

SEQUENCE LISTING

<110> KAHR Medical Ltd.
 PECKER, Iris
 BLOCH, Itai

<120> PD1-4-1BBL VARIANT FUSION PROTEIN AND METHODS OF USE THEREOF

<130> 77792

<150> 62/696,365
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 <151> 2018-12-31

<160> 169

<170> PatentIn version 3.5

<210> 1
 <211> 362
 <212> PRT
 <213> Artificial sequence

<220>
 <223> ORIGINAL PD1-41BBL with signal peptide and His Tag

<400> 1

His His His His His His Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg
 1 5 10 15

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
 20 25 30

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
 35 40 45

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
 50 55 60

Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg
 65 70 75 80

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
85 90 95

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

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
115 120 125

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
130 135 140

Ser Pro Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Gly Ala Cys Pro
145 150 155 160

Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro
165 170 175

Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
180 185 190

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

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
210 215 220

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
225 230 235 240

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
245 250 255

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
260 265 270

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
 275 280 285

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
 290 295 300

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
 305 310 315 320

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
 325 330 335

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

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 355 360

<210> 2
 <211> 150
 <212> PRT
 <213> Artificial sequence

<220>
 <223> ORIGINAL PD1 DOMAIN

<400> 2

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
 1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
 20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
 35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
 50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Phe Gln Thr Leu Val
145 150

<210> 3
<211> 205
<212> PRT
<213> Artificial sequence

<220>
<223> ORIGINAL 41BBL DOMAIN

<400> 3

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
1 5 10 15

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
20 25 30

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
35 40 45

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
50 55 60

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

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
85 90 95

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
100 105 110

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
115 120 125

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

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
145 150 155 160

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
165 170 175

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
180 185 190

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
195 200 205

<210> 4
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> SIGNAL PEPTIDE

<400> 4

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro

1 5 10 15

Asp Thr Thr Gly
20

<210> 5
<211> 356
<212> PRT
<213> Artificial sequence

<220>
<223> ORIGINAL PD1-41BBL without His Tag

<400> 5

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
 130 135 140

Gln Phe Gln Thr Leu Val Gly Ala Cys Pro Trp Ala Val Ser Gly Ala
 145 150 155 160

Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro
 165 170 175

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
 180 185 190

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
 195 200 205

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
 210 215 220

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
 225 230 235 240

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
 245 250 255

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
 260 265 270

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
 275 280 285

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
 290 295 300

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
 305 310 315 320

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val

325

330

335

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

Pro Arg Ser Glu
 355

<210> 6
 <211> 21
 <212> PRT
 <213> Artificial sequence

<220>
 <223> C-terminal segment of PD1

<400> 6

Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln
 1 5 10 15

Phe Gln Thr Leu Val
 20

<210> 7
 <211> 30
 <212> PRT
 <213> Artificial sequence

<220>
 <223> N-terminal segment of the 4-1BBL

<400> 7

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
 1 5 10 15

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
 20 25 30

<210> 8
 <211> 5

<212> PRT
<213> Artificial sequence

<220>
<223> segment of five residues at the N-terminal of PD1

<400> 8

Pro Gly Trp Phe Leu
1 5

<210> 9
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> segment of five residues at the C-terminal of PD1

<400> 9

Phe Gln Thr Leu Val
1 5

<210> 10
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> N-terminal segment of the 4-1BBL domain

<400> 10

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly
1 5 10

<210> 11
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> N-terminal segment of the 4-1BBL domain

<400> 11

Ala Cys Pro Trp Ala Val
1 5

<210> 12
<211> 332
<212> PRT
<213> Artificial sequence

<220>
<223> K105_var1 without His Tag

<400> 12

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Gly Ser Ala Ala
130 135 140

Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala
 145 150 155 160

Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln
 165 170 175

Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly
 180 185 190

Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr
 195 200 205

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln
 210 215 220

Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser
 225 230 235 240

Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala
 245 250 255

Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn
 260 265 270

Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln
 275 280 285

Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp
 290 295 300

Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro
 305 310 315 320

Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 325 330

<210> 13
 <211> 338
 <212> PRT
 <213> Artificial sequence

<220>
 <223> K105_var1 with His Tag

<400> 13

His His His His His His Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro
 1 5 10 15

Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr
 20 25 30

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

Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro
 50 55 60

Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln
 65 70 75 80

Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg
 85 90 95

Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys
 100 105 110

Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg
 115 120 125

Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala
 130 135 140

Gly Gln Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu
 145 150 155 160

Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe
165 170 175

Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser
180 185 190

Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu
195 200 205

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

Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu
225 230 235 240

Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser
245 250 255

Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala
260 265 270

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

His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala
290 295 300

Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly
305 310 315 320

Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg
325 330 335

Ser Glu

<210> 14
<211> 338
<212> PRT
<213> Artificial sequence

<220>
<223> K105_var2 without His Tag

<400> 14

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Gly Ala Arg Ala
130 135 140

Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu
145 150 155 160

Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe
165 170 175

Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser
180 185 190

Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu
195 200 205

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

Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu
225 230 235 240

Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser
245 250 255

Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala
260 265 270

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

His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala
290 295 300

Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly
305 310 315 320

Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg
325 330 335

Ser Glu

<210> 15
<211> 344
<212> PRT
<213> Artificial sequence

<220>
<223> K105_var2 with His Tag

<400> 15

His His His His His His Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro
1 5 10 15

Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr
20 25 30

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

Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro
50 55 60

Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln
65 70 75 80

Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg
85 90 95

Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys
100 105 110

Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg
115 120 125

Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala
130 135 140

Gly Gln Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu
145 150 155 160

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
165 170 175

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
180 185 190

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
195 200 205

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
225 230 235 240

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
245 250 255

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
260 265 270

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

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
290 295 300

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
305 310 315 320

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
325 330 335

Gly Leu Pro Ser Pro Arg Ser Glu
340

<210> 16
<211> 326
<212> PRT
<213> Artificial sequence

<220>
<223> K105_var3 without His Tag

<400> 16

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Gly Leu Arg Glu
130 135 140

Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg
145 150 155 160

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
165 170 175

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
180 185 190

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
195 200 205

Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val
210 215 220

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
225 230 235 240

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
245 250 255

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
260 265 270

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
275 280 285

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
290 295 300

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
305 310 315 320

Pro Ser Pro Arg Ser Glu
325

<210> 17
<211> 332
<212> PRT

<213> Artificial sequence

<220>

<223> K105_var3 with His Tag

<400> 17

His His His His His His Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro
1 5 10 15

Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr
20 25 30

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

Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro
50 55 60

Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln
65 70 75 80

Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg
85 90 95

Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys
100 105 110

Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg
115 120 125

Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala
130 135 140

Gly Gln Gly Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala
145 150 155 160

Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln
165 170 175

Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly
180 185 190

Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr
195 200 205

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln
210 215 220

Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser
225 230 235 240

Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala
245 250 255

Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn
260 265 270

Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln
275 280 285

Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp
290 295 300

Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro
305 310 315 320

Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
325 330

<210> 18
<211> 140
<212> PRT
<213> Artificial sequence

<220>
<223> 140 aa PD1 segment

<400> 18

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln
130 135 140

<210> 19

<211> 128

<212> PRT

<213> Artificial sequence

<220>

<223> 128 aa PD1 segment

<400> 19

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
 1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
 20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
 35 40 45

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
 65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
 85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
 100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
 115 120 125

<210> 20
 <211> 135
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 135 aa PD1 segment

<400> 20

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
 1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
 20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
35 40 45

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

Ser Pro Arg Pro Ala Gly Gln
130 135

<210> 21
<211> 133
<212> PRT
<213> Artificial sequence

<220>
<223> 133 aa PD1 segment

<400> 21

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro
130

<210> 22
<211> 191
<212> PRT
<213> Artificial sequence

<220>
<223> 191 aa 41BBL segment

<400> 22

Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
1 5 10 15

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
20 25 30

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
35 40 45

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys

50

55

60

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

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
85 90 95

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
100 105 110

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
115 120 125

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
130 135 140

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
145 150 155 160

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
165 170 175

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
180 185 190

<210> 23

<211> 197

<212> PRT

<213> Artificial sequence

<220>

<223> 197 aa 41BBL segment

<400> 23

Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly
1 5 10 15

Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln
20 25 30

Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly
35 40 45

Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr
50 55 60

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

Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val
85 90 95

Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro
100 105 110

Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu
115 120 125

Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly
130 135 140

Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His
145 150 155 160

Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr
165 170 175

Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro
180 185 190

Ser Pro Arg Ser Glu
195

<210> 24

<211> 185
<212> PRT
<213> Artificial sequence

<220>
<223> 185 aa 41BBL segment

<400> 24

Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
1 5 10 15

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu
20 25 30

Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly
35 40 45

Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu
50 55 60

Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu
65 70 75 80

Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu
85 90 95

His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu
100 105 110

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

Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly
130 135 140

Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr
145 150 155 160

Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro
165 170 175

Ala Gly Leu Pro Ser Pro Arg Ser Glu
180 185

<210> 25
<211> 199
<212> PRT
<213> Artificial sequence

<220>
<223> 199 aa 41BBL segment

<400> 25

Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg
1 5 10 15

Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu
20 25 30

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

Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser
50 55 60

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

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

Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu
100 105 110

Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val
115 120 125

Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe
130 135 140

Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His
145 150 155 160

Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly
165 170 175

Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly
180 185 190

Leu Pro Ser Pro Arg Ser Glu
195

<210> 26
<211> 381
<212> PRT
<213> Artificial sequence

<220>
<223> ORIGINAL PD1-41BBL with signal peptide and His Tag

<400> 26

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser His His His His His His Pro Gly Trp Phe Leu Asp Ser
20 25 30

