctt cacgatgatt ttgaggaatc taaagcgcgt 1260

gccatggaat ggaccattgg gatgcaaagc gataatggcg gttggggcgc tttcgatgcc 1320

aataacagct atacttatct gaataatacn ccctttgctg atcatggcgc gttacttgat 1380

ccgccaacgg tcgatgtctc ggcacgctgc gtttcaatga tggcgcaagc cggtatctcg 1440

attacagatc ccaaaatgaa agcggcagtt gattatcttc tgaaagagca agaagaggat 1500

ggtagctggt tcgggcgttg gggtgtcaat tacatatatg gcacatggtc ggccttatgt 1560

gcattgaatg tggccgcttt accccatgat catttagctg ttcagaaagc tgtggcttgg 1620

ctgaaaacta ttcaaaatga agatggtggt tggggtgaaa attgcgatag ctatgccctt 1680

gattatagcg gatacgagcc gatggattcg acggcttccc aaacagcatg ggctttattg 1740

ggcttgatgg ctgttgggga agctaattcc gaggccgtga caaagggtat aaactggttg 1800

gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggttay 1860

ccccgtgttt tttatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 113
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 113

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65 70 75 80

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Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Tyr
    130                 135                 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285
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Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510
```

```
Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680
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<210> 114
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 114
atgactgtga ccagctcggc ctccgcgcgt gcgacgcgcg acccgggaaa ttatcagact 60

gccctgcaat cgacggtgcg cgcggcggcg gattggctga tcgccaacca gaagccggac 120

ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc 240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg 360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc 420

ttcacccgct actggctggc actgatcggc gaatggccgt gggagaagac accgaacatc 480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg 780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg tttcccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 115
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 115

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65 70 75 80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
85 90 95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
100 105 110

```
Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Tyr
    130                 135                 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320
```

```
Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540
```

```
Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560


Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575


Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590


Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605


Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620


Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640


Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655


Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670


Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680


<210>  116
<211>  2055
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic BjapSHC1 Derivative

<400>  116
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gccctgcaat cgacggtgcg cgcggcggcg gattggctga tcgccaacca gaagccggac    120

ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg    180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc    240
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gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg 360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc 420

ttcacccgct actggctggc actgatcggc gaatggccgt gggagaagac accgaacatc 480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg 780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg tttcccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 117
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 117

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65 70 75 80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
85 90 95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
100 105 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
115 120 125

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

```
Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350
```

```
Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575
```

```
Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680
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<210> 118
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<220>
<221> misc_feature
<222> (421)..(423)
<223> ntn is ttr or ctn

<400> 118

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gccctgcaat cgacggtgcg cgcggcggcg gattggctga tcgccaacca gaagccggac    120

ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg    180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc    240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc    300
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gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc 420

ntnacccgct actggctggc actgatcggc gaatggccgt gggagaagac accgaacatc 480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg 780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg tttcccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 119
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 119

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65 70 75 80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
85 90 95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
100 105 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
115 120 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Arg
130 135 140

```
Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365
```

```
Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575
```

```
Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680


<210>  120
<211>  2055
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic BjapSHC1 Derivative


<220>
<221>  misc_feature
<222>  (430)..(432)
<223>  ngn is agr or cgn

<400>  120
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gccctgcaat cgacggtgcg cgcggcggcg gattggctga tcgccaacca gaagccggac    120

ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg    180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc    240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc    300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg    360
```

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc 420

ttcacccgcn gntggctggc actgatcggc gaatggccgt gggagaagac accgaacatc 480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg 780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

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tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg tttcccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 121
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 121

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65 70 75 80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
85 90 95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
100 105 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
115 120 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Tyr
130 135 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145 150 155 160

```
Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365
```

```
Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590
```

```
Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680
```

<210> 122
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 122

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ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg    180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc    240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc    300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg    360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc    420

ttcacccgct actggctggc actgatcggc gaatggccgt gggagaagac accgaacatc    480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa    540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg    600
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ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg 780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

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gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

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cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 123
<211> 684

<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 123

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65 70 75 80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
85 90 95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
100 105 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
115 120 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Tyr
130 135 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145 150 155 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
165 170 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
180 185 190

```
Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400
```

```
Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Thr Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620
```

Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625 630 635 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
645 650 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
660 665 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
675 680

<210> 124
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

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ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc 240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg 360

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ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

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aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

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gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagacnccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg tttcccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 125
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 125

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
            20   25   30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
    50   55   60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65   70   75   80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85   90   95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100   105   110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115   120   125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Tyr
    130   135   140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145   150   155   160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165   170   175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180   185   190

```
Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415
```

```
Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys His Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620
```

Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625 630 635 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
645 650 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
660 665 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
675 680

<210> 126
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 126
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ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc 240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

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ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

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aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

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tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

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ccggaattca ccggcaccgg tttcccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 127
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 127

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

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Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
            20                  25                  30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
    50                  55                  60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65                  70                  75                  80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Tyr
    130                 135                 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220
```

```
Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445
```

```
Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Tyr Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655
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Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
660 665 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
675 680

<210> 128
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 128
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ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

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ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

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ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

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gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 129
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 129

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

```
Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
    50                  55                  60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65                  70                  75                  80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Arg
    130                 135                 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255
```

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Thr Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480
```

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

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
               565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
               645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680
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<210> 130
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<220>
<221> misc_feature
<222> (430)..(432)
<223> ngn is agr or cgn

<220>
<221> misc_feature
<222> (1377)..(1377)
<223> n is a, c, g, or t

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ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc 240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg 360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc 420

ttcacccgcn gntggctggc actgatcggc gaatggccgt gggagaagac accgaacatc 480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg 780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

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aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagacnccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

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gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg tttcccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 131
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 131

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
    50                  55                  60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65                  70                  75                  80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Arg
    130                 135                 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
```

```
               245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Thr Pro Phe Cys Asp Tyr
    450                 455                 460
```

```
Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
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675 680

<210> 132
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<220>
<221> misc_feature
<222> (430)..(432)
<223> ngn is agr or cgn

<220>
<221> misc_feature
<222> (1377)..(1377)
<223> n is a, c, g, or t

<400> 132
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gccctgcaat cgacggtgcg cgcggcggcg gattggctga tcgccaacca gaagccggac 120

ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc 240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg 360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc 420

ttcacccgcn gntggctggc actgatcggc gaatggccgt gggagaagac accgaacatc 480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

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aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

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aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagacnccg 1380

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ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

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tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg tttcccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 133
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 133

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

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Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
            20                  25                  30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
    50                  55                  60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65                  70                  75                  80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Tyr
    130                 135                 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240
```

```
Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445
```

```
Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Tyr Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670
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Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
675 680

<210> 134
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

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ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc 240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg 360

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ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

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ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

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aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

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tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

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gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

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cagagtcata gctag 2055

<210> 135
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 135

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

```
Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
    50                  55                  60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65                  70                  75                  80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

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

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

Phe Arg Pro Ala Ala Thr Ser Arg Val Leu Glu Trp Met Ile Arg His
            260                 265                 270
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Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480
```

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

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680
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<210> 136
<211> 2055

<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<220>
<221> misc_feature
<222> (421)..(423)
<223> ntn is ttr or ctn

<400> 136
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ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc 240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg 360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc 420

ntnacccgct actggctggc actgatcggc gaatggccgt gggagaagac accgaacatc 480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg 780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg tttcccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 137
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 137

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

```
Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65                  70                  75                  80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Tyr
    130                 135                 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

Phe Arg Pro Ala Ala Thr Ser Arg Val Leu Glu Trp Met Ile Arg His
            260                 265                 270
```

```
Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

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

```
Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys His Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Tyr Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680
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<210> 138
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 138
atgactgtga ccagctcggc ctccgcgcgt gcgacgcgcg acccgggaaa ttatcagact   60

gccctgcaat cgacggtgcg cgcggcggcg gattggctga tcgccaacca gaagccggac   120

ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg   180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc   240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc   300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg   360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc   420

ttcacccgct actggctggc actgatcggc gaatggccgt gggagaagac accgaacatc   480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa   540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg   600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac   660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag   720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg   780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc   840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc   900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat   960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc   1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg   1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg   1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac   1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc   1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag   1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg   1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc   1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac   1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcca ytggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg ttayccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 139
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 139

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65 70 75 80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
85 90 95

```
Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

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

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300
```

```
Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525
```

```
Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680


<210>  140
<211>  2055
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic BjapSHC1 Derivative


<220>
<221>  misc_feature
<222>  (421)..(423)
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<223> ntn is ttr or ctn

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gccctgcaat cgacggtgcg cgcggcggcg gattggctga tcgccaacca gaagccggac 120

ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc 240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg 360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc 420

ntnacccgct actggctggc actgatcggc gaatggccgt gggagaagac accgaacatc 480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

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gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

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gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

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gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 141
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 141

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65 70 75 80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
85 90 95

```
Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

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

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320
```

```
Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525
```

```
Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Tyr Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680
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<210> 142
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<220>
<221> misc_feature
<222> (421)..(423)
<223> ntn is ttr or ctn

<400> 142
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ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc 240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg 360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc 420

ntnacccgct actggctggc actgatcggc gaatggccgt gggagaagac accgaacatc 480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg 780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg ttayccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 143
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 143

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65 70 75 80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
85 90 95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
100 105 110

```
Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Leu Thr Arg Arg
    130                 135                 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320
```

```
Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Thr Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540
```

```
Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560


Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575


Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590


Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605


Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620


Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640


Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655


Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670


Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680


<210>  144
<211>  2055
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic BjapSHC1 Derivative


<220>
<221>  misc_feature
<222>  (421)..(423)
<223>  ntn is ttr or ctn

<220>
<221>  misc_feature
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<222> (430)..(432)
<223> ngn is agr or cgn

<220>
<221> misc_feature
<222> (1377)..(1377)
<223> n is a, c, g, or t

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gccctgcaat cgacggtgcg cgcggcggcg gattggctga tcgccaacca gaagccggac 120

ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc 240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg 360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc 420

ntnacccgcn gntggctggc actgatcggc gaatggccgt gggagaagac accgaacatc 480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg 600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac 660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg 780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagacnccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg tttcccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 145
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 145

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65 70 75 80

```
Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Arg
    130                 135                 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285
```

```
Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Thr Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510
```

```
Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Tyr Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680


<210>  146
<211>  2055
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic BjapSHC1 Derivative
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<220>
<221> misc_feature
<222> (430)..(432)
<223> ngn is agr or cgn

<220>
<221> misc_feature
<222> (1377)..(1377)
<223> n is a, c, g, or t

<400> 146
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gccctgcaat cgacggtgcg cgcggcggcg gattggctga tcgccaacca gaagccggac 120

ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg 180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc 240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc 300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg 360

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ttcacccgcn gntggctggc actgatcggc gaatggccgt gggagaagac accgaacatc 480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa 540

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gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagacnccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg ttayccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 147
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 147

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
20 25 30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
50 55 60

```
Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65                  70                  75                  80

Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95

Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Leu Thr Arg Arg
    130                 135                 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
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```
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Thr Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

