SEQUENCE LISTING

<110> Vision Global Holdings Ltd.
WONG, Bing Lou

<120> PHARMACEUTICAL COMPOSITION COMPRISING ALBUMIN-BINDING ARGININE DEIMINASE FOR CANCER TARGETING TREATMENT

<130> P6890US01

<140> PCT/US14/020943
<141> 2014-03-06

<150> US 61/773,214
<151> 2013-03-06

<150> US 14/197,236
<151> 2014-03-05

<160> 53

<170> PatentIn version 3.5

<210> 1
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tagtcactta ctccatattt gtcaagttct ctgttagcta agactttagc 50

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gaacttgaca aatatggagt aagtgactat tacaagaacc taatcaacaa 50

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<223> ABD-F5 forward primer, synthesized in laboratory

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agctacgata agcttaaggt aatgcagcta aaatttcatc tatcagtg 48

<210> 7
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<212> DNA
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<212> DNA
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<223> ABD-R8 reverse primer, synthesized in laboratory

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atcgatcgat gtctgtattt gacagtaaat ttaaagg 37

<210> 10
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<220>
<223> ADIhis-R reverse primer, synthesized in laboratory

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<212> DNA
<213> Artificial Sequence

<220>
<223> ADINde-F2 forward primer, synthesized in laboratory

<400> 11
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<210> 12
<211> 48
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<220>
<223> ABD-R10 reverse primer, synthesized in laboratory

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<210> 13
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<223> hisABDNde-F forward primer, synthesized in laboratory

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ggagatatac atatgcatca tcaccatcac catgatgaag ccgtggatg 49

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ttgttattat tgttgttact acccgaaggt aatgcagcta aaatttcatc 50

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aataataaca atggtagcgg cggttctgta tttgacagta aatttaaagg 50

<210> 17
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tagatcaatg gatccttacc acttaacatc tttacgtgat aaag 44

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<223> bcABDnn-R1 reverse primer, synthesized in laboratory

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<223> bcADIn-F forward primer, synthesized in laboratory

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<223> bcADIBam-R reverse primer, synthesized in laboratory

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<211> 410
<212> PRT
<213> Mycoplasma arginini

<400> 23

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1 5 10 15

Ile Gly Glu Leu Glu Ser Val Leu Val His Glu Pro Gly Arg Glu Ile
20 25 30

Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Leu Phe Ser Ala Ile
35 40 45

Leu Glu Ser His Asp Ala Arg Lys Glu His Lys Gln Phe Val Ala Glu
50 55 60

Leu Lys Ala Asn Asp Ile Asn Val Val Glu Leu Ile Asp Leu Val Ala
65 70 75 80

Glu Thr Tyr Asp Leu Ala Ser Gln Glu Ala Lys Asp Lys Leu Ile Glu
85 90 95

Glu Phe Leu Glu Asp Ser Glu Pro Val Leu Ser Glu Glu His Lys Val
100 105 110

Val Val Arg Asn Phe Leu Lys Ala Lys Lys Thr Ser Arg Glu Leu Val
115 120 125

Glu Ile Met Met Ala Gly Ile Thr Lys Tyr Asp Leu Gly Ile Glu Ala
130 135 140

Asp His Glu Leu Ile Val Asp Pro Met Pro Asn Leu Tyr Phe Thr Arg
145 150 155 160

Asp Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Tyr Met Arg
165 170 175

Tyr Lys Val Arg Gln Arg Glu Thr Leu Phe Ser Arg Phe Val Phe Ser
180 185 190

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Asn His Pro Lys Leu Ile Asn Thr Pro Trp Tyr Tyr Asp Pro Ser Leu
        195                 200                 205

Lys Leu Ser Ile Glu Gly Gly Asp Val Phe Ile Tyr Asn Asn Asp Thr
    210                 215                 220

Leu Val Val Gly Val Ser Glu Arg Thr Asp Leu Gln Thr Val Thr Leu
225                 230                 235                 240

Leu Ala Lys Asn Ile Val Ala Asn Lys Glu Cys Glu Phe Lys Arg Ile
                245                 250                 255

Val Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu Asp Thr
            260                 265                 270

Trp Leu Thr Met Leu Asp Lys Asp Lys Phe Leu Tyr Ser Pro Ile Ala
        275                 280                 285

Asn Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val Asn Gly Gly Ala
    290                 295                 300

Glu Pro Gln Pro Val Glu Asn Gly Leu Pro Leu Glu Gly Leu Leu Gln
305                 310                 315                 320

Ser Ile Ile Asn Lys Lys Pro Val Leu Ile Pro Ile Ala Gly Glu Gly
                325                 330                 335

Ala Ser Gln Met Glu Ile Glu Arg Glu Thr His Phe Asp Gly Thr Asn
            340                 345                 350

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

Lys Thr Asn Ala Ala Leu Glu Ala Ala Gly Ile Lys Val Leu Pro Phe
    370                 375                 380

His Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys Met Ser
385                 390                 395                 400

Met Pro Leu Ser Arg Lys Asp Val Lys Trp
                405                 410
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<210> 24
<211> 410
<212> PRT
<213> Lactococcus lactis

<400> 24

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Met Asn Asn Gly Ile Asn Val Asn Ser Glu Ile Gly Lys Leu Lys Ser
1               5                   10                  15
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Val Leu Leu His Arg Pro Gly Ala Glu Val Glu Asn Ile Thr Pro Asp
            20                  25                  30

Thr Met Lys Gln Leu Leu Phe Asp Asp Ile Pro Tyr Leu Lys Ile Ala
        35                  40                  45

Gln Lys Glu His Asp Phe Phe Ala Gln Thr Leu Arg Asp Asn Gly Ala
    50                  55                  60

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

Ser Glu Thr Lys Glu Glu Phe Leu Ser His Leu Leu His Glu Ala Gly
                85                  90                  95

Tyr Arg Pro Gly Arg Thr Tyr Asp Gly Leu Thr Glu Tyr Leu Thr Ser
            100                 105                 110

Met Pro Thr Lys Asp Met Val Glu Lys Val Tyr Ala Gly Val Arg Lys
        115                 120                 125

Asn Glu Leu Asp Ile Lys Arg Thr Ala Leu Ser Asp Met Ala Gly Ser
    130                 135                 140

Asp Ala Glu Asn Tyr Phe Tyr Leu Asn Pro Leu Pro Asn Ala Tyr Phe
145                 150                 155                 160

Thr Arg Asp Pro Gln Ala Ser Met Gly Val Gly Met Thr Ile Asn Lys
                165                 170                 175

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

Met Ala Asn His Pro Arg Phe Lys Asp Thr Pro Ile Trp Arg Asp Arg
        195                 200                 205

Asn His Thr Thr Arg Ile Glu Gly Gly Asp Glu Leu Ile Leu Asn Lys
    210                 215                 220

Thr Thr Val Ala Ile Gly Val Ser Glu Arg Thr Ser Ser Lys Thr Ile
225                 230                 235                 240

Gln Asn Leu Ala Lys Glu Leu Phe Ala Asn Pro Leu Ser Thr Phe Asp
                245                 250                 255

Thr Val Leu Ala Val Glu Ile Pro His Asn His Ala Met Met His Leu
            260                 265                 270

Asp Thr Val Phe Thr Met Ile Asn His Asp Gln Phe Thr Val Phe Pro
        275                 280                 285
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Gly Ile Met Asp Gly Ala Gly Asn Ile Asn Val Phe Ile Leu Arg Pro
    290                 295                 300

Gly Gln Asp Gly Glu Val Glu Ile Glu His Leu Thr Asp Leu Lys Ala
305                 310                 315                 320

Ala Leu Lys Lys Val Leu Asn Leu Ser Glu Leu Asp Leu Ile Glu Cys
                325                 330                 335

Gly Ala Gly Asp Pro Ile Ala Ala Pro Arg Glu Gln Trp Asn Asp Gly
            340                 345                 350

Ser Asn Thr Leu Ala Ile Ala Pro Gly Glu Ile Val Thr Tyr Asp Arg
        355                 360                 365

Asn Tyr Val Thr Val Glu Leu Leu Lys Glu His Gly Ile Lys Val His
    370                 375                 380

Glu Ile Leu Ser Ser Glu Leu Gly Arg Gly Arg Gly Gly Ala Arg Cys
385                 390                 395                 400

Met Ser Gln Pro Leu Trp Arg Glu Asp Leu
                405                 410


<210>  25
<211>  410
<212>  PRT
<213>  Bacillus cereus

<400>  25

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

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

Tyr Leu Gln Gln Leu Leu Phe Asp Asp Ile Pro Tyr Leu Pro Ile Ile
        35                  40                  45

Gln Lys Glu His Asp Tyr Phe Ala Gln Thr Leu Arg Asn Arg Gly Val
    50                  55                  60

Glu Val Leu Tyr Leu Glu Lys Leu Ala Ala Glu Ala Leu Val Asp Lys
65                  70                  75                  80

Lys Leu Arg Glu Glu Phe Val Asp Arg Ile Leu Lys Glu Gly Gln Ala
                85                  90                  95