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

Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr
50 55 60

Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln
65 70 75 80

Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln
85 90 95

Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His
100 105 110

Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys
115 120 125

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

Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His
145 150 155 160

Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Gly
165 170 175

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
180 185 190

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

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
210 215 220

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
225 230 235 240

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
245 250 255

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
260 265 270

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
275 280 285

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
290 295 300

Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
305 310 315 320

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
325 330 335

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
340 345 350

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
355 360 365

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
370 375 380

<210> 27
<211> 288
<212> PRT
<213> Artificial sequence

<220>
<223> aa sequence of full length PD1

<400> 27

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1 5 10 15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
20 25 30

Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
35 40 45

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
50 55 60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65 70 75 80

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
85 90 95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
100 105 110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
130 135 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
165 170 175

Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys
180 185 190

Ser Arg Ala Ala Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln Pro
195 200 205

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

Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val Pro
225 230 235 240

Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly
245 250 255

Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg
260 265 270

Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
275 280 285

<210> 28
<211> 867
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence of full length PD1

<400> 28
atgcagatcc cacaggcgcc ctggccagtc gtctgggcgg tgctacaact gggctggcgg 60
ccaggatggt tcttagactc cccagacagg ccctggaacc ccccccacctt ctccccagcc 120
ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg 180
gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc 240
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg 300
cccaacgggc gtgacttcca catgagcgtg gtcaggggccc ggcgcaatga cagcggcacc 360
tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca 420
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcacc 480
aggccagccg gccagttcca aaccctgggtg gttgggtgtcg tgggcggcct gctgggcagc 540
ctggtgctgc tagtctgggt cctggccgtc atctgctccc gggccgcacg agggacaata 600
ggagccaggc gcaccggcca gcccctgaag gaggaccct cagccgtgcc tgtgttctct 660
gtggactatg gggagctgga tttccagtgg cgagagaaga ccccgagcc ccccggtccc 720
tgtgtccctg agcagacgga gtatgccacc attgtctttc ctagcggaat gggcacctca 780
tccccgccgc gcaggggctc agctgacggc cctcggagtg cccagccact gaggcctgag 840

gatggacact gctcttggcc cctctga

867

<210> 29

<211> 450

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO: 2

<400> 29

ccaggatggt tcttagactc cccagacagg ccctggaacc ccccccacctt ctccccagcc 60

ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg 120

gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc 180

gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg 240

cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc 300

tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca 360

gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcacc 420

aggccagccg gccagttcca aaccctggtg 450

<210> 30

<211> 167

<212> PRT

<213> Artificial sequence

<220>

<223> PD1 amino acid sequence

<400> 30

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1 5 10 15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
20 25 30

Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp

35

40

45

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
 50 55 60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
 65 70 75 80

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
 85 90 95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
 100 105 110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
 115 120 125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
 130 135 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
 145 150 155 160

Arg Pro Ala Gly Gln Phe Gln
 165

<210> 31

<211> 122

<212> PRT

<213> Artificial sequence

<220>

<223> PD1 amino acid sequence

<400> 31

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
 1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
 20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
 35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
 50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
 65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
 85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
 100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg
 115 120

<210> 32
 <211> 420
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 18

<400> 32
 gactcccctg acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
 gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
 aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
 agatctcagc caggccagga ctgccggttc agagttaccc agctgcctaa cggccggggac 240
 ttccacatgt ctgttgtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc 300
 atctctctgg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360

gaaagacgag ctgagggtgcc caccgctcat ccctcacctt ctccaagacc tgccggccag 420

<210> 33

<211> 384

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO: 19

<400> 33

ccttggaacc ctccaacctt ctctcccgct ctgctggtgg ttaccgaggg cgacaatgcc 60

accttcacct gttccttcag caacacctcc gagtccttcg tgctgaactg gtacagaatg 120

tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc 180

caggactgcc gggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt 240

gtgcggggcca gacggaacga ctctggcaca tatctgtgcg gcgccatctc tctggctccc 300

aaggctcaga tcaaagagtc tctgcgggcc gagctgagag tgacagaaag acgagctgag 360

gtgcccaccg ctcatccctc acct 384

<210> 34

<211> 405

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO: 20

<400> 34

ccttggaacc ctccaacctt ctctcccgct ctgctggtgg ttaccgaggg cgacaatgcc 60

accttcacct gttccttcag caacacctcc gagtccttcg tgctgaactg gtacagaatg 120

tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc 180

caggactgcc gggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt 240

gtgcggggcca gacggaacga ctctggcaca tatctgtgcg gcgccatctc tctggctccc 300

aaggctcaga tcaaagagtc tctgcgggcc gagctgagag tgacagaaag acgagctgag 360

gtgcccaccg ctcatccctc accttctcca agacctgccg gccag 405

<210> 35
<211> 399
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO: 21

<400> 35
gactcccctg acagaccttg gaaccctcca accttctctc ccgctctgct ggtgggttacc 60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
aactgggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
agatctcagc caggccagga ctgccggttc agagttaccc agctgcctaa cggccggggac 240
ttccacatgt ctgttgtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc 300
atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
gaaagacgag ctgaggtgcc caccgtcat ccctcacct 399

<210> 36
<211> 254
<212> PRT
<213> Artificial sequence

<220>
<223> aa sequence of full length 41BBL

<400> 36

Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro
1 5 10 15

Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val
20 25 30

Ala Gly Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
35 40 45

Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser

50

55

60

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
 65 70 75 80

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
 85 90 95

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
 100 105 110

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

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
 130 135 140

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
 145 150 155 160

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
 165 170 175

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
 180 185 190

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
 195 200 205

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
 210 215 220

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
 225 230 235 240

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 245 250

<210> 37
<211> 765
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence of full length 41BBL

<400> 37
atggaatacg cctctgacgc ttacttggac cccgaagccc cgtggcctcc cgcgccccgc 60
gctcgcgcct gccgcgtact gccttgggcc ctggtcgcgg ggctgctgct gctgctgctg 120
ctcgtgccc cctgcgccgt cttcctcgcc tgccccctggg ccgtgtccgg ggctcgcgcc 180
tcgcccggct ccgcggccag cccgagactc cgcgagggtc ccgagctttc gcccgcgat 240
cccgcgggcc tcttggacct gcggcagggc atgtttgcgc agctgggtggc ccaaaatgtt 300
ctgctgatcg atgggcccct gagctggtac agtgaccag gcctggcagg cgtgtccctg 360
acggggggcc tgagctacaa agaggacacg aaggagctgg tggaggccaa ggctggagtc 420
tactatgtct tctttcaact agagctgcgg cgcgtggtgg ccggcgaggg ctcaggctcc 480
gtttcacttg cgctgcacct gcagccactg cgctctgctg ctggggccgc cgccctggct 540
ttgaccgtgg acctgccacc cgcctcctcc gaggtctgga actcggcctt cggtttccag 600
ggccgcttgc tgcacctgag tgccggccag cgcctgggcg tccatcttca cactgaggcc 660
agggcacgcc atgcctggca gcttaccag ggccgacag tcttgggact cttccgggtg 720
acccccgaaa tcccagccgg actcccttca ccgaggtcgg aataa 765

<210> 38
<211> 615
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO: 3

<400> 38
gcctgcccct gggccgtgtc cggggctcgc gcctcgccc gctccgcggc cagcccagaga 60

ctccgcgagg gtcccagact ttcgcccagc gatccccgag gcctcttgga cctgcggcag	120
ggcatgtttg cgcagctggg ggcccaaaat gttctgctga tcgatgggcc cctgagctgg	180
tacagtgacc caggcctggc aggcgtgtcc ctgacggggg gcctgagcta caaagaggac	240
acgaaggagc tgggtgggtggc caaggctgga gtctactatg tcttctttca actagagctg	300
cggcgcgtgg tggccggcga gggctcaggc tccgtttcac ttgcgctgca cctgcagcca	360
ctgcgctctg ctgctggggc cgccgccctg gctttgaccg tggacctgcc acccgctcc	420
tccgaggctc ggaactcggc cttcggtttc cagggccgct tgctgcacct gagtgccggc	480
cagcgcctgg gcgtccatct tcacactgag gccagggcac gccatgcctg gcagcttacc	540
cagggcgcca cagtcttggg actcttccgg gtgacccccg aaatcccagc cggactccct	600
tcaccgaggt cgga	615

<210> 39
 <211> 573
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 22

<400> 39	
tctgccgctt ctcccagact gagagaagga cctgagctga gccctgatga tcctgctgga	60
ctgctggatc tgcggcaggg catgtttgct cagttgggtg cccagaacgt gctgctgac	120
gatggccctc tgtcctggta ctctgatcca ggattggctg gcgtgtccct gactggcggc	180
ctgtcttaca aagaggacac caaagaactg gtgggtggcca aggccggcgt gtactacgtg	240
ttctttcagc tggaactgcg gagagtgggtg gctggcgaag gatctggatc tgtgtctctg	300
gccctgcac tgcagcctct gagaagtgct gcaggcgctg ctgcactggc tctgacagtt	360
gatctgcctc ctgcctcctc cgaggccaga aactccgcct ttggcttcca aggcagactg	420
ctgcacctgt ccgctggaca gagactggga gtccatctgc acacagaggc cagagctaga	480
cacgcttggc agttgacaca gggcgctaca gtgctgggcc tgttttagagt gacccctgag	540
attccagccg gcctgccatc tcctagatct gag	573