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

```
Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Tyr Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680
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<210> 148
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

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<221> misc_feature
<222> (421)..(423)
<223> ntn is ttr or ctn

<220>
<221> misc_feature
<222> (430)..(432)
<223> ngn is agr or cgn

<220>
<221> misc_feature
<222> (1377)..(1377)
<223> n is a, c, g, or t

<400> 148
atgactgtga ccagctcggc ctccgcgcgt gcgacgcgcg acccgggaaa ttatcagact   60

gccctgcaat cgacggtgcg cgcggcggcg gattggctga tcgccaacca gaagccggac   120

ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg   180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc   240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc   300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg   360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc   420

ntnacccgcn gntggctggc actgatcggc gaatggccgt gggagaagac accgaacatc   480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa   540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg   600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac   660

gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag   720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg   780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc   840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc   900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat   960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc   1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagacnccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg ttayccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc cttcatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 149
<211> 657
<212> PRT
<213> Burkholderia ambifaria

<400> 149

Met Asn Asp Leu Thr Glu Met Ala Thr Leu Ser Ala Gly Thr Val Pro
1 5 10 15

Ala Gly Leu Asp Ala Ala Val Ala Ser Ala Thr Asp Ala Leu Leu Ala
20 25 30

Ala Gln Asn Ala Asp Gly His Trp Val Tyr Glu Leu Glu Ala Asp Ser
35 40 45

```
Thr Ile Pro Ala Glu Tyr Val Leu Leu Val His Tyr Leu Gly Glu Thr
    50                  55                  60

Pro Asn Leu Glu Leu Glu Gln Lys Ile Gly Arg Tyr Leu Arg Arg Val
65                  70                  75                  80

Gln Gln Ala Asp Gly Gly Trp Pro Leu Phe Thr Asp Gly Ala Pro Asn
                85                  90                  95

Ile Ser Ala Ser Val Lys Ala Tyr Phe Ala Leu Lys Val Ile Gly Asp
            100                 105                 110

Asp Glu Asn Ala Glu His Met Gln Arg Ala Arg Arg Ala Ile Gln Ala
        115                 120                 125

Met Gly Gly Ala Glu Met Ser Asn Val Phe Thr Arg Ile Gln Leu Ala
    130                 135                 140

Leu Tyr Gly Ala Ile Pro Trp Arg Ala Val Pro Met Met Pro Val Glu
145                 150                 155                 160

Ile Met Leu Leu Pro Gln Trp Phe Pro Phe His Leu Ser Lys Val Ser
                165                 170                 175

Tyr Trp Ala Arg Thr Val Ile Val Pro Leu Leu Val Leu Asn Ala Lys
            180                 185                 190

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

Val Asp Pro Pro Val Asn Ala Gly Leu Leu Pro Arg Gln Gly His Gln
    210                 215                 220

Ser Pro Gly Trp Phe Ala Phe Phe Arg Val Val Asp His Ala Leu Arg
225                 230                 235                 240

Ala Ala Asp Gly Leu Phe Pro Asn Tyr Thr Arg Glu Arg Ala Ile Arg
                245                 250                 255
```

```
Gln Ala Val Ser Phe Val Asp Glu Arg Leu Asn Gly Glu Asp Gly Leu
            260                 265                 270

Gly Ala Ile Tyr Pro Ala Met Ala Asn Ala Val Met Met Tyr Asp Val
        275                 280                 285

Leu Gly Tyr Ala Glu Asp His Pro Asn Arg Ala Ile Ala Arg Lys Ser
    290                 295                 300

Ile Glu Lys Leu Leu Val Val Gln Glu Asp Glu Ala Tyr Cys Gln Pro
305                 310                 315                 320

Cys Leu Ser Pro Val Trp Asp Thr Ser Leu Ala Ala His Ala Leu Leu
                325                 330                 335

Glu Thr Gly Asp Ala Arg Ala Glu Glu Ala Val Ile Arg Gly Leu Glu
            340                 345                 350

Trp Leu Arg Pro Leu Gln Ile Leu Asp Val Arg Gly Asp Trp Ile Ser
        355                 360                 365

Arg Arg Pro His Val Arg Pro Gly Gly Trp Ala Phe Gln Tyr Ala Asn
    370                 375                 380

Pro His Tyr Pro Asp Val Asp Asp Thr Ala Val Val Ala Val Ala Met
385                 390                 395                 400

Asp Arg Val Gln Lys Leu Lys His Asn Asp Ala Phe Arg Asp Ser Ile
                405                 410                 415

Ala Arg Ala Arg Glu Trp Val Val Gly Met Gln Ser Ser Asp Gly Gly
            420                 425                 430

Trp Gly Ala Phe Glu Pro Glu Asn Thr Gln Tyr Tyr Leu Asn Asn Ile
        435                 440                 445

Pro Phe Ser Asp His Gly Ala Leu Leu Asp Pro Pro Thr Ala Asp Val
    450                 455                 460

Ser Gly Arg Cys Leu Ser Met Leu Ala Gln Leu Gly Glu Thr Pro Leu
465                 470                 475                 480
```

Asn Ser Glu Pro Ala Arg Arg Ala Leu Asp Tyr Met Leu Lys Glu Gln
485 490 495

Glu Pro Asp Gly Ser Trp Tyr Gly Arg Trp Gly Met Asn Tyr Val Tyr
500 505 510

Gly Thr Trp Thr Ala Leu Cys Ala Leu Asn Ala Ala Gly Leu Thr Pro
515 520 525

Asp Asp Pro Arg Val Lys Arg Gly Ala Gln Trp Leu Leu Ser Ile Gln
530 535 540

Asn Lys Asp Gly Gly Trp Gly Glu Asp Gly Asp Ser Tyr Lys Leu Asn
545 550 555 560

Tyr Arg Gly Phe Glu Gln Ala Pro Ser Thr Ala Ser Gln Thr Ala Trp
565 570 575

Ala Leu Leu Gly Leu Met Ala Ala Gly Glu Val Asn Asn Pro Ala Val
580 585 590

Ala Arg Gly Val Glu Tyr Leu Ile Ala Glu Gln Lys Glu His Gly Leu
595 600 605

Trp Asp Glu Thr Arg Phe Thr Ala Thr Gly Phe Pro Arg Val Phe Tyr
610 615 620

Leu Arg Tyr His Gly Tyr Arg Lys Phe Phe Pro Leu Trp Ala Leu Ala
625 630 635 640

Arg Tyr Arg Asn Leu Lys Arg Asn Asn Ala Thr Arg Val Thr Phe Gly
645 650 655

Leu

<210> 150

<400> 150
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<210> 151
<211> 682
<212> PRT
<213> Burkholderia ambifaria

<400> 151

Met Ile Arg Arg Met Asn Lys Ser Gly Pro Ser Pro Trp Ser Ala Leu
1 5 10 15

Asp Ala Ala Ile Ala Arg Gly Arg Asp Ala Leu Met Arg Leu Gln Gln
20 25 30

Pro Asp Gly Ser Trp Cys Phe Glu Leu Glu Ser Asp Ala Thr Ile Thr
35 40 45

Ala Glu Tyr Ile Leu Met Met His Phe Met Asp Lys Ile Asp Asp Ala
50 55 60

Arg Gln Glu Lys Met Ala Arg Tyr Leu Arg Ala Ile Gln Arg Leu Asp
65 70 75 80

Thr His Gly Gly Trp Asp Leu Tyr Val Asp Gly Asp Pro Asp Val Ser
85 90 95

Cys Ser Val Lys Ala Tyr Phe Ala Leu Lys Ala Ala Gly Asp Ser Glu
100 105 110

His Ala Pro His Met Val Arg Ala Arg Asp Ala Ile Leu Glu Leu Gly
115 120 125

Gly Ala Ala Arg Ser Asn Val Phe Thr Arg Ile Leu Leu Ala Thr Phe
130 135 140

Gly Gln Val Pro Trp Arg Ala Thr Pro Phe Met Pro Ile Glu Phe Val
145 150 155 160

Leu Phe Pro Lys Trp Val Pro Ile Ser Met Tyr Lys Val Ala Tyr Trp
165 170 175

Ala Arg Thr Thr Met Val Pro Leu Leu Val Leu Cys Ser Leu Lys Ala
180 185 190

```
Arg Ala Arg Asn Pro Arg Asn Ile Ala Ile Pro Glu Leu Phe Val Thr
        195                 200                 205

Pro Pro Asp Gln Glu Arg Gln Tyr Phe Pro Pro Ala Arg Gly Met Arg
    210                 215                 220

Arg Ala Phe Leu Ala Leu Asp Arg Val Val Arg His Val Glu Pro Leu
225                 230                 235                 240

Leu Pro Lys Arg Leu Arg Gln Arg Ala Ile Arg His Ala Gln Ala Trp
                245                 250                 255

Cys Ala Glu Arg Met Asn Gly Glu Asp Gly Leu Gly Gly Ile Phe Pro
            260                 265                 270

Pro Ile Val Tyr Ser Tyr Gln Met Met Asp Val Leu Gly Tyr Pro Asp
        275                 280                 285

Asp His Pro Leu Arg Arg Asp Cys Glu Asn Ala Leu Glu Lys Leu Leu
    290                 295                 300

Val Thr Arg Pro Asp Gly Ser Met Tyr Cys Gln Pro Cys Leu Ser Pro
305                 310                 315                 320

Val Trp Asp Thr Ala Trp Ser Thr Met Ala Leu Glu Gln Ala Arg Gly
                325                 330                 335

Val Ala Val Pro Glu Ala Gly Ala Pro Ala Ser Ala Leu Asp Glu Leu
            340                 345                 350

Asp Ala Arg Ile Ala Arg Ala Tyr Asp Trp Leu Ala Glu Arg Gln Val
        355                 360                 365

Asn Asp Leu Arg Gly Asp Trp Ile Glu Asn Ala Pro Ala Asp Thr Gln
    370                 375                 380

Pro Gly Gly Trp Ala Phe Gln Tyr Ala Asn Pro Tyr Tyr Pro Asp Ile
385                 390                 395                 400
```

```
Asp Asp Ser Ala Val Val Thr Ala Met Leu Asp Arg Arg Gly Arg Thr
                405                 410                 415

His Arg Asn Ala Asp Gly Ser His Pro Tyr Ala Ala Arg Val Ala Arg
            420                 425                 430

Ala Leu Asp Trp Met Arg Gly Leu Gln Ser Arg Asn Gly Gly Phe Ala
        435                 440                 445

Ala Phe Asp Ala Asp Cys Asp Arg Leu Tyr Leu Asn Ala Ile Pro Phe
    450                 455                 460

Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Glu Asp Val Ser Gly
465                 470                 475                 480

Arg Val Leu Leu Cys Phe Gly Val Thr Lys Arg Ala Asp Asp Arg Ala
                485                 490                 495

Ser Leu Ala Arg Ala Ile Asp Tyr Val Lys Arg Thr Gln Gln Pro Asp
            500                 505                 510

Gly Ser Trp Trp Gly Arg Trp Gly Thr Asn Tyr Leu Tyr Gly Thr Trp
        515                 520                 525

Ser Val Leu Ala Gly Leu Ala Leu Ala Gly Glu Asp Pro Ser Gln Pro
    530                 535                 540

Tyr Ile Ala Arg Ala Leu Ala Trp Leu Arg Ala Arg Gln His Ala Asp
545                 550                 555                 560