Asp Val Asn Val Ala His Gln Thr Leu Lys Glu Tyr Leu Leu Ser Phe
            100                 105                 110
```

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Ser Asn Glu Glu Leu Ile Gln Lys Ile Met Gly Gly Val Arg Lys Asn
        115                 120                 125

Glu Ile Glu Thr Ser Lys Lys Thr His Leu Tyr Glu Leu Met Glu Asp
    130                 135                 140

His Tyr Pro Phe Tyr Leu Asp Pro Met Pro Asn Leu Tyr Phe Thr Arg
145                 150                 155                 160

Asp Pro Ala Ala Ser Val Gly Asp Gly Leu Thr Ile Asn Lys Met Arg
                165                 170                 175

Glu Pro Ala Arg Arg Arg Glu Ser Leu Phe Met Glu Tyr Ile Ile Lys
            180                 185                 190

Tyr His Pro Arg Phe Ala Lys His Asn Val Pro Ile Trp Leu Asp Arg
        195                 200                 205

Asp Tyr Lys Phe Pro Ile Glu Gly Gly Asp Glu Leu Ile Leu Asn Glu
    210                 215                 220

Glu Thr Ile Ala Ile Gly Val Ser Ala Arg Thr Ser Ala Lys Ala Ile
225                 230                 235                 240

Glu Arg Leu Ala Lys Asn Leu Phe Ser Arg Gln Asn Lys Ile Lys Lys
                245                 250                 255

Val Leu Ala Ile Glu Ile Pro Lys Cys Arg Ala Phe Met His Leu Asp
            260                 265                 270

Thr Val Phe Thr Met Val Asp Tyr Asp Lys Phe Thr Ile His Pro Ala
        275                 280                 285

Ile Gln Gly Pro Lys Gly Asn Met Asn Ile Tyr Ile Leu Glu Lys Gly
    290                 295                 300

Ala Asp Glu Glu Thr Leu Lys Ile Thr His Arg Thr Ser Leu Met Glu
305                 310                 315                 320

Ala Leu Lys Glu Val Leu Asp Leu Ser Glu Leu Val Leu Ile Pro Cys
                325                 330                 335

Gly Gly Gly Asp Val Ile Ala Ser Ala Arg Glu Gln Trp Asn Asp Gly
            340                 345                 350

Ser Asn Thr Leu Ala Ile Ala Pro Gly Val Val Val Thr Tyr Asp Arg
        355                 360                 365

Asn Tyr Val Ser Asn Thr Leu Leu Arg Glu His Gly Ile Glu Val Ile
    370                 375                 380
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Glu Val Leu Ser Ser Glu Leu Ser Arg Gly Arg Gly Gly Pro Arg Cys
385 390 395 400

Met Ser Met Pro Ile Val Arg Lys Asp Ile
405 410

<210> 26
<211> 413
<212> PRT
<213> Bacillus licheniformis

<400> 26

Met Ile Met Thr Thr Pro Ile His Val Tyr Ser Glu Ile Gly Pro Leu
1 5 10 15

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

Pro Glu Tyr Leu Glu Arg Leu Leu Phe Asp Asp Ile Pro Phe Leu Pro
35 40 45

Ala Val Gln Lys Glu His Asp Gln Phe Ala Glu Thr Leu Lys Gln Gln
50 55 60

Gly Ala Glu Val Leu Tyr Leu Glu Lys Leu Thr Ala Glu Ala Leu Asp
65 70 75 80

Asp Ala Leu Val Arg Glu Gln Phe Ile Asp Glu Leu Leu Thr Glu Ser
85 90 95

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

Thr Phe Asp Ala Asp Ser Met Val Glu Gln Val Met Ser Gly Ile Arg
115 120 125

Lys Asn Glu Leu Glu Arg Glu Lys Lys Ser His Leu His Glu Leu Met
130 135 140

Glu Asp His Tyr Pro Phe Tyr Leu Asp Pro Met Pro Asn Leu Tyr Phe
145 150 155 160

Thr Arg Asp Pro Ala Ala Ala Ile Gly Ser Gly Leu Thr Ile Asn Lys
165 170 175

Met Lys Glu Pro Ala Arg Arg Arg Glu Ser Leu Phe Met Arg Tyr Ile
180 185 190

Ile Asn His His Pro Arg Phe Lys Gly His Glu Ile Pro Val Trp Leu
195 200 205

Asp Arg Asp Phe Lys Phe Asn Ile Glu Gly Gly Asp Glu Leu Val Leu

210 215 220

Asn Glu Glu Thr Val Ala Ile Gly Val Ser Glu Arg Thr Thr Ala Gln
225 230 235 240

Ala Ile Glu Arg Leu Val Arg Asn Leu Phe Gln Arg Gln Ser Arg Ile
245 250 255

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

Leu Asp Thr Val Phe Thr Met Val Asp Arg Asp Gln Phe Thr Ile His
275 280 285

Pro Ala Ile Gln Gly Pro Glu Gly Asp Met Arg Ile Phe Val Leu Glu
290 295 300

Arg Gly Lys Thr Ala Asp Glu Ile His Thr Thr Glu Glu His Asn Leu
305 310 315 320

Pro Glu Val Leu Lys Arg Thr Leu Gly Leu Ser Asp Val Asn Leu Ile
325 330 335

Phe Cys Gly Gly Gly Asp Glu Ile Ala Ser Ala Arg Glu Gln Trp Asn
340 345 350

Asp Gly Ser Asn Thr Leu Ala Ile Ala Pro Gly Val Val Val Thr Tyr
355 360 365

Asp Arg Asn Tyr Ile Ser Asn Glu Cys Leu Arg Glu Gln Gly Ile Lys
370 375 380

Val Ile Glu Ile Pro Ser Gly Glu Leu Ser Arg Gly Arg Gly Gly Pro
385 390 395 400

Arg Cys Met Ser Met Pro Leu Tyr Arg Glu Asp Val Lys
405 410

<210> 27
<211> 409
<212> PRT
<213> Mycoplasma arthritidis

<400> 27

Met Ser Val Phe Asp Ser Lys Phe Lys Gly Ile His Val Tyr Ser Glu
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Ile Gly Glu Leu Glu Thr Val Leu Val His Glu Pro Gly Lys Glu Ile
20 25 30

Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Leu Phe Ser Ala Ile
35 40 45

```
Leu Glu Ser His Asp Ala Arg Lys Glu His Lys Glu Phe Val Ala Glu
    50                  55                  60

Leu Lys Lys Arg Gly Ile Asn Val Val Glu Leu Val Asp Leu Ile Val
65                  70                  75                  80

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

Glu Phe Leu Asp Asp Ser Val Pro Val Leu Ser Asp Glu His Arg Ala
            100                 105                 110

Ala Val Lys Lys Phe Leu Gln Ser Gln Lys Ser Thr Arg Ser Leu Val
        115                 120                 125

Glu Tyr Met Ile Ala Gly Ile Thr Lys His Asp Leu Lys Ile Glu Ser
    130                 135                 140

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

Asp Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Tyr Met Arg
                165                 170                 175

Tyr Lys Val Arg Gln Arg Glu Thr Leu Phe Ser Arg Phe Val Phe Ser
            180                 185                 190

Asn His Pro Lys Leu Val Asn Thr Pro Trp Tyr Tyr Asp Pro Ala Glu
        195                 200                 205

Gly Leu Ser Ile Glu Gly Gly Asp Val Phe Ile Tyr Asn Asn Asp Thr
    210                 215                 220

Leu Val Val Gly Val Ser Glu Arg Thr Asp Leu Gln Thr Ile Thr Leu
225                 230                 235                 240

Leu Ala Lys Asn Ile Lys Ala Asn Lys Glu Cys Glu Phe Lys Arg Ile
                245                 250                 255

Val Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu Asp Thr
            260                 265                 270

Trp Leu Thr Met Leu Asp Lys Asp Lys Phe Leu Tyr Ser Pro Ile Ala
        275                 280                 285

Asn Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val Asn Gly Gly Asp
    290                 295                 300

Ala Pro Gln Pro Val Asp Asn Gly Leu Pro Leu Glu Asp Leu Leu Lys
305                 310                 315                 320
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Ser Ile Ile Gly Lys Lys Pro Thr Leu Ile Pro Ile Ala Gly Ala Gly
                325                 330                 335

Ala Ser Gln Ile Asp Ile Glu Arg Glu Thr His Phe Asp Gly Thr Asn
            340                 345                 350

Tyr Leu Ala Val Ala Pro Gly Ile Val Ile Gly Tyr Ala Arg Asn Glu
        355                 360                 365

Lys Thr Asn Ala Ala Leu Glu Ala Ala Gly Ile Thr Val Leu Pro Phe
    370                 375                 380

Arg Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys Met Ser
385                 390                 395                 400

Met Pro Leu Ser Arg Lys Asp Val Lys
                405
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<210> 28
<211> 409
<212> PRT
<213> Mycoplasma hominis

<400> 28

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Met Ser Val Phe Asp Ser Lys Phe Asn Gly Ile His Val Tyr Ser Glu
1               5                   10                  15

Ile Gly Glu Leu Glu Thr Val Leu Val His Glu Pro Gly Arg Glu Ile
            20                  25                  30

Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Leu Phe Ser Ala Ile
        35                  40                  45

Leu Glu Ser His Asp Ala Arg Lys Glu His Gln Ser Phe Val Lys Ile
    50                  55                  60

Met Lys Asp Arg Gly Ile Asn Val Val Glu Leu Thr Asp Leu Val Ala
65                  70                  75                  80

Glu Thr Tyr Asp Leu Ala Ser Lys Ala Ala Lys Glu Glu Phe Ile Glu
                85                  90                  95

Thr Phe Leu Glu Glu Thr Val Pro Val Leu Thr Glu Ala Asn Lys Lys
            100                 105                 110

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

Phe Met Met Ser Gly Ile Thr Lys Tyr Glu Leu Gly Val Glu Ser Glu
    130                 135                 140
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Asn Glu Leu Ile Val Asp Pro Met Pro Asn Leu Tyr Phe Thr Arg Asp
145                 150                 155                 160

Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Phe Met Arg Tyr
                165                 170                 175

Ile Val Arg Arg Arg Glu Thr Leu Phe Ala Arg Phe Val Phe Arg Asn
            180                 185                 190