<210> 40
 <211> 591
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 23

<400> 40
 gctagagctt ctcctggctc tgccgcttct cccagactga gagaaggacc tgagctgagc 60
 cctgatgata ctgctggact gctggatctg cggcagggca tgtttgctca gttggtggcc 120
 cagaacgtgc tgctgatcga tggccctctg tcctgggtact ctgatccagg attggctggc 180
 gtgtccctga ctggcggcct gtcttacaaa gaggacacca aagaactggg ggtggccaag 240
 gccggcgtgt actacgtgtt ctttcagctg gaactgcgga gactgggtggc tggcgaagga 300
 tctggatctg tgtctctggc cctgcatctg cagcctctga gaagtgtctg aggcgtgct 360
 gcactggctc tgacagtga tctgcctcct gcctcctccg aggccagaaa ctccgccttt 420
 ggcttccaag gcagactgct gcacctgtcc gctggacaga gactgggagt ccatctgcac 480
 acagaggcca gagctagaca cgcttggcag ttgacacagg gcgctacagt gctgggcctg 540
 tttagagtga cccctgagat tccagccggc ctgccatctc ctagatctga g 591

<210> 41
 <211> 555
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 24

<400> 41
 ctgagagaag gacctgagct gagccctgat gatcctgctg gactgctgga tctgcggcag 60
 ggcatgtttg ctcatgttgt ggcccagaac gtgctgctga tcgatggccc tctgtcctgg 120
 tactctgata caggattggc tggcgtgtcc ctgactggcg gcctgtctta caaaggaggac 180
 accaaagaac tgggtggtggc caaggccggc gtgtactacg tgttctttca gctggaactg 240

cggagagtgg tggctggcga aggatctgga tctgtgtctc tggccctgca tctgcagcct	300
ctgagaagtg ctgcaggcgc tgctgactg gctctgacag ttgatctgcc tcctgcctcc	360
tccgaggcca gaaactccgc ctttggcttc caaggcagac tgctgcacct gtccgctgga	420
cagagactgg gagtccatct gcacacagag gccagagcta gacacgcttg gcagttgaca	480
cagggcgcta cagtgtggg cctgtttaga gtgaccctg agattccagc cggcctgcca	540
tctcctagat ctgag	555

<210> 42
 <211> 597
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 25

<400> 42	
tctggcgcta gagcttctcc tggctctgcc gcttctccca gactgagaga aggacctgag	60
ctgagccctg atgatcctgc tggactgctg gatctgcggc agggcatgtt tgctcagttg	120
gtggcccaga acgtgctgct gatcgatggc cctctgtcct ggtactctga tccaggattg	180
gctggcgtgt ccctgactgg cggcctgtct taaaagagg acaccaaaga actggtggtg	240
gccaaggccg gcgtgtacta cgtgttcttt cagctggaac tgcggagagt ggtggctggc	300
gaaggatctg gatctgtgtc tctggccctg catctgcagc ctctgagaag tgctgcaggc	360
gctgctgcac tggctctgac agttgatctg cctcctgcct cctccgaggc cagaaactcc	420
gcctttggct tccaaggcag actgctgcac ctgtccgctg gacagagact gggagtccat	480
ctgcacacag aggccagagc tagacacgct tggcagttga cacagggcgc tacagtgtg	540
ggcctgttta gagtgacccc tgagattcca gccggcctgc catctcctag atctgag	597

<210> 43

<400> 43
 000

<210> 44

<211> 340
<212> PRT
<213> Artificial sequence

<220>
<223> var 4

<400> 44

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Gly Ser Gly Ala
130 135 140

Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro
145 150 155 160

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
165 170 175

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
180 185 190

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
195 200 205

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

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
225 230 235 240

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
245 250 255

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
260 265 270

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
275 280 285

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
290 295 300

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
305 310 315 320

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
325 330 335

Pro Arg Ser Glu
340

<210> 45

<211> 333
<212> PRT
<213> Artificial sequence

<220>
<223> var 5

<400> 45

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Gly Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
130 135 140

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
145 150 155 160

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
165 170 175

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
180 185 190

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
195 200 205

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
210 215 220

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
225 230 235 240

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
245 250 255

Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
260 265 270

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
275 280 285

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
290 295 300

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
305 310 315 320

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
325 330

<210> 46
<211> 325
<212> PRT
<213> Artificial sequence

<220>

<223> var 6

<400> 46

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly
130 135 140

Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln
145 150 155 160

Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly
165 170 175

Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr
180 185 190

Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys
195 200 205

Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val
210 215 220

Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro
225 230 235 240

Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu
245 250 255

Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly
260 265 270

Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His
275 280 285

Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr
290 295 300

Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro
305 310 315 320

Ser Pro Arg Ser Glu
325

<210> 47
<211> 331
<212> PRT
<213> Artificial sequence

<220>
<223> var 7

<400> 47

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
 1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
 20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
 35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
 50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
 65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
 85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
 100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
 115 120 125

Ala His Pro Ser Pro Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser
 130 135 140

Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly
 145 150 155 160

Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn
 165 170 175

Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
 180 185 190

Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys
195 200 205

Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu
210 215 220

Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu
225 230 235 240

Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu
245 250 255

Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser
260 265 270

Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg
275 280 285

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
290 295 300

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
305 310 315 320

Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
325 330

<210> 48
<211> 319
<212> PRT
<213> Artificial sequence

<220>
<223> var 8

<400> 48

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Gly Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
130 135 140

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
145 150 155 160

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
165 170 175

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
180 185 190

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
195 200 205

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
 210 215 220

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

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
 245 250 255

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
 260 265 270

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
 275 280 285

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
 290 295 300

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

<210> 49
 <211> 328
 <212> PRT
 <213> Artificial sequence

<220>
 <223> var 9

<400> 49

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
 1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
 20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
 35 40 45

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

Gly Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu
130 135 140

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
145 150 155 160

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
165 170 175

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
180 185 190

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
195 200 205

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
210 215 220

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
225 230 235 240

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
245 250 255

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
260 265 270

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
275 280 285

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
290 295 300

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
305 310 315 320

Gly Leu Pro Ser Pro Arg Ser Glu
325

<210> 50
<211> 320
<212> PRT
<213> Artificial sequence

<220>
<223> var 10

<400> 50

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
35 40 45

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro
130 135 140

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
145 150 155 160

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
165 170 175

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
180 185 190

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
195 200 205

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
210 215 220

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

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
245 250 255

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
260 265 270

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
275 280 285

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
290 295 300

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

<210> 51
<211> 326
<212> PRT
<213> Artificial sequence

<220>
<223> var 11

<400> 51

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
35 40 45

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu
130 135 140

Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg
145 150 155 160

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
165 170 175

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
180 185 190

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
195 200 205

Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val
210 215 220

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
225 230 235 240

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
245 250 255

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
260 265 270

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
275 280 285

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
 290 295 300

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
 305 310 315 320

Pro Ser Pro Arg Ser Glu
 325

<210> 52
 <211> 314
 <212> PRT
 <213> Artificial sequence

<220>
 <223> var 12

<400> 52

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
 1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
 20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
 35 40 45

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
 65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
 85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
 100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

Gly Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
130 135 140

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
145 150 155 160

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
165 170 175

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
180 185 190

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
195 200 205

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
210 215 220

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
225 230 235 240

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
245 250 255

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
260 265 270

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
275 280 285

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

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
305 310

<210> 53
<211> 335
<212> PRT
<213> Artificial sequence

<220>
<223> var 13

<400> 53

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
35 40 45

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

Ser Pro Arg Pro Ala Gly Gln Gly Ser Gly Ala Arg Ala Ser Pro Gly
130 135 140

Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
145 150 155 160

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
165 170 175

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
180 185 190

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
195 200 205

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

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
225 230 235 240

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
245 250 255

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
260 265 270

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
275 280 285

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
290 295 300

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
305 310 315 320

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
325 330 335

<210> 54
 <211> 327
 <212> PRT
 <213> Artificial sequence

<220>
 <223> var 14

<400> 54

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
 1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
 20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
 35 40 45

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
 65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
 85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
 100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
 115 120 125

Ser Pro Arg Pro Ala Gly Gln Gly Ser Ala Ala Ser Pro Arg Leu Arg
 130 135 140

Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu
 145 150 155 160

Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile
165 170 175

Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser
180 185 190

Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val
195 200 205

Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg
210 215 220

Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu
225 230 235 240

Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val
245 250 255

Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe
260 265 270

Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His
275 280 285

Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly
290 295 300

Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly
305 310 315 320

Leu Pro Ser Pro Arg Ser Glu
325

<210> 55
<211> 333
<212> PRT
<213> Artificial sequence

<220>

<223> var 15

<400> 55

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
35 40 45

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

Ser Pro Arg Pro Ala Gly Gln Gly Ala Arg Ala Ser Pro Gly Ser Ala
130 135 140

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
145 150 155 160

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
165 170 175

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
180 185 190

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
195 200 205

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
210 215 220

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
225 230 235 240

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
245 250 255

Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
260 265 270

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
275 280 285

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
290 295 300

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
305 310 315 320

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
325 330

<210> 56
<211> 321
<212> PRT
<213> Artificial sequence

<220>
<223> var 16

<400> 56

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
35 40 45

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

Ser Pro Arg Pro Ala Gly Gln Gly Leu Arg Glu Gly Pro Glu Leu Ser
130 135 140

Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala
145 150 155 160

Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp
165 170 175

Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser
180 185 190

Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr
195 200 205

Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly
210 215 220

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

Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser
245 250 255

Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His
260 265 270

Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg
275 280 285

Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu
290 295 300

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

Glu

<210> 57
<211> 1020
<212> DNA
<213> Artificial sequence

<220>
<223> NA seq of SEQ ID NO: 44, var 4

<400> 57
gatagcccg atcgcccggtg gaacccgccg acctttagcc cggcgctgct ggtggtgacc 60
gaaggcgata acgcgacctt tacctgcagc tttagcaaca ccagcgaaag ctttgtgctg 120