Gly Gly Trp Gly Glu Thr Asn Asp Ser Tyr Ile Asp Pro Ala Leu Ala
                565                 570                 575

Gly Thr Asn Ala Gly Glu Ser Thr Ser Asn Cys Thr Ala Trp Ala Leu
            580                 585                 590

Leu Ala Gln Met Ala Phe Gly Asp Gly Glu Ser Glu Ser Val Arg Arg
        595                 600                 605

Gly Ile Ala Tyr Leu Gln Ser Val Gln Gln Asp Asp Gly Phe Trp Trp
    610                 615                 620
```

```
His Arg Ser His Asn Ala Pro Gly Phe Pro Arg Ile Phe Tyr Leu Lys
625                 630                 635                 640


Tyr His Gly Tyr Thr Ala Tyr Phe Pro Leu Trp Ala Leu Ala Arg Tyr
                645                 650                 655


Arg Arg Leu Ala Gly Gly Val Ser Ala Ala Gly Ala His Ala Val Pro
            660                 665                 670


Ala Ser Thr Gly Ala Asp Ala Ala Leu Ala
        675                 680


<210>  152

<400>  152
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<210>  153
<211>  617
<212>  PRT
<213>  Bacillus anthracis

<400>  153

Met Leu Leu Tyr Glu Lys Ala His Glu Glu Ile Val Arg Arg Ala Thr
1               5                   10                  15


Ala Leu Gln Thr Met Gln Trp Gln Asp Gly Thr Trp Arg Phe Cys Phe
            20                  25                  30


Glu Gly Ala Pro Leu Thr Asp Cys His Met Ile Phe Leu Leu Lys Leu
        35                  40                  45


Leu Gly Arg Asp Lys Glu Ile Glu Pro Phe Val Glu Arg Val Ala Ser
    50                  55                  60


Leu Gln Thr Asn Glu Gly Thr Trp Lys Leu His Glu Asp Glu Val Gly
65                  70                  75                  80


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

```
Lys Lys Tyr Thr Lys Glu Asp Ala Asn Met Lys Arg Ala Glu Asn Phe
            100                 105                 110

Ile Gln Glu Arg Gly Gly Val Ala Arg Ala His Phe Met Thr Lys Phe
        115                 120                 125

Leu Leu Ala Ile His Gly Glu Tyr Glu Tyr Pro Ser Leu Phe His Leu
    130                 135                 140

Pro Thr Pro Ile Met Phe Leu Gln Asn Asp Ser Pro Phe Ser Ile Phe
145                 150                 155                 160

Glu Leu Ser Ser Ser Ala Arg Ile His Leu Ile Pro Met Met Leu Cys
                165                 170                 175

Leu Asn Lys Arg Phe Arg Val Gly Lys Lys Leu Leu Pro Asn Leu Asn
            180                 185                 190

His Ile Ala Gly Gly Gly Gly Glu Trp Phe Arg Glu Asp Arg Ser Pro
        195                 200                 205

Val Phe Gln Thr Leu Leu Ser Asp Val Lys Gln Ile Ile Ser Tyr Pro
    210                 215                 220

Leu Ser Leu His His Lys Gly Tyr Glu Glu Ile Glu Arg Phe Met Lys
225                 230                 235                 240

Glu Arg Ile Asp Glu Asn Gly Thr Leu Tyr Ser Tyr Ala Thr Ala Ser
                245                 250                 255

Phe Tyr Met Ile Tyr Ala Leu Leu Ala Leu Gly His Ser Leu Gln Ser
            260                 265                 270

Ser Met Ile Gln Lys Ala Ile Ala Gly Ile Thr Ser Tyr Ile Trp Lys
        275                 280                 285

Met Glu Arg Gly Asn His Leu Gln Asn Ser Pro Ser Thr Val Trp Asp
    290                 295                 300

Thr Ala Leu Leu Ser Tyr Ala Leu Gln Glu Ala Gln Val Ser Lys Asp
305                 310                 315                 320
```

```
Asn Lys Met Ile Gln Asn Ala Thr Ala Tyr Leu Leu Lys Lys Gln His
                325                 330                 335

Thr Lys Lys Ala Asp Trp Ser Val His Ala Pro Ala Leu Thr Pro Gly
            340                 345                 350

Gly Trp Gly Phe Ser Asp Val Asn Thr Thr Ile Pro Asp Ile Asp Asp
        355                 360                 365

Thr Thr Ala Val Leu Arg Ala Leu Ala Arg Ser Arg Gly Asn Lys Asn
    370                 375                 380

Ile Asp Asn Ala Trp Lys Lys Gly Gly Asn Trp Ile Lys Gly Leu Gln
385                 390                 395                 400

Asn Asn Asp Gly Gly Trp Gly Ala Phe Glu Lys Gly Val Thr Ser Lys
                405                 410                 415

Leu Leu Ala Lys Leu Pro Ile Glu Asn Ala Ser Asp Met Ile Thr Asp
            420                 425                 430

Pro Ser Thr Pro Asp Ile Thr Gly Arg Val Leu Glu Phe Phe Gly Thr
        435                 440                 445

Tyr Ala Gln Asn Glu Leu Pro Glu Lys Gln Ile Gln Arg Ala Ile Asn
    450                 455                 460

Trp Leu Met Asn Val Gln Glu Glu Asn Gly Ser Trp Tyr Gly Lys Trp
465                 470                 475                 480

Gly Ile Cys Tyr Leu Tyr Gly Thr Trp Ala Val Met Thr Gly Leu Arg
                485                 490                 495

Ser Leu Gly Ile Pro Ser Ser Asn Pro Ser Leu Thr Arg Ala Ala Ser
            500                 505                 510

Trp Leu Glu His Ile Gln His Glu Asp Gly Gly Trp Gly Glu Ser Cys
        515                 520                 525
```

```
His Ser Ser Val Glu Lys Arg Phe Val Thr Leu Pro Phe Ser Thr Pro
    530                 535                 540

Ser Gln Thr Ala Trp Ala Leu Asp Ala Leu Ile Ser Tyr Tyr Asp Thr
545                 550                 555                 560

Glu Thr Pro Ala Ile Arg Lys Gly Val Ser Tyr Leu Leu Ser Asn Pro
                565                 570                 575

Tyr Val Asn Glu Arg Tyr Pro Thr Gly Thr Gly Leu Pro Gly Ala Phe
            580                 585                 590

Tyr Ile Arg Tyr His Ser Tyr Ala His Ile Tyr Pro Leu Leu Thr Leu
        595                 600                 605

Ala His Tyr Ile Lys Lys Tyr Arg Lys
    610                 615
```

<210> 154
<211> 1854
<212> DNA
<213> Bacillus anthracis

<400> 154

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atgcaatggc aagatggtac gtggcgattt tgttttgaag gagctccatt aacagattgc    120

catatgattt ttttattaaa attattaggt agagataaag agatagaacc gttcgtagaa    180

agagtagcat cactccaaac aaatgaagga acatggaaat tgcacgaaga tgaagtagga    240

ggtaatttat cagctacaat tcaatcttat gccgccttac ttgcatcgaa aaaatataca    300

aaagaagatg cgaatatgaa acgagcagaa aattttattc aggaacgcgg tggtgtggcg    360

cgtgctcatt ttatgacgaa gtttttatta gcaattcatg gagaatatga atatccttca    420

ctctttcatt taccaacacc aatcatgttt ttacagaatg attccccctt tagtatattt    480

gaattaagta gctcagcacg tattcattta attccgatga tgctatgttt aaataaaaga    540

tttcgagtag ggaaaaagtt attaccaaat ttaaatcaca ttgcgggcgg aggcggagaa    600

tggtttcggg aggatcggtc tccagttttt caaacgttat taagtgatgt aaaacaaatt    660

atatcgtatc cactttcgtt acatcataaa ggatatgagg aaatagaacg ttttatgaaa    720
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gagcgtattg atgaaaatgg aacgttatat agttacgcaa ctgcctcgtt ttatatgatt 780