His Pro Lys Leu Val Lys Thr Pro Trp Tyr Tyr Asp Pro Ala Met Lys
        195                 200                 205

Met Ser Ile Glu Gly Gly Asp Val Phe Ile Tyr Asn Asn Glu Thr Leu
    210                 215                 220

Val Val Gly Val Ser Glu Arg Thr Asp Leu Asp Thr Ile Thr Leu Leu
225                 230                 235                 240

Ala Lys Asn Ile Lys Ala Asn Lys Glu Val Glu Phe Lys Arg Ile Val
                245                 250                 255

Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu Asp Thr Trp
            260                 265                 270

Leu Thr Met Leu Asp Lys Asn Lys Phe Leu Tyr Ser Pro Ile Ala Asn
        275                 280                 285

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

Pro Gln Pro Gln Leu Asn Gly Leu Pro Leu Asp Lys Leu Leu Ala Ser
305                 310                 315                 320

Ile Ile Asn Lys Glu Pro Val Leu Ile Pro Ile Gly Gly Ala Gly Ala
                325                 330                 335

Thr Glu Met Glu Ile Ala Arg Glu Thr Asn Phe Asp Gly Thr Asn Tyr
            340                 345                 350

Leu Ala Ile Lys Pro Gly Leu Val Ile Gly Tyr Asp Arg Asn Glu Lys
        355                 360                 365

Thr Asn Ala Ala Leu Lys Ala Ala Gly Ile Thr Val Leu Pro Phe His
    370                 375                 380

Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys Met Ser Met
385                 390                 395                 400

Pro Leu Ser Arg Lys Asp Val Lys Trp
                405
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<210> 29
<211> 411
<212> PRT
<213> Streptococcus pyogenes

<400> 29

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Met Thr Ala Gln Thr Pro Ile His Val Tyr Ser Glu Ile Gly Lys Leu
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Lys Lys Val Leu Leu His Arg Pro Gly Lys Glu Ile Glu Asn Leu Met
            20                  25                  30

Pro Asp Tyr Leu Glu Arg Leu Leu Phe Asp Asp Ile Pro Phe Leu Glu
        35                  40                  45

Asp Ala Gln Lys Glu His Asp Ala Phe Ala Gln Ala Leu Arg Asp Glu
    50                  55                  60

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

Thr Pro Glu Ile Arg Glu Ala Phe Ile Asp Glu Tyr Leu Ser Glu Ala
                85                  90                  95

Asn Ile Arg Gly Arg Ala Thr Lys Lys Ala Ile Arg Glu Leu Leu Met
            100                 105                 110

Ala Ile Glu Asp Asn Gln Glu Leu Ile Glu Lys Thr Met Ala Gly Val
        115                 120                 125

Gln Lys Ser Glu Leu Pro Glu Ile Pro Ala Ser Glu Lys Gly Leu Thr
    130                 135                 140

Asp Leu Val Glu Ser Ser Tyr Pro Phe Ala Ile Asp Pro Met Pro Asn
145                 150                 155                 160

Leu Tyr Phe Thr Arg Asp Pro Phe Ala Thr Ile Gly Thr Gly Val Ser
                165                 170                 175

Leu Asn His Met Phe Ser Glu Thr Arg Asn Arg Glu Thr Leu Tyr Gly
            180                 185                 190

Lys Tyr Ile Phe Thr His His Pro Ile Tyr Gly Gly Gly Lys Val Pro
        195                 200                 205

Met Val Tyr Asp Arg Asn Glu Thr Thr Arg Ile Glu Gly Gly Asp Glu
    210                 215                 220

Leu Val Leu Ser Lys Asp Val Leu Ala Val Gly Ile Ser Gln Arg Thr
225                 230                 235                 240
```

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Asp Ala Ala Ser Ile Glu Lys Leu Leu Val Asn Ile Phe Lys Gln Asn
                245                 250                 255

Leu Gly Phe Lys Lys Val Leu Ala Phe Glu Phe Ala Asn Asn Arg Lys
            260                 265                 270

Phe Met His Leu Asp Thr Val Phe Thr Met Val Asp Tyr Asp Lys Phe
        275                 280                 285

Thr Ile His Pro Glu Ile Glu Gly Asp Leu Arg Val Tyr Ser Val Thr
    290                 295                 300

Tyr Asp Asn Glu Glu Leu His Ile Val Glu Glu Lys Gly Asp Leu Ala
305                 310                 315                 320

Asp Leu Leu Ala Ala Asn Leu Gly Val Glu Lys Val Asp Leu Ile Arg
                325                 330                 335

Cys Gly Gly Asp Asn Leu Val Ala Ala Gly Arg Glu Gln Trp Asn Asp
            340                 345                 350

Gly Ser Asn Thr Leu Thr Ile Ala Pro Gly Val Val Val Val Tyr Asn
        355                 360                 365

Arg Asn Thr Ile Thr Asn Ala Ile Leu Glu Ser Lys Gly Leu Lys Leu
    370                 375                 380

Ile Lys Ile His Gly Ser Glu Leu Val Arg Gly Arg Gly Gly Pro Arg
385                 390                 395                 400

Cys Met Ser Met Pro Phe Glu Arg Glu Asp Ile
                405                 410
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<210> 30
<211> 409
<212> PRT
<213> Streptococcus pneumonia

<400> 30

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Met Ser Ser His Pro Ile Gln Val Phe Ser Glu Ile Gly Lys Leu Lys
1               5                   10                  15

Lys Val Met Leu His Arg Pro Gly Lys Glu Leu Glu Asn Leu Leu Pro
            20                  25                  30

Asp Tyr Leu Glu Arg Leu Leu Phe Asp Asp Ile Pro Phe Leu Glu Asp
        35                  40                  45

Ala Gln Lys Glu His Asp Ala Phe Ala Gln Ala Leu Arg Asp Glu Gly
    50                  55                  60

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

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

Ile Arg Asp Arg Gln Thr Lys Val Ala Ile Arg Glu Leu Leu His Gly
100 105 110

Ile Lys Asp Asn Gln Glu Leu Val Glu Lys Thr Met Ala Gly Ile Gln
115 120 125

Lys Val Glu Leu Pro Glu Ile Pro Asp Glu Ala Lys Asp Leu Thr Asp
130 135 140

Leu Val Glu Ser Asp Tyr Pro Phe Ala Ile Asp Pro Met Pro Asn Leu
145 150 155 160

Tyr Phe Thr Arg Asp Pro Phe Ala Thr Ile Gly Asn Ala Val Ser Leu
165 170 175

Asn His Met Phe Ala Asp Thr Arg Asn Arg Glu Thr Leu Tyr Gly Lys
180 185 190

Tyr Ile Phe Lys Tyr His Pro Ile Tyr Gly Gly Lys Val Asp Leu Val
195 200 205

Tyr Asn Arg Glu Glu Asp Thr Arg Ile Glu Gly Gly Asp Glu Leu Val
210 215 220

Leu Ser Lys Asp Val Leu Ala Val Gly Ile Ser Gln Arg Thr Asp Ala
225 230 235 240

Ala Ser Ile Glu Lys Leu Leu Val Asn Ile Phe Lys Lys Asn Val Gly
245 250 255

Phe Lys Lys Val Leu Ala Phe Glu Phe Ala Asn Asn Arg Lys Phe Met
260 265 270

His Leu Asp Thr Val Phe Thr Met Val Asp Tyr Asp Lys Phe Thr Ile
275 280 285

His Pro Glu Ile Glu Gly Asp Leu His Val Tyr Ser Val Thr Tyr Glu
290 295 300

Asn Glu Lys Leu Lys Ile Val Glu Glu Lys Gly Asp Leu Ala Glu Leu
305 310 315 320

Leu Ala Gln Asn Leu Gly Val Glu Lys Val His Leu Ile Arg Cys Gly
325 330 335

Gly Gly Asn Ile Val Ala Ala Ala Arg Glu Gln Trp Asn Asp Gly Ser

340 345 350

Asn Thr Leu Thr Ile Ala Pro Gly Val Val Val Val Tyr Asp Arg Asn
355 360 365

Thr Val Thr Asn Lys Ile Leu Glu Glu Tyr Gly Leu Arg Leu Ile Lys
370 375 380

Ile Arg Gly Ser Glu Leu Val Arg Gly Arg Gly Gly Pro Arg Cys Met
385 390 395 400

Ser Met Pro Phe Glu Arg Glu Glu Val
405

<210> 31
<211> 402
<212> PRT
<213> Mycobacterium tuberculosis

<400> 31

Met Gly Val Glu Leu Gly Ser Asn Ser Glu Val Gly Ala Leu Arg Val
1 5 10 15

Val Ile Leu His Arg Pro Gly Ala Glu Leu Arg Arg Leu Thr Pro Arg
20 25 30

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

Gln Asp Glu His Asp Glu Phe Ala Glu Leu Leu Ala Ser Arg Gly Ala
50 55 60

Glu Val Leu Leu Leu Ser Asp Leu Leu Thr Glu Ala Leu His His Ser
65 70 75 80

Gly Ala Ala Arg Met Gln Gly Ile Ala Ala Ala Val Asp Ala Pro Arg
85 90 95

Leu Gly Leu Pro Leu Ala Gln Glu Leu Ser Ala Tyr Leu Arg Ser Leu
100 105 110

Asp Pro Gly Arg Leu Ala His Val Leu Thr Ala Gly Met Thr Phe Asn
115 120 125

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

His His Gly Gly Asp Phe Val Ile Glu Pro Leu Pro Asn Leu Val Phe
145 150 155 160

Thr Arg Asp Ser Ser Ile Trp Ile Gly Pro Arg Val Val Ile Pro Ser
165 170 175

Leu Ala Leu Arg Ala Arg Val Arg Glu Ala Ser Leu Thr Asp Leu Ile
180 185 190

Tyr Ala His His Pro Arg Phe Thr Gly Val Arg Arg Ala Tyr Glu Ser
195 200 205

Arg Thr Ala Pro Val Glu Gly Gly Asp Val Leu Leu Leu Ala Pro Gly
210 215 220

Val Val Ala Val Gly Val Gly Glu Arg Thr Thr Pro Ala Gly Ala Glu
225 230 235 240

Ala Leu Ala Arg Ser Leu Phe Asp Asp Asp Leu Ala His Thr Val Leu
245 250 255

Ala Val Pro Ile Ala Gln Gln Arg Ala Gln Met His Leu Asp Thr Val
260 265 270

Cys Thr Met Val Asp Thr Asp Thr Met Val Met Tyr Ala Asn Val Val
275 280 285

Asp Thr Leu Glu Ala Phe Thr Ile Gln Arg Thr Pro Asp Gly Val Thr
290 295 300

Ile Gly Asp Ala Ala Pro Phe Ala Glu Ala Ala Ala Lys Ala Met Gly
305 310 315 320

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

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

Gly Val Val Val Ala Tyr Glu Arg Asn Val Gln Thr Asn Ala Arg Leu
355 360 365

Gln Asp Ala Gly Ile Glu Val Leu Thr Ile Ala Gly Ser Glu Leu Gly
370 375 380

Thr Gly Arg Gly Gly Pro Arg Cys Met Ser Cys Pro Ala Ala Arg Asp
385 390 395 400

Pro Leu

<210> 32
<211> 417
<212> PRT
<213> Pseudomonas plecoglossicida

<400> 32