aactggtatc gcatgagccc gagcaaccag accgataaac tggcggcggtt tccggaagat	180
cgcagccagc cgggccagga ttgccgcttt cgcgtgaccc agctgccgaa cggccgcgat	240
tttcatatga gcgtggtgcg cgcgcgccgc aacgatagcg gcacctatct gtgcggcgcg	300
attagcctgg cgccgaaagc gcagattaaa gaaagcctgc gcgcgggaact gcgcgtgacc	360
gaacgccgcg cggaagtgcc gaccgcgcgc cgcagcccga gcccgcgccc ggccggccag	420
ggcagcggcg cgcgcgcgag cccgggcagc gcggcgagcc cgcgcctgcg cgaaggcccg	480
gaactgagcc cggatgatcc ggccgggcctg ctggatctgc gccagggcgc gtttgcgcag	540
ctggtggcg agaacgtgct gctgattgat ggcccgtga gctggtatag cgatccgggc	600
ctggcgggcg tgagcctgac cggcggcctg agctataaag aagataccaa agaactggtg	660
gtggcgaaaag cgggcgtgta ttatgtgttt tttcagctgg aactgcgccg cgtggtggcg	720
ggcgaaggca gcggcagcgt gagcctggcg ctgcatctgc agccgctgcg cagcgcggcg	780
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agcgcgtttg gctttcaggg ccgcctgctg catctgagcg cgggccagcg cctgggcgtg	900
catctgcata ccgaagcgcg cgcgcgccat gcgtggcagc tgacccaggg cgcgaccgtg	960
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<210> 58

<211> 999

<212> DNA

<213> Artificial sequence

<220>

<223> NA seq of SEQ ID NO: 45, var 5

<400> 58

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aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac	180
agatctcagc caggccagga ctgccggttc agagttaccc agctgcctaa cggccgggac	240

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gaaagacgag ctgaggtgcc caccgctcat ccctcacctg gatctggcgc tagagcatct	420
cctggctctg ctgcctctcc tagactgaga gagggacctg agctgtctcc tgatgacct	480
gctggcctgc tggatctgag acagggcatg tttgctcagc tggtgccca gaacgtgctg	540
ctgattgatg gccctctgtc ctggtactct gatcctggat tggctggcgt gtccctgact	600
ggcggcctgt cttacaaaga ggacaccaaa gaactggtgg tggccaaggc cggcgtgtac	660
tacgtgttct ttcagctgga actgcggaga gtggtggccg gcgaaggatc tggatctgtg	720
tctctggcac tgcattctgca gcccctgaga tctgctgcag gcgctgctgc tctggctctg	780
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gccaggcacg cctggcagtt gacacaaggt gctacagtgc tgggcctgtt cagagtgacc	960
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<210> 59

<211> 975

<212> DNA

<213> Artificial sequence

<220>

<223> NA seq of SEQ ID NO: 46, var 6

<400> 59

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aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac	180
agatctcagc caggccagga ctgccggttc agagttaccc agctgcctaa cggccgggac	240
ttccacatgt ctgttgtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc	300
atctctcttg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca	360
gaaagacgag ctgaggtgcc caccgctcat ccctcacctg gatctgctgc ttcccctaga	420

ctgagagagg gccctgagct gtccccctgat gatcctgctg gattgctgga cctgcggcag	480
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tactctgatc caggattggc tggcgtgtcc ctgactggcg gcctgtctta caaagaggac	600
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cggagagtgg tggctggcga aggatctgga tctgtgtctc tggccctgca tctgcagcct	720
ctgagaagtg ctgcaggcgc tgctgcactg gctctgacag ttgatctgcc tcctgcctcc	780
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cagagactgg gagtgcacct ccatacagag gccagagcta gacacgcttg gcagttgaca	900
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<210> 60
 <211> 992
 <212> DNA
 <213> Artificial sequence

<220>
 <223> NA seq of SEQ ID NO: 47, var 7

<400> 60	
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actggtacag aatgtcccct agcaaccaga ccgacaagct ggccgccttt cctgaggaca	180
gatctcagcc aggccaggac tgccggttca gagttacca gctgcctaac ggccgggact	240
tccacatgtc tgttgtgcgg gccagacgga acgactctgg cacatatctg tgcggcgcca	300
tctctctggc tcccaaggct cagatcaaag agtctctgcg ggccgagctg agagtgcag	360
aaagacgagc tgagggtgcc accgctcatc cctcacctgg agccagagct tctcctggat	420
ctgctgcttc ccctagactg agagagggcc ctgagctgtc ccctgatgat cctgctggat	480
tgctggacct gcggcagggc atgtttgctc agttgggtggc ccagaacgtg ctgctgatcg	540

atggccctct gtcctggtag tctgatccag gattggctgg cgtgtccctg actggcggcc	600
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tctttcagct ggaactgcgg agagtgggtg ctggcgaagg atctggatct gtgtctctgg	720
ccctgcatct gcagcctctg agaagtgctg caggcgctgc tgcactggct ctgacagttg	780
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tgcactctgtc tgccggacag agactgggag tgcacctcca tacagaggcc agagctagac	900
acgcttggca gttgacacag ggcgctacag tgctgggcct gtttagagtg acccctgaga	960
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<210> 61
 <211> 956
 <212> DNA
 <213> Artificial sequence

<220>
 <223> NA seq of SEQ ID NO: 48, var 8

<400> 61	
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actggtacag aatgtcccct agcaaccaga ccgacaagct ggccgccttt cctgaggaca	180
gatctcagcc aggccaggac tgccggttca gagttaccca gctgcctaac ggccgggact	240
tccacatgtc tgttgtgcgg gccagacgga acgactctgg cacatatctg tgcggcgcca	300
tctctctggc tcccaaggct cagatcaaag agtctctgcg ggccgagctg agagtacag	360
aaagacgagc tgagggtgccc accgctcatc cctcacctgg actgagagag ggccctgagc	420
tgtcccctga tgatcctgct ggattgctgg acctgcggca gggcatgttt gctcagttgg	480
tggcccagaa cgtgctgctg atcgatggcc ctctgtcctg gtactctgat ccaggattgg	540
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ccaaggccgg cgtgtactac gtgttctttc agctggaact gcggagagtg gtggctggcg	660
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ctgctgcact ggctctgaca gttgatctgc ctctgcctc ctccgaggcc agaaactccg	780
cctttggctt ccaaggcaga ctgctgcatc tgtctgccgg acagagactg ggagtgcacc	840
tccatacaga ggccagagct agacacgctt ggcagttgac acagggcgct acagtgctgg	900
gcctgttttag agtgaccctt gagatcccag ctggcctgcc atctcctaga tctgag	956

<210> 62
 <211> 984
 <212> DNA
 <213> Artificial sequence

<220>
 <223> NA seq of SEQ ID NO: 49, var 9

<400> 62	
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tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc	180
caggactgcc ggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt	240
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aaggctcaga tcaaagagtc tctgcgggcc gagctgagag tgacagaaag acgagctgag	360
gtgcccaccg ctcatccctc acctggatct ggcgctagag catctcctgg ctctgctgcc	420
tctcctagac tgagagaggg acctgagctg tctcctgatg atcctgctgg cctgctggat	480
ctgagacagg gcatgtttgc tcagctggtg gcccagaacg tgctgctgat tgatggccct	540
ctgtcctggt actctgatcc tggattggct ggcgtgtccc tgactggcgg cctgtcttac	600
aaagaggaca ccaaagaact ggtggtggcc aaggccggcg tgtactacgt gttctttcag	660
ctggaactgc ggagagtggg ggccggcgaa ggatctggat ctgtgtctct ggcactgcat	720
ctgcagcccc tgagatctgc tgcaggcgct gctgctctgg ctctgacagt tgatctgcct	780
cctgcctcct ccgaggccag aaactccgcc tttggcttcc aaggcagact gctgcatctg	840
tctgccggcc agagactggg agtccatctg catacagagg ctagagccag gcacgcctgg	900

cagttgacac aaggtgctac agtgctgggc ctgttcagag tgaccccaga gattccagcc	960
ggcctgcctt ctccaagatc cgag	984

<210> 63
 <211> 960
 <212> DNA
 <213> Artificial sequence

<220>
 <223> NA seq of SEQ ID NO: 50, var 10

<400> 63	
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tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc	180
caggactgcc ggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt	240
gtgcggggcca gacggaacga ctctggcaca tatctgtgcg gcgccatctc tctggctccc	300
aaggctcaga tcaaagagtc tctgcgggcc gagctgagag tgacagaaaag acgagctgag	360
gtgcccaccg ctcatccctc acctggatct gctgcttccc ctagactgag agagggccct	420
gagctgtccc ctgatgatcc tgctggattg ctggacctgc ggcagggcat gtttgctcag	480
ttgggtggccc agaactgct gctgatcgat ggccctctgt cctgggtactc tgatccagga	540
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gtcgccaagg ccggcgtgta ctacgtgttc tttcagctgg aactgcggag agtggtggct	660
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ggcgctgctg cactggctct gacagttgat ctgcctcctg cctcctccga ggccagaaac	780
tccgcctttg gcttccaagg cagactgctg catctgtctg ccggacagag actgggagtg	840
cacctcata cagaggccag agctagacac gcttggcagt tgacacaggg cgctacagtg	900
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<210> 64
 <211> 978