tatgctttac ttgcgttagg gcattctctt caatcatcaa tgattcaaaa ggctatagct 840

gggataacat cttatatatg gaagatggaa agagggaatc atttgcaaaa ctctccttca 900

accgtgtggg atacagcttt attaagctat gcgttacaag aggctcaagt ttcaaaggat 960

aataagatga ttcaaaatgc aacagcgtat ttattaaaaa aacagcatac aaaaaaagct 1020

gattggagcg tacatgctcc ggcgcttact cctggcggtt ggggtttttc ggatgtgaat 1080

acgacaattc cagatataga tgatacaaca gctgtgctaa gggcattggc acgaagtaga 1140

ggaaacaaaa atatagataa tgcttggaag aaaggggggca attggattaa aggattacaa 1200

aataatgatg gtggctgggg agcatttgaa aaaggtgtga cgagcaaatt attagcaaaa 1260

ttaccaatcg aaaacgcaag tgatatgatt acagatcctt ctacgccaga tattacgggg 1320

agagtgttag agtttttcgg gacgtatgca caaaacgaat tgcctgagaa acagatacaa 1380

agggcaataa attggttaat gaatgtacaa gaggaaaatg gatcatggta tgggaaatgg 1440

gggatttgtt atctatatgg tacgtgggct gttatgactg gtttacggtc actcggaatt 1500

ccgtctagca atccttcatt gacacgagca gcttcatggc ttgaacatat acagcatgaa 1560

gatggtggtt ggggagaatc atgccacagt agtgtggaga aaaggttcgt tactttacca 1620

tttagtacac catcccaaac tgcatgggcg ttagatgctc tcatttctta ctatgataca 1680

gaaacgccag ctattcgaaa aggtgtttca tatttgcttt cgaatcctta tgtgaatgaa 1740

agatatccta ctggaacagg tttaccaggt gcgttttata ttaggtatca tagctatgcc 1800

catatatatc cactacttac tttggcacat tatataaaaa aatatagaaa ataa 1854

<210> 155
<211> 720
<212> PRT
<213> Frankia alni

<400> 155

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

Ala Met Gly Arg Pro Asp Leu Val Thr Thr Thr Gly Gly Ala Glu Ile
20 25 30

```
Pro Phe Val Leu Val Ala Ala Thr Ala Ser Thr Val Gly Val Ala Leu
        35                  40                  45

Ala Leu Arg Arg Pro Arg His Pro Val Gly Trp Leu Phe Leu Ala Leu
    50                  55                  60

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

Gly Ala Val Ala Arg Pro Gly Arg Leu Pro Ala Ala Asp Leu Val Ala
                85                  90                  95

Ile Tyr Ala Asp Ala Gly Phe Ile Pro Trp Leu Val Leu Val Ala Leu
            100                 105                 110

Ile Leu His Leu Thr Pro Thr Gly Arg Pro Leu Ser Ala Arg Trp Gly
        115                 120                 125

Arg Ile Ala Leu Ala Thr Ala Val Ala Gly Gly Leu Trp Leu Leu Val
    130                 135                 140

Gly Leu Val Thr Thr Glu Thr Met Gln Pro Pro Phe Gln Ser Val Thr
145                 150                 155                 160

Asn Pro Leu Leu Ile Gly Gly Pro Leu Gly Pro Leu Leu Val Ala Arg
                165                 170                 175

Arg Val Leu Gly Leu Ala Thr Gly Ala Gly Val Val Leu Ala Ala Val
            180                 185                 190

Ser Leu Ile Val Arg Phe Arg Arg Ser Val Asp Val Glu Arg Arg Gln
        195                 200                 205

Leu Leu Trp Val Ala Val Ala Ala Val Pro Leu Pro Val Leu Met Ala
    210                 215                 220

Ala Ser Phe Ala Ala Ser Tyr Ala Gly Asn Asn Thr Ala Ala Gly Leu
225                 230                 235                 240

Ala Ala Ala Thr Leu Ile Gly Leu Leu Ala Ile Gly Ala Gly Leu Ala
                245                 250                 255
```

```
Ile Gly Gln Tyr His Leu Tyr Asp Val Glu Glu Ile Leu Ser Arg Ala
            260                 265                 270

Val Thr Tyr Leu Leu Val Ser Gly Leu Leu Ala Ala Ser Tyr Ala Thr
        275                 280                 285

Val Val Ile Val Val Gly Gln Ser Leu Ala Gly Arg Thr Gly Arg Ser
    290                 295                 300

Gln Ile Ser Ala Val Leu Ala Thr Leu Ala Ala Val Ala Val Thr Ala
305                 310                 315                 320

Pro Ala Tyr Arg Lys Ile Gln Glu Gly Val Asp Arg Arg Phe Ser Arg
                325                 330                 335

Arg Arg Phe Glu Thr Leu Gln Val Ile Arg Arg Tyr Leu Arg Asp Pro
            340                 345                 350

Asp Pro Asp Val Ala Val Glu Glu Val Leu Arg Arg Ala Leu Gly Asp
        355                 360                 365

Pro Thr Leu Ala Val Ala Tyr Leu Val Asp Asp Arg Arg Gln Trp Val
    370                 375                 380

Ser Ala Asp Gly Gln Pro Ala Asn Pro Gly Asn Ser Phe Met Ala Ala
385                 390                 395                 400

Val Glu Val Tyr Arg Arg Gly Arg Pro Ile Ala Arg Val Thr Phe Asp
                405                 410                 415

Arg Gly Arg Ala Gln Pro Gly Leu Val Arg Ala Ala Ala Thr Ala Ala
            420                 425                 430

Thr Ala Glu Leu Asp Asn Ala Gly Leu Arg Ala Ala Val Ala Leu Gln
        435                 440                 445

Leu Val Glu Val Arg Gln Ser Arg Thr Arg Ile Ala Ala Ala Gln Phe
    450                 455                 460
```

```
Ala Glu Arg Arg Thr Ile Glu Arg Asn Leu His Asp Gly Ala Gln Gln
465                 470                 475                 480

Arg Leu Leu Ala Leu Ala Leu Gln Leu Arg Ala Val Gln Leu Gly Gly
                485                 490                 495

Asp Glu Ala Ser Leu Arg Gln Ala Ile Ser Thr Gly Ile Asp Gln Leu
            500                 505                 510

Gln Ala Ala Val Val Glu Leu Arg Glu Leu Ala Asn Gly Leu His Pro
        515                 520                 525

Ala Val Leu Ala Asp Gly Gly Leu Ala Ala Ala Leu Asp Asp Val Ala
    530                 535                 540

Ala Arg Thr Pro Val Pro Ile Lys Ile Ser Ala Pro Asp Arg Arg Tyr
545                 550                 555                 560

Pro Pro Asp Leu Glu Ala Ala Ala Trp Phe Ile Ala Cys Glu Ala Met
                565                 570                 575

Ala Asn Ala Val Lys His Ala His Pro Thr Thr Ile Ala Val Asp Val
            580                 585                 590

Ser Ala Pro Asp Gly Gln Leu Ile Val Glu Val Arg Asp Asp Gly Ile
        595                 600                 605

Gly Gly Ala Gln Pro Ser Gly Pro Gly Leu Arg Gly Ile Ala Asp Arg
    610                 615                 620

Ala Glu Ala Phe Gly Gly Ser Leu Thr Val His Thr Asp Pro Gly Thr
625                 630                 635                 640

Gly Thr Thr Ile Arg Ala Leu Leu His Arg Arg Ser Pro Leu Ser Ser
                645                 650                 655

Gly Arg Arg Ser Val Met Ile Glu Gly Cys Val Asp Val Val Ala Val
            660                 665                 670

Arg Arg Phe Arg Cys Arg Ser Ser Arg Gly Ser Gly Ser Arg Arg Arg
        675                 680                 685
```

```
Arg Ser Ser Trp Arg Cys Gly Gly Ile Cys Gly Ser Arg Cys Arg Thr
    690                 695                 700


Gly Met Ser Arg Ser Cys Ser Arg Asn Ala Ala Ser Lys Leu Ile Thr
705                 710                 715                 720


<210>  156

<400>  156
000

<210>  157
<211>  685
<212>  PRT
<213>  Rhodopseudomonas palent

<400>  157

Met Asp Ser Ile Leu Ala Pro Arg Ala Asp Ala Pro Arg Asn Ile Asp
1               5                   10                  15


Gly Ala Leu Arg Glu Ser Val Gln Gln Ala Ala Asp Trp Leu Val Ala
            20                  25                  30


Asn Gln Lys Pro Asp Gly His Trp Val Gly Arg Ala Glu Thr Asn Ala
        35                  40                  45


Thr Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu
    50                  55                  60


Asp His Pro Leu Arg Val Arg Leu Gly Arg Ala Leu Leu Asp Thr Gln
65                  70                  75                  80


Arg Pro Asp Gly Ala Trp His Val Phe Tyr Gly Ala Pro Asn Gly Asp
                85                  90                  95


Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly His
            100                 105                 110


Arg Asp Asp Glu Glu Pro Leu Arg Lys Ala Arg Asp Trp Ile Leu Ser
        115                 120                 125
```

```
Lys Gly Gly Leu Ala Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala
    130                 135                 140

Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile Leu Pro Glu
145                 150                 155                 160

Val Ile Trp Leu Pro Thr Trp Phe Pro Phe Ser Ile Tyr Asn Phe Ala
                165                 170                 175

Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu Ser Ala His
            180                 185                 190

Arg Pro Ser Arg Pro Leu Ala Pro Gln Asp Arg Leu Asp Ala Leu Phe
        195                 200                 205

Pro Gln Gly Arg Asp Ser Phe Asn Tyr Asp Leu Pro Ala Arg Leu Gly
    210                 215                 220

Ala Gly Val Trp Asp Val Ile Phe Arg Lys Ile Asp Thr Ile Leu His
225                 230                 235                 240

Arg Leu Gln Asp Trp Gly Ala Arg Arg Gly Pro His Gly Ile Met Arg
                245                 250                 255

Arg Gly Ala Ile Asp His Val Leu Gln Trp Ile Ile Arg His Gln Asp
            260                 265                 270

Tyr Asp Gly Ser Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr Gly Leu
        275                 280                 285

Met Ala Leu His Thr Glu Gly Tyr Ala Met Thr His Pro Val Met Ala
    290                 295                 300

Lys Ala Leu Asp Ala Leu Asn Glu Pro Gly Trp Arg Ile Asp Ile Gly
305                 310                 315                 320

Asp Ala Thr Phe Ile Gln Ala Thr Asn Ser Pro Val Trp Asp Thr Met
                325                 330                 335

Leu Ser Leu Leu Ala Phe Asp Asp Ala Gly Leu Gly Glu Arg Tyr Pro
            340                 345                 350
```

```
Glu Gln Val Glu Arg Ala Val Arg Trp Val Leu Lys Arg Gln Val Leu
        355                 360                 365

Val Pro Gly Asp Trp Ser Val Lys Leu Pro Asp Val Lys Pro Gly Gly
    370                 375                 380

Trp Ala Phe Glu Tyr Ala Asn Asn Phe Tyr Pro Asp Thr Asp Asp Thr
385                 390                 395                 400

Ser Val Ala Leu Met Ala Leu Ala Pro Phe Arg His Asp Pro Lys Trp
                405                 410                 415

Gln Ala Glu Gly Ile Glu Asp Ala Ile Gln Arg Gly Ile Asp Trp Leu
            420                 425                 430

Val Ala Met Gln Cys Lys Glu Gly Gly Trp Gly Ala Phe Asp Lys Asp
        435                 440                 445

Asn Asp Lys Lys Ile Leu Ala Lys Ile Pro Phe Cys Asp Phe Gly Glu
    450                 455                 460

Ala Leu Asp Pro Pro Ser Ala Asp Val Thr Ala His Ile Ile Glu Ala
465                 470                 475                 480

Phe Ala Lys Val Gly Leu Asp Arg Asn His Pro Ser Ile Val Arg Ala
                485                 490                 495

Leu Asp Tyr Leu Lys Arg Glu Gln Glu Pro Glu Gly Pro Trp Phe Gly
            500                 505                 510

Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu Pro Ala
        515                 520                 525

Leu Ala Ala Ile Gly Glu Asp Met Arg Gln Pro Tyr Ile Ala Arg Ala
    530                 535                 540

Cys Asp Trp Leu Ile Ala Arg Gln Gln Ala Asn Gly Gly Trp Gly Glu
545                 550                 555                 560
```