```
Met Ser Thr Glu Lys Gln Lys Tyr Gly Val His Ser Glu Ala Gly Lys
1               5                  10                  15

Leu Arg Lys Val Met Val Cys Ser Pro Gly Leu Ala His Lys Arg Leu
            20                  25                  30

Thr Pro Ser Asn Cys Asp Glu Leu Leu Phe Asp Asp Val Ile Trp Val
        35                  40                  45

Asp Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu
    50                  55                  60

Arg Gly Val Asp Val Leu Glu Met His Asn Leu Leu Thr Asp Ile Val
65                  70                  75                  80

Gln Asp Lys Asn Ala Leu Lys Trp Ile Leu Asp Arg Lys Leu Thr Asp
                85                  90                  95

Asp Thr Val Gly Val Gly Leu Lys Asn Glu Val Arg Ser Trp Leu Glu
            100                 105                 110

Gly Gln Asp Pro Arg His Leu Ala Glu Phe Leu Ile Gly Gly Val Ala
        115                 120                 125

Gly Gln Asp Leu Pro Gln Ser Glu Gly Ala Asp Val Val Lys Met Tyr
    130                 135                 140

Asn Asp Tyr Leu Gly His Ser Ser Phe Ile Leu Pro Pro Leu Pro Asn
145                 150                 155                 160

Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr
                165                 170                 175

Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr
            180                 185                 190

Thr Ala Ile Tyr Lys Phe His Lys Glu Phe Thr Asn Ala Glu Phe Glu
        195                 200                 205

Val Trp Tyr Gly Asp Pro Asp Lys Glu His Gly Ser Ser Thr Leu Glu
    210                 215                 220

Gly Gly Asp Val Met Pro Ile Gly Lys Gly Ile Val Leu Ile Gly Met
225                 230                 235                 240

Gly Glu Arg Thr Ser Arg Gln Ala Ile Gly Gln Leu Ala Arg Asn Leu
                245                 250                 255

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

Ser Arg Ala Ala Met His Leu Asp Thr Val Phe Ser Phe Cys Asp Arg
275 280 285

Asp Leu Val Thr Val Phe Pro Glu Val Val Asn Glu Ile Val Pro Phe
290 295 300

Ile Ile Arg Pro Asp Glu Lys Lys Pro Tyr Gly Met Asp Val Arg Arg
305 310 315 320

Ile Asn Lys Ser Phe Ile Glu Val Val Gly Glu Gln Leu Gly Val Lys
325 330 335

Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg Glu
340 345 350

Gln Trp Asp Asp Gly Asn Asn Val Val Ala Ile Glu Pro Gly Val Val
355 360 365

Ile Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu Arg Lys Ala
370 375 380

Gly Ile Glu Val Ile Thr Ile Ser Ala Gly Glu Leu Gly Arg Gly Arg
385 390 395 400

Gly Gly Gly His Cys Met Thr Cys Pro Ile Val Arg Asp Pro Ile Asp
405 410 415

Tyr

<210> 33
<211> 420
<212> PRT
<213> Pseudomonas putida

<400> 33

Met Ser Ala Glu Lys Gln Lys Tyr Gly Val His Ser Glu Ala Gly Lys
1 5 10 15

Leu Arg Lys Val Met Val Cys Ser Pro Gly Leu Ala His Lys Arg Leu
20 25 30

Thr Pro Ser Asn Cys Asp Glu Leu Leu Phe Asp Asp Val Ile Trp Val
35 40 45

Asp Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu
50 55 60

Arg Gly Val Asp Val Leu Glu Met His Asn Leu Leu Thr Asp Ile Val
65 70 75 80

```
Gln Gln Pro Glu Ala Leu Lys Trp Ile Leu Asp Arg Lys Ile Thr Ser
                85                  90                  95

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

Gly Leu Glu Pro Arg His Leu Ala Glu Phe Leu Ile Gly Gly Val Ala
        115                 120                 125

Gly Gln Asp Leu Pro Val Ser Glu Gly Ala Glu Val Ile Lys Met Tyr
    130                 135                 140

Asn Lys Tyr Leu Gly His Ser Ser Phe Ile Leu Pro Pro Leu Pro Asn
145                 150                 155                 160

Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr
                165                 170                 175

Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr
            180                 185                 190

Thr Ala Ile Tyr Lys Phe His Lys Glu Phe Thr Gly Ala Asp Phe Gln
        195                 200                 205

Val Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Asn Ala Thr Leu Glu
    210                 215                 220

Gly Gly Asp Val Met Pro Val Gly Lys Gly Ile Val Leu Ile Gly Met
225                 230                 235                 240

Gly Glu Arg Thr Ser Arg His Ala Ile Gly Gln Leu Ala Gln Asn Leu
                245                 250                 255

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

Ser Arg Ala Ala Met His Leu Asp Thr Val Phe Ser Phe Cys Asp Arg
        275                 280                 285

Asp Leu Val Thr Val Phe Pro Glu Val Val Lys Glu Ile Lys Pro Phe
    290                 295                 300

Ile Ile Thr Pro Asp Ser Ser Lys Pro Tyr Gly Met Asn Ile Ala Pro
305                 310                 315                 320

Gln Asp Ala Ser Phe Leu Glu Val Val Ser Glu Gln Leu Leu Gly Lys
                325                 330                 335

Lys Asp Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala
            340                 345                 350
```

```
Glu Arg Glu Gln Trp Asp Asp Gly Asn Asn Val Val Ala Leu Glu Pro
        355                 360                 365


Gly Val Val Ile Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu
    370                 375                 380


Arg Lys Ala Gly Ile Glu Val Ile Thr Ile Ser Ala Gly Glu Leu Gly
385                 390                 395                 400


Arg Gly Arg Gly Gly Gly His Cys Met Thr Cys Pro Ile Val Arg Asp
                405                 410                 415


Pro Ile Asp Tyr
            420


<210>  34
<211>  418
<212>  PRT
<213>  Pseudomonas aeruginosa

<400>  34

Met Ser Thr Glu Lys Thr Lys Leu Gly Val His Ser Glu Ala Gly Lys
1               5                   10                  15


Leu Arg Lys Val Met Val Cys Ser Pro Gly Leu Ala His Gln Arg Leu
            20                  25                  30


Thr Pro Ser Asn Cys Asp Glu Leu Leu Phe Asp Asp Val Ile Trp Val
        35                  40                  45


Asn Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu
    50                  55                  60


Arg Gly Ile Asp Val Leu Glu Met His Asn Leu Leu Thr Glu Thr Ile
65                  70                  75                  80


Gln Asn Pro Glu Ala Leu Lys Trp Ile Leu Asp Arg Lys Ile Thr Ala
                85                  90                  95


Asp Ser Val Gly Leu Gly Leu Thr Ser Glu Leu Arg Ser Trp Leu Glu
            100                 105                 110


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


Ala Asp Asp Leu Pro Ala Ser Glu Gly Ala Asn Ile Leu Lys Met Tyr
    130                 135                 140


Arg Glu Tyr Leu Gly His Ser Ser Phe Leu Leu Pro Pro Leu Pro Asn
145                 150                 155                 160


Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr
```

165 170 175

Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr
180 185 190

Thr Ala Ile Tyr Lys Phe His Pro Glu Phe Ala Asn Ala Glu Phe Glu
195 200 205

Ile Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Ser Ser Thr Leu Glu
210 215 220

Gly Gly Asp Val Met Pro Ile Gly Asn Gly Val Val Leu Ile Gly Met
225 230 235 240

Gly Glu Arg Ser Ser Arg Gln Ala Ile Gly Gln Val Ala Gln Ser Leu
245 250 255

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

Ser Arg Ala Ala Met His Leu Asp Thr Val Phe Ser Phe Cys Asp Arg
275 280 285

Asp Leu Val Thr Val Phe Pro Glu Val Val Lys Glu Ile Val Pro Phe
290 295 300

Ser Leu Arg Pro Asp Pro Ser Ser Pro Tyr Gly Met Asn Ile Arg Arg
305 310 315 320

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

Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg
340 345 350

Glu Gln Trp Asp Asp Gly Asn Asn Val Val Cys Leu Glu Pro Gly Val
355 360 365

Val Val Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu Arg Lys
370 375 380