<212> DNA
<213> Artificial sequence

<220>
<223> NA seq of SEQ ID NO: 51, var 11

<400> 64
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tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc 180
caggactgcc ggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt 240
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tggtactctg atccaggatt ggctggcgtg tccctgactg gcggcctgtc ttacaaagag 600
gacaccaaag aactggtggt cgccaaggcc ggcgtgtact acgtgttctt tcagctggaa 660
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tcctccgagg ccagaaactc cgcttttggc ttccaaggca gactgctgca tctgtctgcc 840
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acacagggcg ctacagtgtt gggcctgttt agagtgacct ctgagatccc agctggcctg 960
ccatctccta gatctgag 978

<210> 65
<211> 942
<212> DNA
<213> Artificial sequence

<220>
<223> NA seq of SEQ ID NO: 52, var 12

<400> 65
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tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc 180
caggactgcc ggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt 240
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aaggctcaga tcaaagagtc tctgcgggcc gagctgagag tgacagaaag acgagctgag 360
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cctgctggat tgctggacct gcggcagggc atgtttgctc agttggtggc ccagaacgtg 480
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agagctagac acgcttgga gttgacacag ggcgctacag tgctgggcct gtttagagt 900
acccctgaga tcccagctgg cctgccatct cctagatctg ag 942

<210> 66
<211> 1005
<212> DNA
<213> Artificial sequence

<220>
<223> NA seq of SEQ ID NO: 53, var 13

<400> 66
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accttcacct gttccttcag caacacctcc gagtccttcg tgctgaactg gtacagaatg 120
tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc 180

caggactgcc ggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt	240
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aaggctcaga tcaaagagtc tctgcgggcc gagctgagag tgacagaaag acgagctgag	360
gtgcccaccg ctcatccctc accttctcca agacctgctg gccagggatc tggcgctaga	420
gcatctcctg gctctgctgc ctctcctaga ctgagagagg gacctgagct gtctcctgat	480
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caaggcagac tgctgcatct gtctgccggc cagagactgg gagtccatct gcatacagag	900
gctagagcca ggcacgcctg gcagttgaca caagggtgcta cagtgtctggg cctgttcaga	960
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<210> 67
 <211> 981
 <212> DNA
 <213> Artificial sequence

<220>
 <223> NA seq of SEQ ID NO: 54, var 14

<400> 67	
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tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc	180
caggactgcc ggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt	240
gtgcggggcca gacggaacga ctctggcaca tatctgtgcg gcgccatctc tctggctccc	300

aaggctcaga tcaaagagtc tctgcgggcc gagctgagag tgacagaaag acgagctgag	360
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cctagactga gagagggccc tgagctgtcc cctgatgatc ctgctggatt gctggacctg	480
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gaactgcgga gagtgggtggc tggcgaagga tctggatctg tgtctctggc cctgcatctg	720
cagcctctga gaagtgtgc aggcgctgct gcactggctc tgacagttga tctgcctcct	780
gcctcctccg aggccagaaa ctccgccttt ggcttccaag gcagactgct gcatctgtct	840
gccggacaga gactgggagt gcacctccat acagaggcca gagctagaca cgcttggcag	900
ttgacacagg gcgctacagt gctgggcctg tttagagtga cccctgagat cccagctggc	960
ctgccatctc ctagatctga g	981

<210> 68

<211> 999

<212> DNA

<213> Artificial sequence

<220>

<223> NA seq of SEQ ID NO: 55, var 15

<400> 68

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tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc	180
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<210> 69
 <211> 963
 <212> DNA
 <213> Artificial sequence

<220>
 <223> NA seq of SEQ ID NO: 56, var 16

<400> 69	
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tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc	180
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gtgcacctcc atacagaggc cagagctaga cacgcttggc agttgacaca gggcgctaca	900
gtgctgggcc tgttttagagt gaccctgag atcccagctg gcctgccatc tcctagatct	960
gag	963

<210> 70
 <211> 996
 <212> DNA
 <213> Artificial sequence

<220>
 <223> NA seq of SEQ ID NO: 12

<400> 70	
gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc	60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg	120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac	180
agatctcagc caggccagga ctgccggttc agagttaccc agctgcctaa cggccgggac	240
ttccacatgt ctgttgtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc	300
atctctctgg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca	360
gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagacc tgctggccag	420
ggatctgccg cttctcctag actgagagag ggccctgagc tgtctcctga tgatcctgct	480
ggactgctgg acctgagaca gggcatgttt gcccagctgg tggcccagaa tgtgctgctg	540
attgacggcc ctctgtcctg gtactctgat ccaggattgg ctggcgtgtc cctgactggc	600
ggcctgtctt acaaagagga caccaaagaa ctggtggtcg ccaaggccgg cgtgtactac	660
gtgttctttc agctggaact gcggagagtg gtggctggcg aaggatctgg atctgtgtct	720
ctggccctgc atctgcagcc tctgagaagt gctgcaggcg ctgctgcact ggctctgaca	780

gttgatctgc ctctgcctc ctccgaggcc agaaactccg cttttggctt ccaaggcaga	840
ctgctgcatc tgtctgccgg acagagactg ggagtgcacc tccatacaga ggccagagct	900
agacacgctt ggcagttgac acagggcgct acagtgctgg gcctgttttag agtgaccct	960
gagattccag ccggcctgcc atctccaaga tctgag	996

<210> 71
 <211> 1014
 <212> DNA
 <213> Artificial sequence

<220>
 <223> NA seq of SEQ ID NO: 14

<400> 71	
gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc	60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg	120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac	180
agatctcagc caggccagga ctgccggttc agagttaccc agctgcctaa cggccgggac	240
ttccacatgt ctgttgctgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc	300
atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca	360
gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagacc tgctggacag	420
ggcgccagag cttctcctgg atctgctgct tcccctagac tgagagaggg ccctgagctg	480
tcccctgatg atcctgctgg attgctggac ctgcggcagg gcatgtttgc tcagttggtg	540
gcccagaacg tgctgctgat cgatggccct ctgtcctggt actctgatcc aggattggct	600
ggcgtgtccc tgactggcgg cctgtcttac aaagaggaca ccaaagaact ggtggtcgcc	660
aaggccggcg tgtactacgt gttctttcag ctggaactgc ggagagtggg ggctggcgaa	720
ggatctggat ctgtgtctct ggccctgcat ctgcagcctc tgagaagtgc tgcaggcgct	780
gctgcactgg ctctgacagt tgatctgcct cctgcctcct ccgaggccag aaactccgcc	840
tttggcttcc aaggcagact gctgcatctg tctgccggac agagactggg agtgcacctc	900

catacagagg ccagagctag acacgcttgg cagttgacac agggcgctac agtgctgggc	960
ctgttttagag tgaccctga gatcccagct ggctgcat ctcctagatc tgag	1014

<210> 72
 <211> 978
 <212> DNA
 <213> Artificial sequence

<220>
 <223> NA seq of SEQ ID NO: 16

<400> 72	
gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc	60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg	120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac	180
agatctcagc caggccagga ctgccggttc agagttaccc agctgcctaa cggccgggac	240
ttccacatgt ctgttgtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc	300
atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca	360
gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagacc tgctggccag	420
ggactgagag agggacctga actgtctcct gatgatcctg ccggcctgct ggatctgaga	480
cagggcatgt ttgcccagct ggtggcccag aatgtgctgc tgattgacgg ccctctgtcc	540
tggtactctg atccaggatt ggctggcgtg tccctgactg gcggcctgtc ttacaaagag	600
gacaccaaag aactggtggt cgccaaggcc ggcgtgtact acgtgttctt tcagctggaa	660
ctgcggagag tgggtggctgg cgaaggatct ggatctgtgt ctctggccct gcatctgcag	720
cctctgagaa gtgctgcagg cgctgctgca ctggctctga cagttgatct gcctcctgcc	780
tcctccgagg ccagaaactc cgcctttggc ttccaaggca gactgctgca tctgtctgcc	840
ggacagagac tgggagtgca cctccataca gaggccagag ctagacacgc ttggcagttg	900
acacagggcg ctacagtgtt gggcctgttt agagtgaccc ctgagatccc tgctggactg	960
ccctctccaa gatctgag	978

<210> 73
 <211> 150
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 73 PD1 ECD Full with CYS73>SER SUBSTITUTION

<400> 73

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
 1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
 20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
 35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
 50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg Phe Arg Val Thr Gln Leu
 65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
 85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
 100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
 115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
 130 135 140

Gln Phe Gln Thr Leu Val
 145 150

<210> 74
 <211> 450
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO:73

<400> 74
 cccggctggt ttctggactc tccagacaga ccttggaacc ctccaacctt ctctcccgct 60
 ctgctggtgg ttaccgaggg cgacaatgcc accttcacct gttccttcag caacacctcc 120
 gagtccttcg tgctgaactg gtacagaatg tcccctagca accagaccga caagctggcc 180
 gcctttcctg aggacagatc tcagccaggc caggactctc gggtcagagt taccagctg 240
 cctaacggcc gggacttcca catgtctgtt gtgcgggccg gacggaacga ctctggcaca 300
 tatctgtgcg gcgccatctc tctggctccc aaggctcaga tcaaagagtc tctgcgggcc 360
 gagctgagag tgacagaaag acgagctgag gtgcccaccg ctcatccctc accttctcca 420
 agacctgctg gccagtttca gacactcgtg 450