Ser Cys Val Ser Tyr Met Asp Ala Lys Gln Ala Gly Glu Gly Thr Ala
565 570 575

Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Ile Ala Ala Asp
580 585 590

Arg Pro Gln Asp Arg Asp Ala Ile Glu Arg Gly Cys Leu Tyr Leu Thr
595 600 605

Glu Thr Gln Arg Asp Gly Thr Trp Gln Glu Val His Tyr Thr Gly Thr
610 615 620

Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn Asp Pro
625 630 635 640

Leu Leu Ser Lys Arg Leu Met Gln Gly Pro Glu Leu Ser Arg Ser Phe
645 650 655

Met Leu Arg Tyr Asp Leu Tyr Arg His Tyr Phe Pro Met Met Ala Ile
660 665 670

Gly Arg Val Leu Arg Gln Arg Gly Asp Arg Ser Gly His
675 680 685

<210> 158

<400> 158
000

<210> 159
<211> 679
<212> PRT
<213> Streptomyces coelicolor

<400> 159

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

Ala Ala Ser Ala Ser Asp Thr Asp Ile Thr Ile Pro Ala Ala Ala Ala
20 25 30

Gly Val Pro Glu Ala Ala Ala Arg Ala Thr Arg Arg Ala Thr Asp Phe
35 40 45

```
Leu Leu Ala Lys Gln Asp Ala Glu Gly Trp Trp Lys Gly Asp Leu Glu
    50                  55                  60

Thr Asn Val Thr Met Asp Ala Glu Asp Leu Leu Leu Arg Gln Phe Leu
65                  70                  75                  80

Gly Ile Gln Asp Glu Glu Thr Thr Arg Ala Ala Ala Leu Phe Ile Arg
                85                  90                  95

Gly Glu Gln Arg Glu Asp Gly Thr Trp Ala Thr Phe Tyr Gly Gly Pro
            100                 105                 110

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

Gly Asp Ser Pro Glu Ala Pro His Met Ala Arg Ala Ala Glu Trp Ile
    130                 135                 140

Arg Ser Arg Gly Gly Ile Ala Ser Ala Arg Val Phe Thr Arg Ile Trp
145                 150                 155                 160

Leu Ala Leu Phe Gly Trp Trp Lys Trp Asp Asp Leu Pro Glu Leu Pro
                165                 170                 175

Pro Glu Leu Ile Tyr Phe Pro Thr Trp Val Pro Leu Asn Ile Tyr Asp
            180                 185                 190

Phe Gly Cys Trp Ala Arg Gln Thr Ile Val Pro Leu Thr Ile Val Ser
        195                 200                 205

Ala Lys Arg Pro Val Arg Pro Ala Pro Phe Pro Leu Asp Glu Leu His
    210                 215                 220

Thr Asp Pro Ala Arg Pro Asn Pro Pro Arg Pro Leu Ala Pro Val Ala
225                 230                 235                 240

Ser Trp Asp Gly Ala Phe Gln Arg Ile Asp Lys Ala Leu His Ala Tyr
                245                 250                 255
```

```
Arg Lys Val Ala Pro Arg Arg Leu Arg Arg Ala Ala Met Asn Ser Ala
            260                 265                 270

Ala Arg Trp Ile Ile Glu Arg Gln Glu Asn Asp Gly Cys Trp Gly Gly
        275                 280                 285

Ile Gln Pro Pro Ala Val Tyr Ser Val Ile Ala Leu Tyr Leu Leu Gly
    290                 295                 300

Tyr Asp Leu Glu His Pro Val Met Arg Ala Gly Leu Glu Ser Leu Asp
305                 310                 315                 320

Arg Phe Ala Val Trp Arg Glu Asp Gly Ala Arg Met Ile Glu Ala Cys
                325                 330                 335

Gln Ser Pro Val Trp Asp Thr Cys Leu Ala Thr Ile Ala Leu Ala Asp
            340                 345                 350

Ala Gly Val Pro Glu Asp His Pro Gln Leu Val Lys Ala Ser Asp Trp
        355                 360                 365

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

Pro Gly Pro Pro Gly Gly Trp Ala Phe Glu Phe His Asn Asp Asn Tyr
385                 390                 395                 400

Pro Asp Ile Asp Asp Thr Ala Glu Val Val Leu Ala Leu Arg Arg Val
                405                 410                 415

Arg His His Asp Pro Glu Arg Val Glu Lys Ala Ile Gly Arg Gly Val
            420                 425                 430

Arg Trp Asn Leu Gly Met Gln Ser Lys Asn Gly Ala Trp Gly Ala Phe
        435                 440                 445

Asp Val Asp Asn Thr Ser Ala Phe Pro Asn Arg Leu Pro Phe Cys Asp
    450                 455                 460

Phe Gly Glu Val Ile Asp Pro Pro Ser Ala Asp Val Thr Ala His Val
465                 470                 475                 480
```

```
Val Glu Met Leu Ala Val Glu Gly Leu Ala His Asp Pro Arg Thr Arg
                485                 490                 495

Arg Gly Ile Gln Trp Leu Leu Asp Ala Gln Glu Thr Asp Gly Ser Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ser Val Ile
        515                 520                 525

Pro Ala Leu Thr Ala Ala Gly Leu Pro Thr Ser His Pro Ala Ile Arg
    530                 535                 540

Arg Ala Val Arg Trp Leu Glu Ser Val Gln Asn Glu Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Asp Leu Arg Ser Tyr Arg Tyr Val Arg Glu Trp Ser Gly Arg
                565                 570                 575

Gly Ala Ser Thr Ala Ser Gln Thr Gly Trp Ala Leu Met Ala Leu Leu
            580                 585                 590

Ala Ala Gly Glu Arg Asp Ser Lys Ala Val Glu Arg Gly Val Ala Trp
        595                 600                 605

Leu Ala Ala Thr Gln Arg Glu Asp Gly Ser Trp Asp Glu Pro Tyr Phe
    610                 615                 620

Thr Gly Thr Gly Phe Pro Trp Asp Phe Ser Ile Asn Tyr Asn Leu Tyr
625                 630                 635                 640

Arg Gln Val Phe Pro Leu Thr Ala Leu Gly Arg Tyr Val His Gly Glu
                645                 650                 655

Pro Phe Ala Lys Lys Pro Arg Ala Ala Asp Ala Pro Ala Glu Ala Ala
            660                 665                 670

Pro Ala Glu Val Lys Gly Ser
        675
```

<210> 160

<400> 160
000

<210> 161
<211> 725
<212> PRT
<213> Zymomonas mobilis

<400> 161

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
115 120 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
130 135 140

Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145 150 155 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
165 170 175

```
Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380
```

```
Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605
```

```
Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720

Ile Asp Leu Asn Asn
                725
```

<210> 162
<211> 2178
<212> DNA
<213> Zymomonas mobilis

<400> 162

```
atgggtattg acagaatgaa tagcttaagt cgcttgttaa tgaagaagat tttcggggct     60

gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga    120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg    180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc    240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg    300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt    360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat    420
```

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

```
gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtttatgctg   2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg   2160

attgatttga ataattga                                                 2178
```

<210> 163
<211> 725
<212> PRT
<213> Zymomonas mobilis

<400> 163

```
Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1               5                   10                  15


Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
            20                  25                  30


Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
        35                  40                  45


Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
    50                  55                  60


Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65                  70                  75                  80


Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
                85                  90                  95


Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
            100                 105                 110


Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
        115                 120                 125


Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
    130                 135                 140


Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160
```

```
Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365

Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380
```

```
Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590
```

```
Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720

Ile Asp Leu Asn Asn
                725
```

<210> 164
<211> 2178
<212> DNA
<213> Zymomonas mobilis

<400> 164

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atgggtattg acagaatgaa tagcttaagt cgcttgttaa tgaagaagat tttcggggct     60

gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga    120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg    180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc    240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg    300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt    360
```

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65 70 75 80

```
Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110

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

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

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

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300
```

```
Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510
```

```
Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Trp Tyr Leu Gly
        595                 600                 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
    610                 615                 620

Lys Gln Ala Ile Glu Arg Arg
625                 630
```

<210> 172
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 172
atgggtattg acagaatgaa tagcttaagt cgcttgttaa tgaagaagat tttcggggct 60

gaaaaaacct cgtataaacc ggcttccgat accataatcg gaacggatac cctgaaaaga 120

ccgaaccggc ggcctgaacc gacggcaaaa gtcgacaaaa cgatattcaa gactatgggg 180

aatagtctga ataataccct tgtttcagcc tgtgactggt tgatcggaca acaaaagccc 240

gatggtcatt gggtcggtgc cgtggaatcc aatgcttcga tggaagcaga atggtgtctg 300

gccttgtggt ttttgggtct ggaagatcat ccgcttcgtc caagattggg caatgctctt 360

ttggaaatgc agcgggaaga tggctcttgg ggagtctatt tcggcgctgg aaatggcgat 420

atcaatgcca cggttgaagc ctatgcggcc ttgcggtctt tggggtattc tgccgataat 480

cctgttttga aaaaagcggc agcatggatt gctgaaaaag gcggattaaa aaatatccgt 540

gtctttaccc gttattggct ggcgttgatc ggggaatggc cttgggaaaa gacccctaac 600

cttccccctg aaattatctg gttccctgat aattttgtct tttcgattta taattttgcc 660

caatgggcgc gggcaaccat ggtgccgatt gctattctgt ccgcgagacg accaagccgc 720

ccgctgcgcc ctcaagaccg attggatgaa ctgtttccag aaggccgcgc tcgctttgat 780

tatgaattgc cgaaaaaaga aggcatcgat ctttggtcgc aatttttccg aaccactgac 840

cgtggattac attgggttca gtccaatctg ttaaagcgca atagcttgcg tgaagccgct 900

atccgtcatg ttttggaatg gattatccgg catcaggatg ccgatggcgg ttggggtgga 960

attcagccac cttgggtcta tggtttgatg gcgttacatg gtgaaggcta tcagctttat 1020

catccggtga tggccaaggc tttgtcggct ttggatgatc ccggttggcg acatgacaga 1080

ggcgagtctt cttggataca ggccaccaat agtccggtat gggatacaat gttggccttg 1140

atggcgttaa aagacgccaa ggccgaggat cgttttacgc cggaaatgga taaggccgcc 1200

gattggcttt tggctcgaca ggtcaaagtc aaaggcgatt ggtcaatcaa actgcccgat 1260

gttgaacccg gtggatgggc atttgaatat gccaatgatc gctatcccga taccgatgat 1320

accgccgtcg ctttgatcgc cctttcctct tatcgtgata aggaggagtg gcaaaagaaa 1380

ggcgttgagg acgccattac ccgtggggtt aattggttga tcgccatgca aagcgaatgt 1440

ggcggttggg gagcctttga taaggataat aacagaagta tcctttccaa aattcctttt 1500

tgtgatttcg gagaatctat tgatccgcct tcagtcgatg taacggcgca tgttttagag 1560

gcctttggca ccttgggact gtcccgcgat atgccggtca tccaaaaagc gatcgactat 1620

gtccgttccg aacaggaagc cgaaggcgcg tggtttggtc gttggggcgt taattatatc 1680

tatggcaccg gtgcggttct gcctgctttg gcggcgatcg gtgaagatat gacccagcct 1740

tacatcacca aggcttgcga ttggctggtc gcacatcagc aggaagacgg cggttggggc 1800

gaaagctgct cttcctatat ggagattgat tccattggga agggcccaac cacgccgtcc 1860

cagactgctt gggctttgat ggggttgatc gcggccaatc gtcccgaaga ttatgaagcc 1920

attgccaagg gatgccatta tctgattgat cgccaagagc aggatggtag ctggaaagaa 1980

gaagaattca ccggcaccgg attccccggt tatggcgtgg gtcagacgat caagttggat 2040

gatccggctt tatcgaaacg attgcttcaa ggcgctgaac tgtcacgggc gtggatgctg 2100

cgttatgatt tttatcggca attcttcccg attatggcgt taagtcgggc agagagactg 2160

attgatttga ataattga 2178

<210> 173
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC1 Derivative

<400> 173

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
115 120 125

Ser Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
130 135 140

```
Val Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145                 150                 155                 160

Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Phe Thr Arg Tyr Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Gly Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365
```

```
Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Ile Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575
```

```
Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590

Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605

Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620

Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640

Ile Ala Lys Gly Cys His Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655

Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Phe Pro Gly Tyr Gly
            660                 665                 670

Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685

Leu Gln Gly Ala Glu Leu Ser Arg Ala Trp Met Leu Arg Tyr Asp Phe
    690                 695                 700

Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720

Ile Asp Leu Asn Asn
                725
```

<210> 174
<211> 1977
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 174

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atgactgtat cgacttcctc ggcttttcat catagcccgt tgtctgatga tgttgagccg     60

attatccaaa aggccacccg tgccttgctt gagaagcagc agcaggatgg ccattgggtt    120

tttgaattgg aagccgatgc aaccattccc gctgaataca tcctgttaaa gcattatttg    180
```

ggtgaacccg aagatttaga aatagaggcc aagataggtc gctatttgcg tcgtattcag 240

ggcgagcatg gcggatggtc tttgttttat ggtggtgatc ttgatttgag cgccacggtc 300

aaagcctatt ttgccttgaa aatgatcgga gattctcctg atgcgcctca tatgcttcga 360

gccagaaatg aaattttggc acggggtggg gcgatgcgtg ccaatgtctt tacacgtatt 420

caattagctc tgttcggggc aatgtcatgg gagcatgtcc ctcaaatgcc cgtagagttg 480

atgttgatgc cggaatggtt tccggttcac atcaataaaa tggcctattg ggcaagaacc 540

gttttagtcc cgttattggt tttacaggcg ttaaagcctg tcgcccgtaa tcggcgcggt 600

atcttggttg atgaattatt tgtgccggat gttttaccga cccttcagga aagcggtgac 660

cctatatggc gtcgtttttt ttcggcactt gataaggtat tgcataaagt agaaccttat 720

tggccgaaaa atatgcgcgc gaaggctatt catagctgtg tccattttgt gaccgagcgt 780

ttgaatggtg aagacgggtt gggtgctatt tatccggcga ttgccaatag cgtcatgatg 840

tatgatgcct tgggatatcc cgaaaaccat ccagaaagag ccattgcccg tcgggctgtc 900

gaaaaattga tggtgttaga tggcacggaa gatcagggtg ataaagaagt ctactgtcag 960

ccttgtttat ccccgatttg ggataccgct ttggttgccc atgccatgtt ggaagtcgga 1020

ggcgatgagg ctgaaaaatc ggctatttct gccttgagct ggttaaagcc gcaacaaatt 1080

ttggatgtaa agggcgattg ggcatggcgg cggcctgatc tcagacccgg gggatgggcc 1140

tttcaatata gaaatgacta ttatcccgat gtcgatgata cggctgttgt gactatggcg 1200

atggatcgag ccgcaaaatt gtcggatctt cacgatgatt ttgaggaatc taaagcgcgt 1260

gccatggaat ggaccattgg gatgcaaagc gataatggcg gttggggcgc tttcgatgcc 1320

aataacagct atacttatct gaataatatt ccctttgctg atcatggcgc gttacttgat 1380

ccgccaacgg tcgatgtctc ggcacgctgc gtttcaatga tggcgcaagc cggtatctcg 1440

attacagatc ccaaaatgaa agcggcagtt gattatcttc tgaaagagca agaagaggat 1500

ggtagctggt tcgggcgttg gggtgtcaat tacatatatg gcacatggtc ggccttatgt 1560

gcattgaatg tggccgcttt accccatgat catttagctg ttcagaaagc tgtggcttgg 1620

ctgaaaacta ttcaaaatga agatggtggt tggggtgaaa attgcgatag ctatgccctt 1680

gattatagcg gatacgagcc gatggattcg acggcttccc aaacagcatg ggctttattg 1740

ggcttgatgg ctgttgggga agctaattcc gaggccgtga caaagggtat aaactggttg 1800

gcacaaaatc aggatgaaga aggattgtgg aaagaagatt attatagtgg cggtggtttt 1860

ccccgtgttt ggtatcttcg gtatcacggt tattccaaat attttcctct ttgggcttta 1920

gcgcgctatc gcaatttgaa aaaagccaat cagccgattg ttcattatgg gatgtaa 1977

<210> 175
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic ZmoSHC2 Derivative

<400> 175

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1 5 10 15

Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
50 55 60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65 70 75 80

Gly Glu His Gly Gly Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
85 90 95

Ser Ala Thr Val Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
100 105 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
115 120 125

Gly Gly Ala Met Arg Ala Asn Val Phe Thr Arg Ile Gln Leu Ala Leu
130 135 140

```
Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Val Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365
```

```
Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Ile Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
                485                 490                 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
            500                 505                 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
        515                 520                 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
    530                 535                 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545                 550                 555                 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
                565                 570                 575
```

```
Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
            580                 585                 590

Val Thr Lys Gly Ile Asn Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
        595                 600                 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Phe Pro Arg Val Trp
    610                 615                 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625                 630                 635                 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
                645                 650                 655

Gly Met
```

<210> 176
<211> 2055
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 176

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atgactgtga ccagctcggc ctccgcgcgt gcgacgcgcg acccgggaaa ttatcagact     60

gccctgcaat cgacggtgcg cgcggcggcg gattggctga tcgccaacca gaagccggac    120

ggccattggg tcggccgcgc cgagtccaat gcctgcatgg aggcgcaatg gtgcctcgcg    180

ctgtggttca tggggctcga ggaccatccg ctgcgcaagc gcctgggcca gtcgctgctc    240

gacagccagc gcccggacgg cgcctggcag gtctatttcg gcgcccccaa tggcgacatc    300

aacgcgactg tcgaggccta tgccgcgctc cgctcgctgg gcttccgcga cgacgagccg    360

gcggtgcgcc gggcgcggga atggatcgag gccaagggcg gcctgcgcaa catccgcgtc    420

ttcacccgct actggctggc actgatcggc gaatggccgt gggagaagac accgaacatc    480

ccgccggagg tgatctggtt tccgctctgg tttccgttct cgatctacaa tttcgcgcaa    540

tgggcccgcg ccaccttgat gccgatcgcc gtgctgtcgg cgcggcggcc gagccggccg    600

ctgccgccgg agaaccgcct cgatgcgctg tttccgcatg gacggaaggc gttcgactac    660
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gaactgccgg tcaaggccgg cgccggcggc tgggacaggt tcttccgcgg cgccgacaag 720

gttctgcaca agctgcagaa cctcggcaac cgtctcaatc tcggcctgtt ccgcccggcg 780

gccaccagcc gcgtgctgga atggatgatc cgccatcagg atttcgacgg cgcctggggc 840

ggcatccagc cgccctggat ctacgggctg atggcgctct atgccgaagg ctatccgctc 900

aatcatcccg tgctcgcaaa gggcctcgac gcgctgaacg atcccggctg gcgcgtcgat 960

gtcggtgacg ccacctacat ccaggccacc aacagcccgg tctgggacac gatcctgacc 1020

ttgctcgcct tcgacgatgc cggcgtgctc ggcgactatc ccgaggccgt cgacaaggcg 1080

gtcgactggg tgctgcagcg gcaggtgcgc gtgcccggcg actggtcgat gaagctgccg 1140

catgtcaagc ccggcggctg ggcgttcgaa tacgccaaca actactatcc cgacacggac 1200

gacaccgcgg tcgcgctgat cgcgctggcg ccactgcgcc acgatccgaa atggaaggcc 1260

aaagggatcg acgaggctat ccagctcggt gtcgactggc tgatcggcat gcagagccag 1320

ggcggcggct ggggcgcgtt cgacaaggac aacaaccaga agatcctgac caagatcccg 1380

ttctgcgatt atggcgaggc gctcgatccg ccctcggtcg acgtcaccgc ccacatcatc 1440

gaggcgttcg gcaagctcgg catctcgcgc aaccatccgt cgatggtgca ggcgctggac 1500

tatattcgcc gtgagcagga gccgagcggt ccgtggttcg gccgctgggg cgtcaattac 1560

gtctacggca ccggcgcggt gctgccggcg ctggccgcga tcggcgagga catgacccag 1620

ccctatatcg gccgcgcctg cgactggctg gttgcccatc agcaggccga tggcggctgg 1680

ggcgagagct gcgcctccta catggatgtc agcgcggtcg gccgcggcac cacaacggcc 1740

tcgcagaccg cctgggcgct gatggcgctg ctcgccgcca atcgccccca ggacaaggac 1800

gcgatcgagc gtggctgcat gtggctggtc gagcgccagt cggccggcac ctgggacgag 1860

ccggaattca ccggcaccgg tttcccgggc tacggcgtcg gccagaccat caagctgaac 1920

gatcccgcgc tgtcgcagcg gctgatgcag ggcccggaat tgtcccgcgc ctggatgctc 1980

cgctacggca tgtaccgcca ctacttcccg ctgatggcgc tcggccgcgc cctacgcccg 2040

cagagtcata gctag 2055

<210> 177
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic BjapSHC1 Derivative

<400> 177

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


Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
            20                  25                  30


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


Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
    50                  55                  60


Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65                  70                  75                  80


Asp Ser Gln Arg Pro Asp Gly Ala Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95


Asn Gly Asp Ile Asn Ala Thr Val Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110


Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125


Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Phe Thr Arg Tyr
    130                 135                 140


Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160


Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175


Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190
```

```
Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220

Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Val Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415
```

```
Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430

Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Ile Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Met Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620
```

```
Gly Thr Gly Phe Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655

Ala Trp Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670

Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680
```

<210> 178
<211> 631
<212> PRT
<213> Alicyclobacillus acidocaldarius

<400> 178

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

Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
            20                  25                  30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
        35                  40                  45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
    50                  55                  60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65                  70                  75                  80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
                85                  90                  95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110

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

```
Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
                165                 170                 175

Ile Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Asp Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

Gly Ala Lys Gly Gly Gly Gly Arg Ile Phe Asp Ala Leu Asp Arg Ala
    210                 215                 220

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Thr Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Asp Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp Ala
```

```
            340                 345                 350

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380

Leu Asn Ser Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Val Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Arg
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Pro Ala Leu Lys Ala Val Gly Ile Asp Val Arg
            500                 505                 510

Glu Pro Phe Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560
```

```
Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Asp Ser Val Arg Arg
                565                 570                 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
        595                 600                 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
    610                 615                 620

Lys Gln Ala Ile Glu Arg Arg
625                 630
```

<210> 179
<211> 382
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic plasmid pET-28a(+) cloning/expression region

<220>
<221> CDS
<222> (109)..(285)

<400> 179

```
agatctcgat cccgcgaaat taatacgact cactataggg gaattgtgag cggataacaa     60

ttcccctcta gaaataattt ttgtttaact ttaagaagga gatatacc atg ggc agc     117
                                                      Met Gly Ser
                                                      1

agc cat cat cat cat cat cac agc agc ggc ctg gtg ccg cgc ggc agc      165
Ser His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
    5                  10                  15

cat atg gct agc atg act ggt gga cag caa atg ggt cgc gga tcc gaa      213
His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Glu
20                  25                  30                  35

ttc gag ctc cgt cga caa gct tgc ggc cgc act cga gca cca cca cca      261
Phe Glu Leu Arg Arg Gln Ala Cys Gly Arg Thr Arg Ala Pro Pro Pro
                40                  45                  50

cca cca ctg aga tcc ggc tgc taa caaagcccga aaggaagctg agttggctgc     315
```

Pro Pro Leu Arg Ser Gly Cys
            55

tgccaccgct gagcaataac tagcataacc ccttggggcc tctaaacggg tcttgagggg   375

tttttg   382

<210> 180
<211> 58
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 180

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1   5   10   15

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
            20   25   30

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

Pro Pro Pro Pro Pro Leu Arg Ser Gly Cys
    50   55

<210> 181
<211> 94
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic plasmid pET-28b(+) cloning/expression region

<220>
<221> CDS
<222> (1)..(72)

<400> 181
ggt cgg gat ccg aat tcg agc tcc gtc gac aag ctt gcg gcc gca ctc   48
Gly Arg Asp Pro Asn Ser Ser Ser Val Asp Lys Leu Ala Ala Ala Leu
1   5   10   15

gag cac cac cac cac cac cac tga gatccggctg ctaacaaagc cc   94
Glu His His His His His His