Ala Gly Val Glu Val Ile Thr Ile Ser Ala Ser Glu Leu Gly Arg Gly
385 390 395 400

Arg Gly Gly Gly His Cys Met Thr Cys Pro Ile Val Arg Asp Pro Ile
405 410 415

Asp Tyr

<210> 35

<211> 409
<212> PRT
<213> Streptococcus pneumoniae

<400> 35

```
Met Ser Ser His Pro Ile Gln Val Phe Ser Glu Ile Gly Lys Leu Lys
1               5                  10                  15

Lys Val Met Leu His Arg Pro Gly Lys Glu Leu Glu Asn Leu Leu Pro
            20                  25                  30

Asp Tyr Leu Glu Arg Leu Leu Phe Asp Asp Ile Pro Phe Leu Glu Asp
        35                  40                  45

Ala Gln Lys Glu His Asp Ala Phe Ala Gln Ala Leu Arg Asp Glu Gly
    50                  55                  60

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

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

Ile Arg Asp Arg Gln Thr Lys Val Ala Ile Arg Glu Leu Leu His Gly
            100                 105                 110

Ile Lys Asp Asn Gln Glu Leu Val Glu Lys Thr Met Ala Gly Ile Gln
        115                 120                 125

Lys Val Glu Leu Pro Glu Ile Pro Asp Glu Ala Lys Asp Leu Thr Asp
    130                 135                 140

Leu Val Glu Ser Asp Tyr Pro Phe Ala Ile Asp Pro Met Pro Asn Leu
145                 150                 155                 160

Tyr Phe Thr Arg Asp Pro Phe Ala Thr Ile Gly Asn Ala Val Ser Leu
                165                 170                 175

Asn His Met Phe Ala Asp Thr Arg Asn Arg Glu Thr Leu Tyr Gly Lys
            180                 185                 190

Tyr Ile Phe Lys Tyr His Pro Ile Tyr Gly Gly Lys Val Asp Leu Val
        195                 200                 205

Tyr Asn Arg Glu Glu Asp Thr Arg Ile Glu Gly Gly Asp Glu Leu Val
    210                 215                 220

Leu Ser Lys Asp Val Leu Ala Val Gly Ile Ser Gln Arg Thr Asp Ala
225                 230                 235                 240

Ala Ser Ile Glu Lys Leu Leu Val Asn Ile Phe Lys Lys Asn Val Gly
                245                 250                 255
```

```
Phe Lys Lys Val Leu Ala Phe Glu Phe Ala Asn Asn Arg Lys Phe Met
            260                 265                 270

His Leu Asp Thr Val Phe Thr Met Val Asp Tyr Asp Lys Phe Thr Ile
        275                 280                 285

His Pro Glu Ile Glu Gly Asp Leu His Val Tyr Ser Val Thr Tyr Glu
    290                 295                 300

Asn Glu Lys Leu Lys Ile Val Glu Glu Lys Gly Asp Leu Ala Glu Leu
305                 310                 315                 320

Leu Ala Gln Asn Leu Gly Val Glu Lys Val His Leu Ile Arg Cys Gly
                325                 330                 335

Gly Gly Asn Ile Val Ala Ala Ala Arg Glu Gln Trp Asn Asp Gly Ser
            340                 345                 350

Asn Thr Leu Thr Ile Ala Pro Gly Val Val Val Val Tyr Asp Arg Asn
        355                 360                 365

Thr Val Thr Asn Lys Ile Leu Glu Glu Tyr Gly Leu Arg Leu Ile Lys
    370                 375                 380

Ile Arg Gly Ser Glu Leu Val Arg Gly Arg Gly Gly Pro Arg Cys Met
385                 390                 395                 400

Ser Met Pro Phe Glu Arg Glu Glu Val
                405


<210>  36
<211>  467
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ABD1: high affinity albumin binding domain, synthesized in laboratory

<400>  36

Met Ser Val Phe Asp Ser Lys Phe Lys Gly Ile His Val Tyr Ser Glu
1               5                   10                  15

Ile Gly Glu Leu Glu Ser Val Leu Val His Glu Pro Gly Arg Glu Ile
            20                  25                  30

Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Leu Phe Ser Ala Ile
        35                  40                  45

Leu Glu Ser His Asp Ala Arg Lys Glu His Lys Gln Phe Val Ala Glu
    50                  55                  60
```

```
Leu Lys Ala Asn Asp Ile Asn Val Val Glu Leu Ile Asp Leu Val Ala
65                  70                  75                  80

Glu Thr Tyr Asp Leu Ala Ser Gln Glu Ala Lys Asp Lys Leu Ile Glu
                85                  90                  95

Glu Phe Leu Glu Asp Ser Glu Pro Val Leu Ser Glu Glu His Lys Val
            100                 105                 110

Val Val Arg Asn Phe Leu Lys Ala Lys Lys Thr Ser Arg Glu Leu Val
        115                 120                 125

Glu Ile Met Met Ala Gly Ile Thr Lys Tyr Asp Leu Gly Ile Glu Ala
    130                 135                 140

Asp His Glu Leu Ile Val Asp Pro Met Pro Asn Leu Tyr Phe Thr Arg
145                 150                 155                 160

Asp Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Tyr Met Arg
                165                 170                 175

Tyr Lys Val Arg Gln Arg Glu Thr Leu Phe Ser Arg Phe Val Phe Ser
            180                 185                 190

Asn His Pro Lys Leu Ile Asn Thr Pro Trp Tyr Tyr Asp Pro Ser Leu
        195                 200                 205

Lys Leu Ser Ile Glu Gly Gly Asp Val Phe Ile Tyr Asn Asn Asp Thr
    210                 215                 220

Leu Val Val Gly Val Ser Glu Arg Thr Asp Leu Gln Thr Val Thr Leu
225                 230                 235                 240

Leu Ala Lys Asn Ile Val Ala Asn Lys Glu Cys Glu Phe Lys Arg Ile
                245                 250                 255

Val Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu Asp Thr
            260                 265                 270

Trp Leu Thr Met Leu Asp Lys Asp Lys Phe Leu Tyr Ser Pro Ile Ala
        275                 280                 285

Asn Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val Asn Gly Gly Ala
    290                 295                 300

Glu Pro Gln Pro Val Glu Asn Gly Leu Pro Leu Glu Gly Leu Leu Gln
305                 310                 315                 320

Ser Ile Ile Asn Lys Lys Pro Val Leu Ile Pro Ile Ala Gly Glu Gly
                325                 330                 335
```

Ala Ser Gln Met Glu Ile Glu Arg Glu Thr His Phe Asp Gly Thr Asn
340 345 350

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

Lys Thr Asn Ala Ala Leu Glu Ala Ala Gly Ile Lys Val Leu Pro Phe
370 375 380

His Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys Met Ser
385 390 395 400

Met Pro Leu Ser Arg Lys Asp Val Lys Trp Gly Ser His His His His
405 410 415

His His Ala Asn Ser Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu
420 425 430

Leu Asp Lys Tyr Gly Val Ser Asp Phe Tyr Lys Arg Leu Ile Asn Lys
435 440 445

Ala Lys Thr Val Glu Gly Val Glu Ala Leu Lys Leu His Ile Leu Ala
450 455 460

Ala Leu Pro
465

<210> 37
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> ABD: albumin binding domain, synthesized in laboratory

<400> 37

Met Ser Val Phe Asp Ser Lys Phe Lys Gly Ile His Val Tyr Ser Glu
1 5 10 15

Ile Gly Glu Leu Glu Ser Val Leu Val His Glu Pro Gly Arg Glu Ile
20 25 30

Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Leu Phe Ser Ala Ile
35 40 45

Leu Glu Ser His Asp Ala Arg Lys Glu His Lys Gln Phe Val Ala Glu
50 55 60

Leu Lys Ala Asn Asp Ile Asn Val Val Glu Leu Ile Asp Leu Val Ala
65 70 75 80

Glu Thr Tyr Asp Leu Ala Ser Gln Glu Ala Lys Asp Lys Leu Ile Glu
85 90 95

```
Glu Phe Leu Glu Asp Ser Glu Pro Val Leu Ser Glu Glu His Lys Val
            100                 105                 110

Val Val Arg Asn Phe Leu Lys Ala Lys Lys Thr Ser Arg Glu Leu Val
        115                 120                 125

Glu Ile Met Met Ala Gly Ile Thr Lys Tyr Asp Leu Gly Ile Glu Ala
    130                 135                 140

Asp His Glu Leu Ile Val Asp Pro Met Pro Asn Leu Tyr Phe Thr Arg
145                 150                 155                 160

Asp Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Tyr Met Arg
                165                 170                 175

Tyr Lys Val Arg Gln Arg Glu Thr Leu Phe Ser Arg Phe Val Phe Ser
            180                 185                 190

Asn His Pro Lys Leu Ile Asn Thr Pro Trp Tyr Tyr Asp Pro Ser Leu
        195                 200                 205

Lys Leu Ser Ile Glu Gly Gly Asp Val Phe Ile Tyr Asn Asn Asp Thr
    210                 215                 220

Leu Val Val Gly Val Ser Glu Arg Thr Asp Leu Gln Thr Val Thr Leu
225                 230                 235                 240

Leu Ala Lys Asn Ile Val Ala Asn Lys Glu Cys Glu Phe Lys Arg Ile
                245                 250                 255

Val Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu Asp Thr
            260                 265                 270

Trp Leu Thr Met Leu Asp Lys Asp Lys Phe Leu Tyr Ser Pro Ile Ala
        275                 280                 285

Asn Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val Asn Gly Gly Ala
    290                 295                 300

Glu Pro Gln Pro Val Glu Asn Gly Leu Pro Leu Glu Gly Leu Leu Gln
305                 310                 315                 320

Ser Ile Ile Asn Lys Lys Pro Val Leu Ile Pro Ile Ala Gly Glu Gly
                325                 330                 335

Ala Ser Gln Met Glu Ile Glu Arg Glu Thr His Phe Asp Gly Thr Asn
            340                 345                 350

Tyr Leu Ala Ile Arg Pro Gly Val Val Ile Gly Tyr Ser Arg Asn Glu
        355                 360                 365
```