<210> 75
 <211> 140
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PD1 -5-5 from var17 (DSP105 var 1 with CYS73>SER SUBSTITUTION)

<400> 75

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
 1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
 20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
 35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
 50 55 60

Gly Gln Asp Ser Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
 65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
 85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
 100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
 115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln
 130 135 140

<210> 76
 <211> 420
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 75 420 bp

<400> 76
 gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
 gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
 aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
 agatctcagc caggccagga ctctcggttc agagtgaccc agctgcctaa cggcagagac 240
 ttccacatgt ccgtcgtgcg ggccagaaga aacgactctg gcacctatct gtgcggcgcc 300
 atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
 gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagacc tgctggccag 420

<210> 77

<211> 146
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -5-5 with His Tag with CYS73>SER SUBSTITUTION

<400> 77

His His His His His His Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro
1 5 10 15

Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr
20 25 30

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

Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro
50 55 60

Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg Phe Arg Val Thr Gln
65 70 75 80

Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg
85 90 95

Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys
100 105 110

Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg
115 120 125

Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala
130 135 140

Gly Gln
145

<210> 78
 <211> 438
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO:77 438 bp

<400> 78
 caccaccacc atcaccacga ctctccagac agaccttgga accctccaac cttctctccc 60
 gctctgctgg tggttaccga gggcgacaat gccaccttca cctgttcctt cagcaacacc 120
 tccgagtcct tcgtgctgaa ctggtacaga atgtccccta gcaaccagac cgacaagctg 180
 gccgcctttc ctgaggacag atctcagcca ggccaggact ctcggttcag agtgacccag 240
 ctgcctaacg gcagagactt ccacatgtcc gtcgtgcggg ccagaagaaa cgactctggc 300
 acctatctgt gcggcgccat ctctctggct cccaaggctc agatcaaaga gtctctgcgg 360
 gccgagctga gagtgacaga aagacgagct gaggtgcca ccgctcatcc ctcaccttct 420
 ccaagacctg ctggccag 438

<210> 79
 <211> 135
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PD1 -10-5 (with CYS73>SER SUBSTITUTION)

<400> 79

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
 1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
 20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
 35 40 45

Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg

50

55

60

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

Ser Pro Arg Pro Ala Gly Gln
130 135

<210> 80
<211> 405
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO:79 405 bp

<400> 80
ccttgggaacc ctccaacctt ctctcccgct ctgctggtgg ttaccgaggg cgacaatgcc 60
accttcacct gttccttcag caacacctcc gagtccttcg tgctgaactg gtacagaatg 120
tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc 180
caggactctc gggttcagagt taccagctg cctaacggcc gggacttcca catgtctggt 240
gtgcggggcca gacggaacga ctctggcaca tatctgtgcg gcgccatctc tctggctccc 300
aaggctcaga tcaaagagtc tctgcgggcc gagctgagag tgacagaaag acgagctgag 360
gtgcccaccg ctcatccctc accttctcca agacctgctg gccag 405

<210> 81
<211> 128

<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -10-12 (with CYS73>SER SUBSTITUTION)

<400> 81

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
35 40 45

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

<210> 82
<211> 384
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO:81 384 bp

<400> 82

```

ccttgaacc ctccaacctt ctctcccgt ctgctggtgg ttaccgaggg cgacaatgcc      60
accttcacct gttccttcag caacacctcc gagtccttcg tgctgaactg gtacagaatg    120
tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc    180
caggactctc ggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt    240
gtgcggggcca gacggaacga ctctggcaca tatctgtgcg gcgccatctc tctggctccc    300
aaggctcaga tcaaagagtc tctgcgggcc gagctgagag tgacagaaaag acgagctgag    360
gtgcccaccg ctcacccctc acct                                           384

```

```

<210> 83
<211> 133
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> PD1 -5-12 (New, from V20) (with CYS73>SER SUBSTITUTION)

```

```

<400> 83

```

```

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1           5           10           15

```

```

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20           25           30

```

```

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35           40           45

```

```

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50           55           60

```

```

Gly Gln Asp Ser Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65           70           75           80

```

```

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85           90           95

```

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro
130

<210> 84
<211> 399
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO:83 399 bp

<400> 84
gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
agatctcagc caggccagga ctctcggttc agagttaccc agctgcctaa cggccggggac 240
ttccacatgt ctgttgtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc 300
atctctcttg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
gaaagacgag ctgaggtgcc caccgctcat ccctcacct 399

<210> 85
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -11-12

<400> 85

Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly
1 5 10 15

Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe
 20 25 30

Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu
 35 40 45

Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe
 50 55 60

Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val
 65 70 75 80

Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser
 85 90 95

Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg
 100 105 110

Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
 115 120 125

<210> 86
 <211> 381
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 85 381 bp

<400> 86
 tggaaccctc caaccttctc tcccgtctctg ctggtgggta ccgagggcga caatgccacc 60
 ttcacctgtt ccttcagcaa cacctccgag tccttcgtgc tgaactggta cagaatgtcc 120
 cctagcaacc agaccgacaa gctggccgcc tttcctgagg acagatctca gccaggccag 180
 gactgtcggg tcagagtgc ccagctgcct aacggcagag acttccacat gtccgtcgtg 240
 cgggccagaa gaaacgactc tggcacctat ctgtgcggcg ccatctctct ggctcccaag 300
 gctcagatca aagagtctct gcgggccgag ctgagagtga cagaaagacg agctgaggtg 360

cccaccgctc atccctcacc t

381

<210> 87
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -11-12 (New, from V18) (with CYS73>SER SUBSTITUTION)

<400> 87

Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly
1 5 10 15

Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe
20 25 30

Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu
35 40 45

Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg Phe
50 55 60

Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val
65 70 75 80

Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser
85 90 95

Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg
100 105 110

Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

<210> 88
<211> 381
<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO: 87 381 bp

<400> 88

```
tggaaccctc caaccttctc tcccgctctg ctggtgggta ccgagggcga caatgccacc      60
ttcacctgtt ccttcagcaa cacctccgag tccttcgtgc tgaactggta cagaatgtcc      120
cctagcaacc agaccgacaa gctggccgcc tttcctgagg acagatctca gccaggccag      180
gactctcggg tcagagtgc ccagctgcct aacggcagag acttccacat gtccgtcgtg      240
cgggccagaa gaaacgactc tggcacctat ctgtgcggcg ccatctctct ggctcccaag      300
gctcagatca aagagtctct gcgggccgag ctgagagtga cagaaagacg agctgagggtg      360
cccaccgctc atccctcacc t                                     381
```

<210> 89

<211> 134

<212> PRT

<213> Artificial sequence

<220>

<223> PD1 -11-5

<400> 89

```
Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly
1              5              10              15
```

```
Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe
          20              25              30
```

```
Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu
          35              40              45
```

```
Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe
          50              55              60
```

```
Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val
65              70              75              80
```

Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser
85 90 95

Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg
100 105 110

Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser
115 120 125

Pro Arg Pro Ala Gly Gln
130

<210> 90
<211> 402
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO: 89 402 bp

<400> 90
tggaaccctc caaccttctc tcccgctctg ctggtgggta ccgagggcga caatgccacc 60
ttcacctgtt ccttcagcaa cacctccgag tccttcgtgc tgaactggta cagaatgtcc 120
cctagcaacc agaccgacaa gctggccgcc tttcctgagg acagatctca gccaggccag 180
gactgtcggg tccagagtgc ccagctgcct aacggcagag acttccacat gtccgtcgtg 240
cgggccagaa gaaacgactc tggcacctat ctgtgcggcg ccatctctct ggctcccaag 300
gctcagatca aagagtctct gcgggccgag ctgagagtga cagaaagacg agctgaggtg 360
cccaccgctc atccctcacc ttctccaaga cctgctggcc ag 402

<210> 91
<211> 134
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -11-5 (New, from V19) (with CYS73>SER SUBSTITUTION)

<400> 91

Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly
1 5 10 15

Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe
20 25 30

Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu
35 40 45

Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg Phe
50 55 60

Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val
65 70 75 80

Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser
85 90 95

Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg
100 105 110

Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser
115 120 125

Pro Arg Pro Ala Gly Gln
130

<210> 92

<211> 402

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO: 91 402 bp

<400> 92

tggaaccctc caaccttctc tcccgtctctg ctggtgggta ccgagggcga caatgccacc

60

100

105

110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
 115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala
 130 135

<210> 94
 <211> 414
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 93 414 bp

<400> 94
 gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
 gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
 aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
 agatctcagc caggccagga ctgtcggttc agagtgaccc agctgcctaa cggcagagac 240
 ttccacatgt ccgtcgtgcg ggccagaaga aacgactctg gcacctatct gtgcggcgcc 300
 atctctctgg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
 gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagacc tgct 414

<210> 95
 <211> 138
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PD1 -5-7 (New, from V21) (with CYS73>SER SUBSTITUTION)

<400> 95

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
 1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Ser Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala
130 135

<210> 96
<211> 414
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO: 95 414 bp

<400> 96
gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
agatctcagc caggccagga ctctcggttc agagtgaccc agctgcctaa cggcagagac 240

ttccacatgt ccgtcgtgcg ggccagaaga aacgactctg gcacctatct gtgcggcgcc 300
atctctctgg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagacc tgct 414

<210> 97
<211> 332
<212> PRT
<213> Artificial sequence

<220>
<223> DSP105 var17 (var1 with substitution of CYS73 in the PD1 domain to SER) without His tag

<400> 97

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Ser Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Gly Ser Ala Ala
130 135 140

Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala
145 150 155 160

Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln
165 170 175

Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly
180 185 190

Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr
195 200 205

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln
210 215 220

Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser
225 230 235 240

Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala
245 250 255

Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn
260 265 270

Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln
275 280 285

Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp
290 295 300

Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro
305 310 315 320

Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 325 330

<210> 98
 <211> 996
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 97 996 bp

<400> 98
 gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
 gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
 aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
 agatctcagc caggccagga ctctcggttc agagtgaccc agctgcctaa cggcagagac 240
 ttccacatgt ccgtcgtgcg ggccagaaga aacgactctg gcacctatct gtgcggcgcc 300
 atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
 gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagacc tgctggccag 420
 ggatctgccc cttctcctag actgagagag ggccctgagc tgtctcctga tgatcctgct 480
 ggactgctgg acctgagaca gggcatgttt gctcagctgg tggcccagaa cgtgctgctg 540
 attgatggcc ctctgtcctg gtactctgat cctggattgg ctggcgtgtc cctgactggc 600
 ggccctgtctt acaaagagga caccaaagaa ctggtggctc ccaaggccgg cgtgtactac 660
 gtgttctttc agctggaact gcggagagtg gtggctggcg aaggatctgg atctgtgtct 720
 ctggccctgc atctgcagcc tctgagaagt gctgcaggcg ctgctgcact ggctctgaca 780
 gttgatctgc ctctgcctc ctccgaggcc agaaactccg cctttggctt ccaaggcaga 840
 ctgctgcata tgtctgccgg acagagactg ggagtgcacc tccatacaga ggccagagct 900
 agacacgctt ggcagttgac acagggcgct acagtgctgg gcctgttttag agtgacacct 960
 gagatcccag ccggcctgcc atctccaaga tctgaa 996

<210> 99

<211> 338
<212> PRT
<213> Artificial sequence

<220>
<223> DSP105 var17 (var1 with substitution of CYS73 in the PD1 domain
to SER) with His tag

<400> 99

His His His His His His Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro
1 5 10 15

Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr
20 25 30

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

Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro
50 55 60

Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg Phe Arg Val Thr Gln
65 70 75 80

Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg
85 90 95

Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys
100 105 110

Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg
115 120 125

Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala
130 135 140

Gly Gln Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu
145 150 155 160

Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe
165 170 175

Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser
180 185 190

Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu
195 200 205

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

Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu
225 230 235 240

Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser
245 250 255

Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala
260 265 270

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

His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala
290 295 300

Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly
305 310 315 320

Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg
325 330 335

Ser Glu

<210> 100
 <211> 1014
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 99 1014 bp

<400> 100
 caccaccacc atcaccacga ctctccagac agaccttgga accctccaac cttctctccc 60
 gctctgctgg tggttaccga gggcgacaat gccaccttca cctgttcctt cagcaacacc 120
 tccgagtcct tcgtgctgaa ctggtacaga atgtccccta gcaaccagac cgacaagctg 180
 gccgcctttc ctgaggacag atctcagcca ggccaggact ctcggttcag agtgaccag 240
 ctgcctaacg gcagagactt ccacatgtcc gtcgtgcggg ccagaagaaa cgactctggc 300
 acctatctgt gcggcgccat ctctctggct cccaaggctc agatcaaaga gtctctgcgg 360
 gccgagctga gagtgacaga aagacgagct gaggtgcca ccgctcatcc ctcaccttct 420
 ccaagacctg ctggccaggg atctgccgct tctcctagac tgagagaggg ccctgagctg 480
 tctcctgatg atcctgctgg actgctggac ctgagacagg gcatgtttgc tcagctggtg 540
 gcccagaacg tgctgctgat tgatggccct ctgtcctggt actctgatcc tggattggct 600
 ggctgtgtccc tgactggcgg cctgtcttac aaagaggaca ccaaagaact ggtggtcgcc 660
 aaggccggcg tgtactacgt gttctttcag ctggaactgc ggagagtggg ggctggcgaa 720
 ggatctggat ctgtgtctct ggccctgcat ctgcagcctc tgagaagtgc tgcaggcgct 780
 gctgcactgg ctctgacagt tgatctgcct cctgcctcct ccgaggccag aaactccgcc 840
 tttggcttcc aaggcagact gctgcatctg tctgccggac agagactggg agtgacctc 900
 catacagagg ccagagctag acacgcttgg cagttgacac agggcgctac agtgctgggc 960
 ctgttttagag tgacacctga gatcccagcc ggcttgccat ctccaagatc tgaa 1014

<210> 101
 <211> 319
 <212> PRT
 <213> Artificial sequence

<220>

<223> DSP105 var18

<400> 101

Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly
1 5 10 15

Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe
20 25 30

Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu
35 40 45

Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg Phe
50 55 60

Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val
65 70 75 80

Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser
85 90 95

Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg
100 105 110

Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Gly
115 120 125

Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
130 135 140

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
145 150 155 160

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
165 170 175

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
180 185 190

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
195 200 205

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
210 215 220

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

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
245 250 255

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
260 265 270

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
275 280 285

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
290 295 300

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

<210> 102
<211> 957
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO: 101 957 bp

<400> 102
tggaaccctc caaccttctc tcccgctctg ctggtgggta ccgagggcga caatgccacc 60
ttcacctgtt ccttcagcaa cacctccgag tccttcgtgc tgaactggta cagaatgtcc 120

cctagcaacc agaccgacaa gctggccgcc tttcctgagg acagatctca gccaggccag 180
 gactctcggg tcagagtgaac ccagctgcct aacggcagag acttccacat gtccgtcgtg 240
 cgggccagaa gaaacgactc tggcacctat ctgtgcggcg ccatctctct ggctcccaag 300
 gctcagatca aagagtctct gcgggccgag ctgagagtga cagaaagacg agctgagggtg 360
 cccaccgctc atccctcacc tggatctgcc gcttctccta gactgagaga gggccctgag 420
 ctgtctcctg atgatcctgc tggactgctg gacctgagac agggcatgtt tgctcagctg 480
 gtggcccaga acgtgctgct gattgatggc cctctgtcct ggtactctga tcctggattg 540
 gctggcgtgt ccctgactgg cggcctgtct tacaagagg acaccaaaga actggtgggtc 600
 gccaaaggccg gcgtgtacta cgtgttcttt cagctggaac tgcggagagt ggtggctggc 660
 gaaggatctg gatctgtgtc tctggccctg catctgcagc ctctgagaag tgctgcaggc 720
 gctgctgcac tggctctgac agttgatctg cctcctgcct cctccgaggc cagaaactcc 780
 gcctttggct tccaaggcag actgctgcat ctgtctgccg gacagagact gggagtgcac 840
 ctccatacag aggccagagc tagacacgct tggcagttga cacagggcgc tacagtgtg 900
 ggctgttcta gaggacacc tgagatccca gccggcctgc catctccaag atctgaa 957

<210> 103
 <211> 326
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP105 var19

<400> 103

Trp	Asn	Pro	Pro	Thr	Phe	Ser	Pro	Ala	Leu	Leu	Val	Val	Thr	Glu	Gly
1				5					10					15	

Asp	Asn	Ala	Thr	Phe	Thr	Cys	Ser	Phe	Ser	Asn	Thr	Ser	Glu	Ser	Phe
			20						25				30		

Val	Leu	Asn	Trp	Tyr	Arg	Met	Ser	Pro	Ser	Asn	Gln	Thr	Asp	Lys	Leu
		35					40					45			

Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg Phe
50 55 60

Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val
65 70 75 80

Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser
85 90 95

Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg
100 105 110

Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser
115 120 125

Pro Arg Pro Ala Gly Gln Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu
130 135 140

Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg
145 150 155 160

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
165 170 175

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
180 185 190

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
195 200 205

Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val
210 215 220

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
225 230 235 240

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
245 250 255

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
260 265 270

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
275 280 285

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
290 295 300

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
305 310 315 320

Pro Ser Pro Arg Ser Glu
325

<210> 104
<211> 978
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO: 103 977 bp

<400> 104
tggaaccctc caaccttctc tcccgctctg ctggtgggta ccgagggcga caatgccacc 60
ttcacctgtt ccttcagcaa cacctccgag tccttcgtgc tgaactggta cagaatgtcc 120
cctagcaacc agaccgacaa gctggccgcc tttcctgagg acagatctca gccaggccag 180
gactctcggg tcagagtgac ccagctgcct aacggcagag acttccacat gtccgtcgtg 240
cgggccagaa gaaacgactc tggcacctat ctgtgcggcg ccatctctct ggctcccaag 300
gctcagatca aagagtctct gcgggccgag ctgagagtga cagaaagacg agctgaggtg 360
cccaccgctc atccctcacc ttctccaaga cctgctggcc agggatctgc cgcttctcct 420
agactgagag agggccctga gctgtctcct gatgatcctg ctggactgct ggacctgaga 480

cagggcatgt ttgctcagct ggtggcccag aacgtgctgc tgattgatgg ccctctgtcc 540
 tgggtactctg atcctggatt ggctggcgtg tccctgactg gcggcctgtc ttacaaagag 600
 gacaccaaag aactggtggt cgccaaggcc ggctgtgact acgtgttctt tcagctggaa 660
 ctgcggagag tgggtggctgg cgaaggatct ggatctgtgt ctctggccct gcatctgcag 720
 cctctgagaa gtgctgcagg cgctgctgca ctggctctga cagttgatct gcctcctgcc 780
 tcctccgagg ccagaaactc cgcctttggc ttccaaggca gactgctgca tctgtctgcc 840
 ggacagagac tgggagtgc cctccataca gaggccagag ctagacacgc ttggcagttg 900
 acacagggcg ctacagtgtt gggcctgttt agagtgcac ctgagatccc agccggcctg 960
 ccatctccaa gatctgaa 978