```
            20


<210>  182
<211>  23
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Synthetic Construct

<400>  182

Gly Arg Asp Pro Asn Ser Ser Ser Val Asp Lys Leu Ala Ala Ala Leu
1               5                   10                  15


Glu His His His His His His
            20


<210>  183
<211>  93
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic plasmid pET-28c(+) cloning/expression region


<220>
<221>  CDS
<222>  (1)..(93)

<400>  183
ggt cgg atc cga att cga gct ccg tcg aca agc ttg cgg ccg cac tcg       48
Gly Arg Ile Arg Ile Arg Ala Pro Ser Thr Ser Leu Arg Pro His Ser
1               5                   10                  15

agc acc acc acc acc acc act gag atc cgg ctg cta aca aag ccc          93
Ser Thr Thr Thr Thr Thr Thr Glu Ile Arg Leu Leu Thr Lys Pro
            20                  25                  30


<210>  184
<211>  31
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Synthetic Construct

<400>  184
```

Gly Arg Ile Arg Ile Arg Ala Pro Ser Thr Ser Leu Arg Pro His Ser
1   5   10   15

Ser Thr Thr Thr Thr Thr Thr Glu Ile Arg Leu Leu Thr Lys Pro
            20   25   30

<210> 185
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic SHC derivative

<220>
<221> VARIANT
<222> (77)..(77)
<223> T77X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y

<220>
<221> VARIANT
<222> (92)..(92)
<223> I92X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y

<220>
<221> VARIANT
<222> (129)..(129)
<223> F129X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (132)..(132)
<223> M132X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (224)..(224)
<223> A224X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (432)..(432)
<223> I432X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y.

<220>

<221> VARIANT
<222> (579)..(579)
<223> Q579X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (601)..(601)
<223> F601X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<400> 185

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


Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
            20                  25                  30


Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
        35                  40                  45


Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
    50                  55                  60


Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Xaa Trp Ala Leu
65                  70                  75                  80


Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Xaa Glu Ala Tyr Val
                85                  90                  95


Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
            100                 105                 110


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


Xaa Thr Arg Xaa Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
    130                 135                 140


Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145                 150                 155                 160


Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
```

```
                165                 170                 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
            180                 185                 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
        195                 200                 205

Gly Ala Lys Gly Gly Gly Gly Trp Ile Phe Asp Ala Leu Asp Arg Xaa
    210                 215                 220

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225                 230                 235                 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
                245                 250                 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
            260                 265                 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
        275                 280                 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
    290                 295                 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
305                 310                 315                 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
                325                 330                 335

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

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
        355                 360                 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
    370                 375                 380
```

```
Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385                 390                 395                 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
                405                 410                 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Xaa
            420                 425                 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
        435                 440                 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
    450                 455                 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465                 470                 475                 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
                485                 490                 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
            500                 505                 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
        515                 520                 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
    530                 535                 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545                 550                 555                 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
                565                 570                 575

Gly Val Xaa Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
            580                 585                 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Xaa Pro Gly Asp Phe Tyr Leu Gly
```

595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 186
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic SHC derivative

<220>
<221> VARIANT
<222> (129)..(129)
<223> S129X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (145)..(145)
<223> V145X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (182)..(182)
<223> F182X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (185)..(185)
<223> Y185X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (282)..(282)
<223> G282X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (498)..(498)
<223> I498X has X selected from: A, B, C, D, E, F, G, H, I, K, L, M, N,

P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (646)..(646)
<223> H646X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (668)..(668)
<223> F668X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<400> 186

Met Gly Ile Asp Arg Met Asn Ser Leu Ser Arg Leu Leu Met Lys Lys
1 5 10 15

Ile Phe Gly Ala Glu Lys Thr Ser Tyr Lys Pro Ala Ser Asp Thr Ile
20 25 30

Ile Gly Thr Asp Thr Leu Lys Arg Pro Asn Arg Arg Pro Glu Pro Thr
35 40 45

Ala Lys Val Asp Lys Thr Ile Phe Lys Thr Met Gly Asn Ser Leu Asn
50 55 60

Asn Thr Leu Val Ser Ala Cys Asp Trp Leu Ile Gly Gln Gln Lys Pro
65 70 75 80

Asp Gly His Trp Val Gly Ala Val Glu Ser Asn Ala Ser Met Glu Ala
85 90 95

Glu Trp Cys Leu Ala Leu Trp Phe Leu Gly Leu Glu Asp His Pro Leu
100 105 110

Arg Pro Arg Leu Gly Asn Ala Leu Leu Glu Met Gln Arg Glu Asp Gly
115 120 125

Xaa Trp Gly Val Tyr Phe Gly Ala Gly Asn Gly Asp Ile Asn Ala Thr
130 135 140

Xaa Glu Ala Tyr Ala Ala Leu Arg Ser Leu Gly Tyr Ser Ala Asp Asn
145 150 155 160

```
Pro Val Leu Lys Lys Ala Ala Ala Trp Ile Ala Glu Lys Gly Gly Leu
                165                 170                 175

Lys Asn Ile Arg Val Xaa Thr Arg Xaa Trp Leu Ala Leu Ile Gly Glu
            180                 185                 190

Trp Pro Trp Glu Lys Thr Pro Asn Leu Pro Pro Glu Ile Ile Trp Phe
        195                 200                 205

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

Ala Thr Met Val Pro Ile Ala Ile Leu Ser Ala Arg Arg Pro Ser Arg
225                 230                 235                 240

Pro Leu Arg Pro Gln Asp Arg Leu Asp Glu Leu Phe Pro Glu Gly Arg
                245                 250                 255

Ala Arg Phe Asp Tyr Glu Leu Pro Lys Lys Glu Gly Ile Asp Leu Trp
            260                 265                 270

Ser Gln Phe Phe Arg Thr Thr Asp Arg Xaa Leu His Trp Val Gln Ser
        275                 280                 285

Asn Leu Leu Lys Arg Asn Ser Leu Arg Glu Ala Ala Ile Arg His Val
    290                 295                 300

Leu Glu Trp Ile Ile Arg His Gln Asp Ala Asp Gly Gly Trp Gly Gly
305                 310                 315                 320

Ile Gln Pro Pro Trp Val Tyr Gly Leu Met Ala Leu His Gly Glu Gly
                325                 330                 335

Tyr Gln Leu Tyr His Pro Val Met Ala Lys Ala Leu Ser Ala Leu Asp
            340                 345                 350

Asp Pro Gly Trp Arg His Asp Arg Gly Glu Ser Ser Trp Ile Gln Ala
        355                 360                 365
```

```
Thr Asn Ser Pro Val Trp Asp Thr Met Leu Ala Leu Met Ala Leu Lys
    370                 375                 380

Asp Ala Lys Ala Glu Asp Arg Phe Thr Pro Glu Met Asp Lys Ala Ala
385                 390                 395                 400

Asp Trp Leu Leu Ala Arg Gln Val Lys Val Lys Gly Asp Trp Ser Ile
                405                 410                 415

Lys Leu Pro Asp Val Glu Pro Gly Gly Trp Ala Phe Glu Tyr Ala Asn
            420                 425                 430

Asp Arg Tyr Pro Asp Thr Asp Asp Thr Ala Val Ala Leu Ile Ala Leu
        435                 440                 445

Ser Ser Tyr Arg Asp Lys Glu Glu Trp Gln Lys Lys Gly Val Glu Asp
    450                 455                 460

Ala Ile Thr Arg Gly Val Asn Trp Leu Ile Ala Met Gln Ser Glu Cys
465                 470                 475                 480

Gly Gly Trp Gly Ala Phe Asp Lys Asp Asn Asn Arg Ser Ile Leu Ser
                485                 490                 495

Lys Xaa Pro Phe Cys Asp Phe Gly Glu Ser Ile Asp Pro Pro Ser Val
            500                 505                 510

Asp Val Thr Ala His Val Leu Glu Ala Phe Gly Thr Leu Gly Leu Ser
        515                 520                 525

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

Gln Glu Ala Glu Gly Ala Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
545                 550                 555                 560

Tyr Gly Thr Gly Ala Val Leu Pro Ala Leu Ala Ala Ile Gly Glu Asp
                565                 570                 575

Met Thr Gln Pro Tyr Ile Thr Lys Ala Cys Asp Trp Leu Val Ala His
            580                 585                 590
```

```
Gln Gln Glu Asp Gly Gly Trp Gly Glu Ser Cys Ser Ser Tyr Met Glu
        595                 600                 605


Ile Asp Ser Ile Gly Lys Gly Pro Thr Thr Pro Ser Gln Thr Ala Trp
    610                 615                 620


Ala Leu Met Gly Leu Ile Ala Ala Asn Arg Pro Glu Asp Tyr Glu Ala
625                 630                 635                 640


Ile Ala Lys Gly Cys Xaa Tyr Leu Ile Asp Arg Gln Glu Gln Asp Gly
                645                 650                 655


Ser Trp Lys Glu Glu Glu Phe Thr Gly Thr Gly Xaa Pro Gly Tyr Gly
            660                 665                 670


Val Gly Gln Thr Ile Lys Leu Asp Asp Pro Ala Leu Ser Lys Arg Leu
        675                 680                 685


Leu Gln Gly Ala Glu Leu Ser Arg Ala Phe Met Leu Arg Tyr Asp Phe
    690                 695                 700


Tyr Arg Gln Phe Phe Pro Ile Met Ala Leu Ser Arg Ala Glu Arg Leu
705                 710                 715                 720


Ile Asp Leu Asn Asn
                725
```

<210> 187
<211> 658
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic SHC derivative

<220>
<221> VARIANT
<222> (85)..(85)
<223> G85X has X selected from: A, C, D, E, F, G, H, I, K , L, M, N, P, Q, R, S, T, V, W or Y.

<220>

<221> VARIANT
<222> (100)..(100)
<223> V100X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (137)..(137)
<223> F137X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (140)..(140)
<223> I140X has X selected from: A,, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (233)..(233)
<223> V233X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (450)..(450)
<223> I450X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (598)..(598)
<223> N598X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y

<220>
<221> VARIANT
<222> (620)..(620)
<223> F620X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W or Y.