Lys Thr Asn Ala Ala Leu Glu Ala Ala Gly Ile Lys Val Leu Pro Phe
370 375 380

His Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys Met Ser
385 390 395 400

Met Pro Leu Ser Arg Lys Asp Val Lys Trp Ala Gln His Asp Glu Ala
405 410 415

Val Asp Ala Asn Ser Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu
420 425 430

Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn Asn
435 440 445

Ala Lys Thr Val Glu Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala
450 455 460

Ala Leu Pro
465

<210> 38
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> ABD: albumin binding domain, synthesized in laboratory

<400> 38

Met Ser Val Phe Asp Ser Lys Phe Lys Gly Ile His Val Tyr Ser Glu
1 5 10 15

Ile Gly Glu Leu Glu Ser Val Leu Val His Glu Pro Gly Arg Glu Ile
20 25 30

Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Leu Phe Ser Ala Ile
35 40 45

Leu Glu Ser His Asp Ala Arg Lys Glu His Lys Gln Phe Val Ala Glu
50 55 60

Leu Lys Ala Asn Asp Ile Asn Val Val Glu Leu Ile Asp Leu Val Ala
65 70 75 80

Glu Thr Tyr Asp Leu Ala Ser Gln Glu Ala Lys Asp Lys Leu Ile Glu
85 90 95

Glu Phe Leu Glu Asp Ser Glu Pro Val Leu Ser Glu Glu His Lys Val
100 105 110

```
Val Val Arg Asn Phe Leu Lys Ala Lys Lys Thr Ser Arg Glu Leu Val
        115                 120                 125

Glu Ile Met Met Ala Gly Ile Thr Lys Tyr Asp Leu Gly Ile Glu Ala
    130                 135                 140

Asp His Glu Leu Ile Val Asp Pro Met Pro Asn Leu Tyr Phe Thr Arg
145                 150                 155                 160

Asp Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Tyr Met Arg
                165                 170                 175

Tyr Lys Val Arg Gln Arg Glu Thr Leu Phe Ser Arg Phe Val Phe Ser
            180                 185                 190

Asn His Pro Lys Leu Ile Asn Thr Pro Trp Tyr Tyr Asp Pro Ser Leu
        195                 200                 205

Lys Leu Ser Ile Glu Gly Gly Asp Val Phe Ile Tyr Asn Asn Asp Thr
    210                 215                 220

Leu Val Val Gly Val Ser Glu Arg Thr Asp Leu Gln Thr Val Thr Leu
225                 230                 235                 240

Leu Ala Lys Asn Ile Val Ala Asn Lys Glu Cys Glu Phe Lys Arg Ile
                245                 250                 255

Val Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu Asp Thr
            260                 265                 270

Trp Leu Thr Met Leu Asp Lys Asp Lys Phe Leu Tyr Ser Pro Ile Ala
        275                 280                 285

Asn Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val Asn Gly Gly Ala
    290                 295                 300

Glu Pro Gln Pro Val Glu Asn Gly Leu Pro Leu Glu Gly Leu Leu Gln
305                 310                 315                 320

Ser Ile Ile Asn Lys Lys Pro Val Leu Ile Pro Ile Ala Gly Glu Gly
                325                 330                 335

Ala Ser Gln Met Glu Ile Glu Arg Glu Thr His Phe Asp Gly Thr Asn
            340                 345                 350

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

Lys Thr Asn Ala Ala Leu Glu Ala Ala Gly Ile Lys Val Leu Pro Phe
    370                 375                 380
```

His Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys Met Ser
385 390 395 400

Met Pro Leu Ser Arg Lys Asp Val Lys Trp His His His His His His
405 410 415

Ala Gln His Asp Glu Ala Val Asp Ala Asn Ser Leu Ala Glu Ala Lys
420 425 430

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

Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu
450 455 460

Ile Asp Glu Ile Leu Ala Ala Leu Pro
465 470

<210> 39
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> ABD: albumin binding domain, synthesized in laboratory

<400> 39

Met Ser Val Phe Asp Ser Lys Phe Lys Gly Ile His Val Tyr Ser Glu
1 5 10 15

Ile Gly Glu Leu Glu Ser Val Leu Val His Glu Pro Gly Arg Glu Ile
20 25 30

Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Leu Phe Ser Ala Ile
35 40 45

Leu Glu Ser His Asp Ala Arg Lys Glu His Lys Gln Phe Val Ala Glu
50 55 60

Leu Lys Ala Asn Asp Ile Asn Val Val Glu Leu Ile Asp Leu Val Ala
65 70 75 80

Glu Thr Tyr Asp Leu Ala Ser Gln Glu Ala Lys Asp Lys Leu Ile Glu
85 90 95

Glu Phe Leu Glu Asp Ser Glu Pro Val Leu Ser Glu Glu His Lys Val
100 105 110

Val Val Arg Asn Phe Leu Lys Ala Lys Lys Thr Ser Arg Glu Leu Val
115 120 125

Glu Ile Met Met Ala Gly Ile Thr Lys Tyr Asp Leu Gly Ile Glu Ala
130 135 140

```
Asp His Glu Leu Ile Val Asp Pro Met Pro Asn Leu Tyr Phe Thr Arg
145                 150                 155                 160

Asp Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Tyr Met Arg
                165                 170                 175

Tyr Lys Val Arg Gln Arg Glu Thr Leu Phe Ser Arg Phe Val Phe Ser
            180                 185                 190

Asn His Pro Lys Leu Ile Asn Thr Pro Trp Tyr Tyr Asp Pro Ser Leu
        195                 200                 205

Lys Leu Ser Ile Glu Gly Gly Asp Val Phe Ile Tyr Asn Asn Asp Thr
    210                 215                 220

Leu Val Val Gly Val Ser Glu Arg Thr Asp Leu Gln Thr Val Thr Leu
225                 230                 235                 240

Leu Ala Lys Asn Ile Val Ala Asn Lys Glu Cys Glu Phe Lys Arg Ile
                245                 250                 255

Val Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu Asp Thr
            260                 265                 270

Trp Leu Thr Met Leu Asp Lys Asp Lys Phe Leu Tyr Ser Pro Ile Ala
        275                 280                 285

Asn Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val Asn Gly Gly Ala
    290                 295                 300

Glu Pro Gln Pro Val Glu Asn Gly Leu Pro Leu Glu Gly Leu Leu Gln
305                 310                 315                 320

Ser Ile Ile Asn Lys Lys Pro Val Leu Ile Pro Ile Ala Gly Glu Gly
                325                 330                 335

Ala Ser Gln Met Glu Ile Glu Arg Glu Thr His Phe Asp Gly Thr Asn
            340                 345                 350

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

Lys Thr Asn Ala Ala Leu Glu Ala Ala Gly Ile Lys Val Leu Pro Phe
    370                 375                 380

His Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys Met Ser
385                 390                 395                 400

Met Pro Leu Ser Arg Lys Asp Val Lys Trp Ala Gln His Asp Glu Ala
                405                 410                 415
```

Val Asp Ala Asn Ser Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu
420 425 430

Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn Asn
435 440 445

Ala Lys Thr Val Glu Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala
450 455 460

Ala Leu Pro His His His His His His
465 470

<210> 40
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> ABD: albumin binding domain, synthesized in laboratory

<400> 40

Met His His His His His His Asp Glu Ala Val Asp Ala Asn Ser Leu
1 5 10 15

Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val
20 25 30

Ser Asp Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly
35 40 45

Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro Ser Gly Ser
50 55 60

Asn Asn Asn Asn Asn Asn Gly Ser Gly Gly Ser Val Phe Asp Ser Lys
65 70 75 80

Phe Lys Gly Ile His Val Tyr Ser Glu Ile Gly Glu Leu Glu Ser Val
85 90 95

Leu Val His Glu Pro Gly Arg Glu Ile Asp Tyr Ile Thr Pro Ala Arg
100 105 110

Leu Asp Glu Leu Leu Phe Ser Ala Ile Leu Glu Ser His Asp Ala Arg
115 120 125

Lys Glu His Lys Gln Phe Val Ala Glu Leu Lys Ala Asn Asp Ile Asn
130 135 140

Val Val Glu Leu Ile Asp Leu Val Ala Glu Thr Tyr Asp Leu Ala Ser
145 150 155 160

```
Gln Glu Ala Lys Asp Lys Leu Ile Glu Glu Phe Leu Glu Asp Ser Glu
                165                 170                 175

Pro Val Leu Ser Glu Glu His Lys Val Val Val Arg Asn Phe Leu Lys
            180                 185                 190

Ala Lys Lys Thr Ser Arg Glu Leu Val Glu Ile Met Met Ala Gly Ile
        195                 200                 205

Thr Lys Tyr Asp Leu Gly Ile Glu Ala Asp His Glu Leu Ile Val Asp
    210                 215                 220

Pro Met Pro Asn Leu Tyr Phe Thr Arg Asp Pro Phe Ala Ser Val Gly
225                 230                 235                 240

Asn Gly Val Thr Ile His Tyr Met Arg Tyr Lys Val Arg Gln Arg Glu
                245                 250                 255

Thr Leu Phe Ser Arg Phe Val Phe Ser Asn His Pro Lys Leu Ile Asn
            260                 265                 270

Thr Pro Trp Tyr Tyr Asp Pro Ser Leu Lys Leu Ser Ile Glu Gly Gly
        275                 280                 285

Asp Val Phe Ile Tyr Asn Asn Asp Thr Leu Val Val Gly Val Ser Glu
    290                 295                 300

Arg Thr Asp Leu Gln Thr Val Thr Leu Leu Ala Lys Asn Ile Val Ala
305                 310                 315                 320

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

Trp Thr Asn Leu Met His Leu Asp Thr Trp Leu Thr Met Leu Asp Lys
            340                 345                 350

Asp Lys Phe Leu Tyr Ser Pro Ile Ala Asn Asp Val Phe Lys Phe Trp
        355                 360                 365

Asp Tyr Asp Leu Val Asn Gly Gly Ala Glu Pro Gln Pro Val Glu Asn
    370                 375                 380

Gly Leu Pro Leu Glu Gly Leu Leu Gln Ser Ile Ile Asn Lys Lys Pro
385                 390                 395                 400

Val Leu Ile Pro Ile Ala Gly Glu Gly Ala Ser Gln Met Glu Ile Glu
                405                 410                 415

Arg Glu Thr His Phe Asp Gly Thr Asn Tyr Leu Ala Ile Arg Pro Gly
            420                 425                 430
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Val Val Ile Gly Tyr Ser Arg Asn Glu Lys Thr Asn Ala Ala Leu Glu
435 440 445

Ala Ala Gly Ile Lys Val Leu Pro Phe His Gly Asn Gln Leu Ser Leu
450 455 460

Gly Met Gly Asn Ala Arg Cys Met Ser Met Pro Leu Ser Arg Lys Asp
465 470 475 480

Val Lys Trp

<210> 41
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> His-ABD-PolyN-bcADI, synthesized in laboratory

<400> 41

Met Gly His His His His His His Asp Glu Ala Val Asp Ala Asn Ser
1 5 10 15

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
20 25 30

Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu
35 40 45

Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro Ser Gly
50 55 60

Ser Asn Asn Asn Asn Asn Asn Gly Ser Gly Gly Lys His Pro Ile His
65 70 75 80

Val Thr Ser Glu Ile Gly Glu Leu Gln Thr Val Leu Leu Lys Arg Pro
85 90 95

Gly Lys Glu Val Glu Asn Leu Thr Pro Asp Tyr Leu Gln Gln Leu Leu
100 105 110

Phe Asp Asp Ile Pro Tyr Leu Pro Ile Ile Gln Lys Glu His Asp Tyr
115 120 125

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

Lys Leu Ala Ala Glu Ala Leu Val Asp Lys Lys Leu Arg Glu Glu Phe
145 150 155 160

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

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Gln Thr Leu Lys Glu Tyr Leu Leu Ser Phe Ser Asn Glu Glu Leu Ile
            180                 185                 190

Gln Lys Ile Met Glu Thr Gly Gly Val Arg Lys Asn Glu Ile Glu Thr
        195                 200                 205

Ser Lys Lys Thr His Leu Tyr Glu Leu Met Glu Thr Glu Asp His Tyr
    210                 215                 220

Pro Phe Tyr Leu Asp Pro Met Glu Thr Pro Asn Leu Tyr Phe Thr Arg
225                 230                 235                 240

Asp Pro Ala Ala Ser Val Gly Asp Gly Leu Thr Ile Asn Lys Met Glu
                245                 250                 255

Thr Arg Glu Pro Ala Arg Arg Arg Glu Ser Leu Phe Met Glu Thr Glu
            260                 265                 270

Tyr Ile Ile Lys Tyr His Pro Arg Phe Glu Lys His Asn Val Pro Ile
        275                 280                 285

Trp Leu Asp Arg Asp Tyr Lys Phe Pro Ile Glu Gly Gly Asp Glu Leu
    290                 295                 300

Ile Leu Asn Glu Glu Thr Ile Ala Ile Gly Val Ser Ala Arg Thr Ser
305                 310                 315                 320

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

Lys Ile Lys Lys Val Leu Ala Ile Glu Ile Pro Lys Cys Arg Ala Phe
            340                 345                 350

Met Glu Thr His Leu Asp Thr Val Phe Thr Met Glu Thr Val Asp Tyr
        355                 360                 365

Asp Lys Phe Thr Ile His Pro Ala Ile Gln Gly Pro Lys Gly Asn Met
    370                 375                 380

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

Lys Ile Thr His Arg Thr Ser Leu Met Glu Thr Glu Ala Leu Lys Glu
                405                 410                 415

Val Leu Gly Leu Ser Glu Leu Val Leu Ile Pro Cys Gly Gly Gly Asp
            420                 425                 430

Val Ile Ala Ser Ala Arg Glu Gln Trp Asn Asp Gly Ser Asn Thr Leu
        435                 440                 445
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Ala Ile Ala Pro Gly Val Val Val Thr Tyr Asp Arg Asn Tyr Val Ser
450 455 460

Asn Thr Leu Leu Arg Glu His Gly Ile Glu Val Ile Glu Val Leu Ser
465 470 475 480

Ser Glu Leu Ser Arg Gly Arg Gly Gly Pro Arg Cys Met Glu Thr Ser
485 490 495

Met Glu Thr Pro Ile Val Arg Lys Asp Ile
500 505

<210> 42
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> ABD-Intein-CBD, synthesized in laboratory

<400> 42

Met Ala Gln His Asp Glu Ala Val Asp Ala Asn Ser Leu Ala Glu Ala
1 5 10 15

Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr
20 25 30

Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala
35 40 45

Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro Glu Phe Leu Glu Gly Ser
50 55 60

Ser Cys Ile Thr Gly Asp Ala Leu Val Ala Leu Pro Glu Gly Glu Ser
65 70 75 80

Val Arg Ile Ala Asp Ile Val Pro Gly Ala Arg Pro Asn Ser Asp Asn
85 90 95

Ala Ile Asp Leu Lys Val Leu Asp Arg His Gly Asn Pro Val Leu Ala
100 105 110

Asp Arg Leu Phe His Ser Gly Glu His Pro Val Tyr Thr Val Arg Thr
115 120 125

Val Glu Gly Leu Arg Val Thr Gly Thr Ala Asn His Pro Leu Leu Cys
130 135 140

Leu Val Asp Val Ala Gly Val Pro Thr Leu Leu Trp Lys Leu Ile Asp
145 150 155 160

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Glu Ile Lys Pro Gly Asp Tyr Ala Val Ile Gln Arg Ser Ala Phe Ser
                165                 170                 175

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

Thr Tyr Thr Val Gly Val Pro Gly Leu Val Arg Phe Leu Glu Ala His
        195                 200                 205

His Arg Asp Pro Asp Ala Gln Ala Ile Ala Asp Glu Leu Thr Asp Gly
    210                 215                 220

Arg Phe Tyr Tyr Ala Lys Val Ala Ser Val Thr Asp Ala Gly Val Gln
225                 230                 235                 240

Pro Val Tyr Ser Leu Arg Val Asp Thr Ala Asp His Ala Phe Ile Thr
                245                 250                 255

Asn Gly Phe Val Ser His Ala Thr Gly Leu Thr Gly Leu Asn Ser Gly
            260                 265                 270

Leu Thr Thr Asn Pro Gly Val Ser Ala Trp Gln Val Asn Thr Ala Tyr
        275                 280                 285

Thr Ala Gly Gln Leu Val Thr Tyr Asn Gly Lys Thr Tyr Lys Cys Leu
    290                 295                 300

Gln Pro His Thr Ser Leu Ala Gly Trp Glu Pro Ser Asn Val Pro Ala
305                 310                 315                 320

Leu Trp Gln Leu Gln Gly Asp Pro Ile Thr Ile Thr Ile Thr Lys
                325                 330                 335


<210>  43
<211>  636
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CBD-Intein-ADI, synthesized in laboratory

<400>  43

Met Lys Ile Glu Glu Gly Lys Leu Thr Asn Pro Gly Val Ser Ala Trp
1               5                   10                  15

Gln Val Asn Thr Ala Tyr Thr Ala Gly Gln Leu Val Thr Tyr Asn Gly
            20                  25                  30

Lys Thr Tyr Lys Cys Leu Gln Pro His Thr Ser Leu Ala Gly Trp Glu
        35                  40                  45

Pro Ser Asn Val Pro Ala Leu Trp Gln Leu Gln Asn Asn Gly Asn Asn
    50                  55                  60
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Gly Leu Glu Leu Arg Glu Ser Gly Ala Ile Ser Gly Asp Ser Leu Ile