<400> 187

Met Thr Val Ser Thr Ser Ser Ala Phe His His Ser Pro Leu Ser Asp
1 5 10 15

Asp Val Glu Pro Ile Ile Gln Lys Ala Thr Arg Ala Leu Leu Glu Lys
20 25 30

Gln Gln Gln Asp Gly His Trp Val Phe Glu Leu Glu Ala Asp Ala Thr
35 40 45

```
Ile Pro Ala Glu Tyr Ile Leu Leu Lys His Tyr Leu Gly Glu Pro Glu
    50                  55                  60

Asp Leu Glu Ile Glu Ala Lys Ile Gly Arg Tyr Leu Arg Arg Ile Gln
65                  70                  75                  80

Gly Glu His Gly Xaa Trp Ser Leu Phe Tyr Gly Gly Asp Leu Asp Leu
                85                  90                  95

Ser Ala Thr Xaa Lys Ala Tyr Phe Ala Leu Lys Met Ile Gly Asp Ser
            100                 105                 110

Pro Asp Ala Pro His Met Leu Arg Ala Arg Asn Glu Ile Leu Ala Arg
        115                 120                 125

Gly Gly Ala Met Arg Ala Asn Val Xaa Thr Arg Xaa Gln Leu Ala Leu
    130                 135                 140

Phe Gly Ala Met Ser Trp Glu His Val Pro Gln Met Pro Val Glu Leu
145                 150                 155                 160

Met Leu Met Pro Glu Trp Phe Pro Val His Ile Asn Lys Met Ala Tyr
                165                 170                 175

Trp Ala Arg Thr Val Leu Val Pro Leu Leu Val Leu Gln Ala Leu Lys
            180                 185                 190

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

Pro Asp Val Leu Pro Thr Leu Gln Glu Ser Gly Asp Pro Ile Trp Arg
    210                 215                 220

Arg Phe Phe Ser Ala Leu Asp Lys Xaa Leu His Lys Val Glu Pro Tyr
225                 230                 235                 240

Trp Pro Lys Asn Met Arg Ala Lys Ala Ile His Ser Cys Val His Phe
                245                 250                 255

Val Thr Glu Arg Leu Asn Gly Glu Asp Gly Leu Gly Ala Ile Tyr Pro
```

```
            260                 265                 270

Ala Ile Ala Asn Ser Val Met Met Tyr Asp Ala Leu Gly Tyr Pro Glu
        275                 280                 285

Asn His Pro Glu Arg Ala Ile Ala Arg Arg Ala Val Glu Lys Leu Met
    290                 295                 300

Val Leu Asp Gly Thr Glu Asp Gln Gly Asp Lys Glu Val Tyr Cys Gln
305                 310                 315                 320

Pro Cys Leu Ser Pro Ile Trp Asp Thr Ala Leu Val Ala His Ala Met
                325                 330                 335

Leu Glu Val Gly Gly Asp Glu Ala Glu Lys Ser Ala Ile Ser Ala Leu
            340                 345                 350

Ser Trp Leu Lys Pro Gln Gln Ile Leu Asp Val Lys Gly Asp Trp Ala
        355                 360                 365

Trp Arg Arg Pro Asp Leu Arg Pro Gly Gly Trp Ala Phe Gln Tyr Arg
    370                 375                 380

Asn Asp Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Thr Met Ala
385                 390                 395                 400

Met Asp Arg Ala Ala Lys Leu Ser Asp Leu His Asp Asp Phe Glu Glu
                405                 410                 415

Ser Lys Ala Arg Ala Met Glu Trp Thr Ile Gly Met Gln Ser Asp Asn
            420                 425                 430

Gly Gly Trp Gly Ala Phe Asp Ala Asn Asn Ser Tyr Thr Tyr Leu Asn
        435                 440                 445

Asn Xaa Pro Phe Ala Asp His Gly Ala Leu Leu Asp Pro Pro Thr Val
    450                 455                 460

Asp Val Ser Ala Arg Cys Val Ser Met Met Ala Gln Ala Gly Ile Ser
465                 470                 475                 480
```

Ile Thr Asp Pro Lys Met Lys Ala Ala Val Asp Tyr Leu Leu Lys Glu
485 490 495

Gln Glu Glu Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Ile
500 505 510

Tyr Gly Thr Trp Ser Ala Leu Cys Ala Leu Asn Val Ala Ala Leu Pro
515 520 525

His Asp His Leu Ala Val Gln Lys Ala Val Ala Trp Leu Lys Thr Ile
530 535 540

Gln Asn Glu Asp Gly Gly Trp Gly Glu Asn Cys Asp Ser Tyr Ala Leu
545 550 555 560

Asp Tyr Ser Gly Tyr Glu Pro Met Asp Ser Thr Ala Ser Gln Thr Ala
565 570 575

Trp Ala Leu Leu Gly Leu Met Ala Val Gly Glu Ala Asn Ser Glu Ala
580 585 590

Val Thr Lys Gly Ile Xaa Trp Leu Ala Gln Asn Gln Asp Glu Glu Gly
595 600 605

Leu Trp Lys Glu Asp Tyr Tyr Ser Gly Gly Gly Xaa Pro Arg Val Phe
610 615 620

Tyr Leu Arg Tyr His Gly Tyr Ser Lys Tyr Phe Pro Leu Trp Ala Leu
625 630 635 640

Ala Arg Tyr Arg Asn Leu Lys Lys Ala Asn Gln Pro Ile Val His Tyr
645 650 655

Gly Met

<210> 188
<211> 684
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic SHC derivative

<220>
<221> VARIANT
<222> (88)..(88)
<223> A88X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (104)..(104)
<223> V104X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (141)..(141)
<223> F141X, has X selected from: A, C, D, E, F, G, H, I, K, L, M, N,
       P, Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (144)..(144)
<223> Y144X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (241)..(241)
<223> V241X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (459)..(459)
<223> I459X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (607)..(607)
<223> M607X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y.

<220>
<221> VARIANT
<222> (628)..(628)
<223> F628X has X selected from: A, C, D, E, F, G, H, I, K, L, M, N, P,
       Q, R, S, T, V, W or Y.

<400> 188

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

Asn Tyr Gln Thr Ala Leu Gln Ser Thr Val Arg Ala Ala Ala Asp Trp
            20                  25                  30

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

Ser Asn Ala Cys Met Glu Ala Gln Trp Cys Leu Ala Leu Trp Phe Met
    50                  55                  60

Gly Leu Glu Asp His Pro Leu Arg Lys Arg Leu Gly Gln Ser Leu Leu
65                  70                  75                  80

Asp Ser Gln Arg Pro Asp Gly Xaa Trp Gln Val Tyr Phe Gly Ala Pro
                85                  90                  95

Asn Gly Asp Ile Asn Ala Thr Xaa Glu Ala Tyr Ala Ala Leu Arg Ser
            100                 105                 110

Leu Gly Phe Arg Asp Asp Glu Pro Ala Val Arg Arg Ala Arg Glu Trp
        115                 120                 125

Ile Glu Ala Lys Gly Gly Leu Arg Asn Ile Arg Val Xaa Thr Arg Xaa
    130                 135                 140

Trp Leu Ala Leu Ile Gly Glu Trp Pro Trp Glu Lys Thr Pro Asn Ile
145                 150                 155                 160

Pro Pro Glu Val Ile Trp Phe Pro Leu Trp Phe Pro Phe Ser Ile Tyr
                165                 170                 175

Asn Phe Ala Gln Trp Ala Arg Ala Thr Leu Met Pro Ile Ala Val Leu
            180                 185                 190

Ser Ala Arg Arg Pro Ser Arg Pro Leu Pro Pro Glu Asn Arg Leu Asp
        195                 200                 205

Ala Leu Phe Pro His Gly Arg Lys Ala Phe Asp Tyr Glu Leu Pro Val
    210                 215                 220
```

```
Lys Ala Gly Ala Gly Gly Trp Asp Arg Phe Phe Arg Gly Ala Asp Lys
225                 230                 235                 240

Xaa Leu His Lys Leu Gln Asn Leu Gly Asn Arg Leu Asn Leu Gly Leu
                245                 250                 255

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

Gln Asp Phe Asp Gly Ala Trp Gly Gly Ile Gln Pro Pro Trp Ile Tyr
        275                 280                 285

Gly Leu Met Ala Leu Tyr Ala Glu Gly Tyr Pro Leu Asn His Pro Val
    290                 295                 300

Leu Ala Lys Gly Leu Asp Ala Leu Asn Asp Pro Gly Trp Arg Val Asp
305                 310                 315                 320

Val Gly Asp Ala Thr Tyr Ile Gln Ala Thr Asn Ser Pro Val Trp Asp
                325                 330                 335

Thr Ile Leu Thr Leu Leu Ala Phe Asp Asp Ala Gly Val Leu Gly Asp
            340                 345                 350

Tyr Pro Glu Ala Val Asp Lys Ala Val Asp Trp Val Leu Gln Arg Gln
        355                 360                 365

Val Arg Val Pro Gly Asp Trp Ser Met Lys Leu Pro His Val Lys Pro
    370                 375                 380

Gly Gly Trp Ala Phe Glu Tyr Ala Asn Asn Tyr Tyr Pro Asp Thr Asp
385                 390                 395                 400

Asp Thr Ala Val Ala Leu Ile Ala Leu Ala Pro Leu Arg His Asp Pro
                405                 410                 415

Lys Trp Lys Ala Lys Gly Ile Asp Glu Ala Ile Gln Leu Gly Val Asp
            420                 425                 430
```

```
Trp Leu Ile Gly Met Gln Ser Gln Gly Gly Gly Trp Gly Ala Phe Asp
        435                 440                 445

Lys Asp Asn Asn Gln Lys Ile Leu Thr Lys Xaa Pro Phe Cys Asp Tyr
    450                 455                 460

Gly Glu Ala Leu Asp Pro Pro Ser Val Asp Val Thr Ala His Ile Ile
465                 470                 475                 480

Glu Ala Phe Gly Lys Leu Gly Ile Ser Arg Asn His Pro Ser Met Val
                485                 490                 495

Gln Ala Leu Asp Tyr Ile Arg Arg Glu Gln Glu Pro Ser Gly Pro Trp
            500                 505                 510

Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ala Val Leu
        515                 520                 525

Pro Ala Leu Ala Ala Ile Gly Glu Asp Met Thr Gln Pro Tyr Ile Gly
    530                 535                 540

Arg Ala Cys Asp Trp Leu Val Ala His Gln Gln Ala Asp Gly Gly Trp
545                 550                 555                 560

Gly Glu Ser Cys Ala Ser Tyr Met Asp Val Ser Ala Val Gly Arg Gly
                565                 570                 575

Thr Thr Thr Ala Ser Gln Thr Ala Trp Ala Leu Met Ala Leu Leu Ala
            580                 585                 590

Ala Asn Arg Pro Gln Asp Lys Asp Ala Ile Glu Arg Gly Cys Xaa Trp
        595                 600                 605

Leu Val Glu Arg Gln Ser Ala Gly Thr Trp Asp Glu Pro Glu Phe Thr
    610                 615                 620

Gly Thr Gly Xaa Pro Gly Tyr Gly Val Gly Gln Thr Ile Lys Leu Asn
625                 630                 635                 640

Asp Pro Ala Leu Ser Gln Arg Leu Met Gln Gly Pro Glu Leu Ser Arg
                645                 650                 655
```

```
Ala Phe Met Leu Arg Tyr Gly Met Tyr Arg His Tyr Phe Pro Leu Met
            660                 665                 670


Ala Leu Gly Arg Ala Leu Arg Pro Gln Ser His Ser
        675                 680
```