65                  70                  75                  80

Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu Asp
                85                  90                  95

Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys Leu
            100                 105                 110

Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu Val
        115                 120                 125

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

His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu Ser
145                 150                 155                 160

Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser Leu
                165                 170                 175

Gln Leu Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile Tyr Trp
            180                 185                 190

Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val Phe Asp
        195                 200                 205

Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile Ile Val
    210                 215                 220

His Asn Cys Ser Val Phe Asp Ser Lys Phe Lys Gly Ile His Val Tyr
225                 230                 235                 240

Ser Glu Ile Gly Glu Leu Glu Ser Val Leu Val His Glu Pro Gly Arg
                245                 250                 255

Glu Ile Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Cys Phe Ser
            260                 265                 270

Ala Ile Leu Glu Ser His Asp Ala Arg Lys Glu His Lys Gln Phe Val
        275                 280                 285

Ala Glu Leu Lys Ala Asn Asp Ile Asn Val Val Glu Leu Ile Asp Leu
    290                 295                 300

Val Ala Glu Thr Tyr Asp Leu Ala Ser Gln Glu Ala Lys Asp Lys Leu
305                 310                 315                 320

Ile Glu Glu Phe Leu Glu Asp Ser Glu Pro Val Leu Ser Glu Glu His
                325                 330                 335
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Lys Val Val Val Arg Asn Phe Leu Lys Ala Lys Lys Thr Ser Arg Glu
340 345 350

Leu Val Glu Ile Met Met Ala Gly Ile Thr Lys Tyr Asp Leu Gly Ile
355 360 365

Glu Ala Asp His Glu Leu Ile Val Asp Pro Met Pro Asn Leu Tyr Phe
370 375 380

Thr Arg Asp Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Tyr
385 390 395 400

Met Arg Tyr Lys Val Arg Gln Arg Glu Thr Leu Phe Ser Arg Phe Val
405 410 415

Phe Ser Asn His Pro Lys Leu Ile Asn Thr Pro Trp Tyr Tyr Asp Pro
420 425 430

Ser Leu Lys Leu Ser Ile Ala Gly Gly Asp Val Phe Ile Tyr Asn Asn
435 440 445

Asp Thr Leu Val Val Gly Val Ser Glu Arg Thr Asp Leu Gln Thr Val
450 455 460

Thr Leu Leu Ala Lys Asn Ile Val Ala Asn Lys Glu Ser Glu Phe Lys
465 470 475 480

Arg Ile Val Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu
485 490 495

Asp Thr Trp Leu Thr Met Leu Asp Lys Asp Lys Phe Leu Tyr Ser Pro
500 505 510

Ile Ala Asn Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val Asn Gly
515 520 525

Gly Ala Glu Pro Gln Pro Val Glu Asn Gly Leu Pro Leu Glu Gly Leu
530 535 540

Leu Gln Ser Ile Ile Asn Lys Lys Pro Val Leu Ile Pro Ile Ala Gly
545 550 555 560

Glu Gly Ala Ser Gln Met Glu Ile Glu Arg Glu Thr His Phe Asp Gly
565 570 575

Thr Asn Tyr Leu Ala Ile Arg Pro Gly Val Val Ile Gly Tyr Ser Arg
580 585 590

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

Pro Phe His Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys
610 615 620

Met Ser Met Pro Leu Ser Arg Lys Asp Val Lys Trp
625 630 635

<210> 44
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> His-ABD-PolyN-ADI (DNA), synthesized in laboratory

<400> 44
atgcatcatc accatcacca tgatgaagcc gtggatgcga attccttagc tgaagctaaa 60

gtcttagcta acagagaact tgacaaatat ggagtaagtg actattacaa gaacctaatc 120

aacaatgcca aaactgttga aggtgtaaaa gcactgatag atgaaatttt agctgcatta 180

ccttcgggta gtaacaacaa taataacaat ggtagcggcg gttctgtatt tgacagtaaa 240

tttaaaggaa ttcacgttta ttcagaaatt ggtgaattag aatcagttct agttcacgaa 300

ccaggacgcg aaattgacta tattacacca gctagactag atgaattatg cttctcagct 360

atcttagaaa gccacgatgc tagaaaagaa cacaaacaat tcgtagcaga attaaaagca 420

aacgacatca atgttgttga attaattgat ttagttgctg aaacatatga tttagcatca 480

caagaagcta aagacaaatt aatcgaagaa tttttagaag actcagaacc agttctatca 540

gaagaacaca aagtagttgt aagaaacttc ttaaaagcta aaaaaacatc aagagaatta 600

gtagaaatca tgatggcagg gatcacaaaa tacgatttag gtatcgaagc agatcacgaa 660

ttaatcgttg acccaatgcc aaacctatac ttcacacgtg acccatttgc atcagtaggt 720

aatggtgtaa caatccacta catgcgttac aaagttagac aacgtgaaac attattctca 780

agatttgtat tctcaaatca ccctaaacta attaacactc catggtacta cgacccttca 840

ctaaaattat caatcgcagg tggggacgta tttatctaca acaatgacac attagtagtt 900

ggtgtttctg aaagaactga cttacaaaca gttactttat tagctaaaaa cattgttgct 960

aataaagaat ctgaattcaa acgtattgtt gcaattaacg ttccaaaatg gacaaactta 1020

atgcacttag acacatggct aacaatgtta gacaaggaca aattcctata ctcaccaatc 1080

gctaatgacg tatttaaatt ctgggattat gacttagtaa acggtggagc agaaccacaa 1140

ccagttgaaa acggattacc tctagaagga ttattacaat caatcattaa caaaaaacca 1200

gttttaattc ctatcgcagg tgaaggtgct tcacaaatgg aaatcgaaag agaaacacac 1260

ttcgatggta caaactactt agcaattaga ccaggtgttg taattggtta ctcacgtaac 1320

gaaaaaacaa acgctgctct agaagctgca ggcattaaag ttcttccatt ccacggtaac 1380

caattatcat taggtatggg taacgctcgt tgtatgtcaa tgcctttatc acgtaaagat 1440

gttaagtggt aa 1452

<210> 45
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> His-ABD-PolyN-bcADI (DNA), synthesized in laboratory

<400> 45
atgggtcatc atcaccatca ccatgatgaa gccgtggatg cgaacagctt agctgaagct 60

aaagtcttag ctaacagaga acttgacaaa tatggagtaa gtgactatta caagaaccta 120

atcaacaatg ccaaaactgt tgaaggtgta aaagcactga tagatgaaat tttagctgca 180

ttaccttcgg gtagtaacaa caataataac aatggtagcg gcggtaaaca tccgatacat 240

gttacttcag aaattgggga attacaaacg gttttattaa aacgaccggg taaagaagtg 300

gaaaacttga cgccagatta tttgcagcaa ttattatttg acgatattcc atacctacca 360

attattcaaa aagagcatga ttattttgca caaacgttac gcaatcgggg tgttgaagtt 420

ctttatttag aaaaactagc cgctgaggcg ttagtagata aaaaacttcg agaagaattt 480

gttgatcgta ttttaaaaga aggacaggcc gacgtaaatg ttgcacatca aactttaaaa 540

gaatatttac tttccttttc aaatgaagaa ttaattcaaa aaattatggg cggtgtacgg 600

aaaaacgaaa ttgaaacaag taagaagaca catttatatg aattaatgga agatcattat 660

ccgttttact tagatccaat gcctaattta tattttactc gtgatccagc agctagcgtg 720

ggcgatggct taacgataaa taagatgaga gaaccagcgc gtagacgtga atcattattc 780

atggagtaca tcattaaata tcatccaaga tttgaaaaac ataatgtacc aatctggtta 840

gatcgtgatt ataaatttcc aattgaaggt ggcgacgagc taattttaaa tgaagaaaca 900

attgcgattg gagtatctgc tcgtacttca gctaaagcaa ttgaacgttt agcaaaaaat 960

ctctttagcc gacaaaataa aattaagaaa gtgttagcaa tagaaattcc aaaatgccga 1020

gcatttatgc atttagatac agtatttaca atggttgatt atgataagtt tacaattcac 1080

ccagctattc aagggccaaa agggaatatg aatatttata ttttagaaaa aggatcagat 1140

gaggaaactc ttaaaattac acatcgtact tctttaatgg aagcattaaa agaggtatta 1200

ggcttaagtg aattagttct tattccatgt ggaggaggag atgtaattgc ttctgctcgt 1260

gaacaatgga atgatggctc gaacacatta gcaatcgcgc caggtgtagt tgttacatat 1320

gatcgcaact atgtatccaa tacgttatta cgggaacacg gtatagaagt gattgaggtg 1380

ctaagttcag aattatctcg tggtcgtggg ggtccacgtt gcatgagtat gccaattgtt 1440

cgtaaagata tttaa 1455

<210> 46
<211> 46
<212> PRT
<213> Artificial Sequence

<220>

<223> ABD without Linker, synthesized in laboratory

<400> 46

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu
20 25 30

Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro
35 40 45

<210> 47
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<223> ABD with Linker, synthesized in laboratory

<400> 47

Ala Gln His Asp Glu Ala Val Asp Ala Asn Ser Leu Ala Glu Ala Lys
1 5 10 15

Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr
20 25 30

Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu
35 40 45

Ile Asp Glu Ile Leu Ala Ala Leu Pro
50 55

<210> 48
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> ABD1 without Linker, synthesized in laboratory

<400> 48

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

Val Ser Asp Phe Tyr Lys Arg Leu Ile Asn Lys Ala Lys Thr Val Glu
20 25 30

Gly Val Glu Ala Leu Lys Leu His Ile Leu Ala Ala Leu Pro
35 40 45

<210> 49
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<223> ABD1 with Linker, synthesized in laboratory

<400> 49

Gly Ser His His His His His His Ala Asn Ser Leu Ala Glu Ala Lys
1 5 10 15

Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp Phe Tyr
20 25 30

Lys Arg Leu Ile Asn Lys Ala Lys Thr Val Glu Gly Val Glu Ala Leu
35 40 45

Lys Leu His Ile Leu Ala Ala Leu Pro
50 55

<210> 50
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 1, synthesized in laboratory

<400> 50

Gly Ser His His His His His His Ala Asn Ser
1 5 10

<210> 51
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 2, synthesized in laboratory

<400> 51

Ala Gln His Asp Glu Ala Val Asp Ala Asn Ser
1 5 10

<210> 52
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 3, synthesized in laboratory

<400> 52

Asp Glu Ala Val Asp Ala Asn Ser
1 5

<210> 53
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 5, synthesized in laboratory

<400> 53

Gly Ser Gly Gly
1