<210> 105
 <211> 325
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP105 var20

<400> 105

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
 1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
 20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
 35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
 50 55 60

Gly Gln Asp Ser Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
 65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly
130 135 140

Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln
145 150 155 160

Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly
165 170 175

Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr
180 185 190

Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys
195 200 205

Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val
210 215 220

Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro
225 230 235 240

Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu
245 250 255

Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly
260 265 270

Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His
 275 280 285

Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr
 290 295 300

Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro
 305 310 315 320

Ser Pro Arg Ser Glu
 325

<210> 106
 <211> 975
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 105 1062 bp

<400> 106
 gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
 gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
 aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
 agatctcagc caggccagga ctctcggttc agagtgaccc agctgcctaa cggcagagac 240
 ttccacatgt ccgtcgtgcg ggccagaaga aacgactctg gcacctatct gtgcggcgcc 300
 atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
 gaaagacgag ctgagggtgcc caccgctcat ccctcacctg gatctgccgc ttctcctaga 420
 ctgagagagg gccctgagct gtctcctgat gatcctgctg gactgctgga cctgagacag 480
 ggcatgtttg ctcagctggt ggcccagaac gtgctgctga ttgatggccc tctgtcctgg 540
 tactctgatc ctggattggc tggcgtgtcc ctgactggcg gcctgtctta caaagaggac 600
 accaaagaac tgggtggtcgc caaggccggc gtgtactacg tgttctttca gctggaactg 660
 cggagagtgg tggctggcga aggatctgga tctgtgtctc tggccctgca tctgcagcct 720

ctgagaagtg ctgcaggcgc tgctgcactg gctctgacag ttgatctgcc tcctgcctcc 780
tccgaggcca gaaactccgc ctttggcttc caaggcagac tgctgcatct gtctgccgga 840
cagagactgg gagtgcacct ccatacagag gccagagcta gacacgcttg gcagttgaca 900
cagggcgcta cagtgtctggg cctgtttaga gtgacacctg agatcccagc cggcctgcca 960
tctccaagat ctgaa 975

<210> 107
<211> 330
<212> PRT
<213> Artificial sequence

<220>
<223> DSP105 var21

<400> 107

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Ser Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Ser Ala Ala Ser Pro
130 135 140

Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
145 150 155 160

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
165 170 175

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
180 185 190

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
195 200 205

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
210 215 220

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
225 230 235 240

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
245 250 255

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
260 265 270

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
275 280 285

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
290 295 300

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile

305 310 315 320

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
325 330

<210> 108
<211> 990
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO: 107 1077 bp

<400> 108
gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
gagggcgaca atgccacctt cacctgttcc ttacgaaca cctccgagtc cttcgtgctg 120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
agatctcagc caggccagga ctctcggttc agagtgaccc agctgcctaa cggcagagac 240
ttccacatgt ccgtcgtgcg ggccagaaga aacgactctg gcacctatct gtgcggcgcc 300
atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
gaaagacgag ctgagggtgcc caccgctcat ccctcacctt ctccaagacc tgctggatct 420
gccgcttctc ctagactgag agagggccct gagctgtctc ctgatgatcc tgctggactg 480
ctggacctga gacagggcat gtttgctcag ctggtggccc agaacgtgct gctgattgat 540
ggccctctgt cctggtactc tgatcctgga ttggctggcg tgtccctgac tggcggcctg 600
tcttacaaag aggacaccaa agaactgggtg gtcgccaagg ccggcgtgta ctacgtgttc 660
tttcagctgg aactgcggag agtgggtggct ggcaaggat ctggatctgt gtctctggcc 720
ctgcatctgc agcctctgag aagtgtgca ggcgctgctg cactggctct gacagttgat 780
ctgcctcctg cctcctccga ggccagaaac tccgcctttg gcttccaagg cagactgctg 840
catctgtctg ccggacagag actgggagtg cacctccata cagaggccag agctagacac 900
gcttggcagt tgacacaggg cgctacagtg ctgggcctgt ttagagtgac acctgagatc 960
ccagccggcc tgccatctcc aagatctgaa 990

<210> 109
<211> 362
<212> PRT
<213> Artificial sequence

<220>
<223> DSP105 var22 362 aa with His tag

<400> 109

His His His His His His Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg
1 5 10 15

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
20 25 30

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
35 40 45

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
50 55 60

Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg
65 70 75 80

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
85 90 95

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

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
115 120 125

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
130 135 140

Ser Pro Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Gly Ala Cys Pro

145		150		155		160									
Trp	Ala	Val	Ser	Gly	Ala	Arg	Ala	Ser	Pro	Gly	Ser	Ala	Ala	Ser	Pro
				165					170					175	
Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	Asp	Pro	Ala	Gly	Leu
			180					185					190		
Leu	Asp	Leu	Arg	Gln	Gly	Met	Phe	Ala	Gln	Leu	Val	Ala	Gln	Asn	Val
		195					200					205			
Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser	Trp	Tyr	Ser	Asp	Pro	Gly	Leu	Ala
	210					215					220				
Gly	Val	Ser	Leu	Thr	Gly	Gly	Leu	Ser	Tyr	Lys	Glu	Asp	Thr	Lys	Glu
225					230					235					240
Leu	Val	Val	Ala	Lys	Ala	Gly	Val	Tyr	Tyr	Val	Phe	Phe	Gln	Leu	Glu
				245					250					255	
Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly	Ser	Val	Ser	Leu	Ala
			260					265					270		
Leu	His	Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly	Ala	Ala	Ala	Leu	Ala
		275					280					285			
Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu	Ala	Arg	Asn	Ser	Ala
	290					295					300				
Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser	Ala	Gly	Gln	Arg	Leu
305					310					315					320
Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg	His	Ala	Trp	Gln	Leu
				325					330					335	
Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg	Val	Thr	Pro	Glu	Ile
			340					345					350		

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 355 360

<210> 110
 <211> 1086
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 109 1086 bp

<400> 110
 caccatcatc accaccatcc tggctggttt ctggacagcc ccgacagacc ttggaaccct 60
 cctacattca gccccgctct gctggtgggt accgagggcg ataatgccac cttcacctgt 120
 agcttcagca acaccagcga gagcttcgtg ctgaactggg acagaatgag ccccagcaac 180
 cagaccgaca agctggccgc ctttcctgag gatagatctc agcccggcca ggactctcgg 240
 ttcagagtta cacagctgcc caacggccgg gacttccaca tgtctgtcgt ccgggccaga 300
 agaaacgaca gcggcacata tctgtgcggc gccatttctc tggcccctaa ggctcagatc 360
 aaagagagcc tgagagccga gctgagagt acagaaagac gggccgaagt gcccacagct 420
 cacccttcac cttctccaag acctgccggc cagtttcaga cactcgtggg agcttgtcct 480
 tgggccggtt ctggcgctag agcctctcct ggatctgccg cttctcccag actgagagag 540
 ggacctgagc tgagccctga tgatcctgct ggactgctgg atctgagaca gggcatgttt 600
 gcccagctgg tggcccagaa tgtgtgctg attgatggcc ctctgtcctg gtacagcgat 660
 cctggacttg ctggcgtag cctgactggc ggcctgagct acaaagagga caccaaagaa 720
 ctggtggtgg ccaaggccgg cgtgtactac gtgttctttc agctggaact gcggagagt 780
 gtggccggcg aaggatctgg atctgtgtct ctggctctgc atctgcagcc tctgagatct 840
 gctgctgggt ctgctgctct ggccctgaca gttgatctgc ctctgcctc tagcgaggcc 900
 agaaaactccg cctttggctt ccaaggcaga ctgctgcacc tgagcgctgg acagagactg 960
 ggagtccatc tgcacacaga agccagagct agacacgcct ggcagctgac acaaggcgct 1020

acagtgtggtg gcctgttcag agtgaccctt gagattccag ccggcctgcc atctcctaga 1080
tctgag 1086

<210> 111
<211> 356
<212> PRT
<213> Artificial sequence

<220>
<223> DSP105 var22 362 aa

<400> 111

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg Phe Arg Val Thr Gln Leu
65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Phe Gln Thr Leu Val Gly Ala Cys Pro Trp Ala Val Ser Gly Ala
 145 150 155 160

Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro
 165 170 175

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
 180 185 190

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
 195 200 205

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
 210 215 220

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
 225 230 235 240

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
 245 250 255

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
 260 265 270

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
 275 280 285

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
 290 295 300

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
 305 310 315 320

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
 325 330 335

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

Pro Arg Ser Glu
 355

<210> 112
 <211> 1068
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 111 1086 bp

<400> 112
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 ctgctggtgg ttaccgaggg cgataatgcc accttcacct gtagcttcag caacaccagc 120
 gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc 180
 gcctttcctg aggatagatc tcagcccggc caggactctc gggttcagagt tacacagctg 240
 cccaacggcc gggacttcca catgtctgtc gtccgggccca gaagaaacga cagcggcaca 300
 tatctgtgcg gcgccatttc tctggcccct aaggctcaga tcaaagagag cctgagagcc 360
 gagctgagag tgacagaaaag acgggccgaa gtgcccacag ctccaccttc accttctcca 420
 agacctgccg gccagtttca gacactcgtg ggagcttgct cttgggccgt ttctggcgct 480
 agagcctctc ctggatctgc cgcttctccc agactgagag agggacctga gctgagccct 540
 gatgatcctg ctggactgct ggatctgaga cagggcattg ttgcccagct ggtggcccag 600
 aatgtgctgc tgattgatgg ccctctgtcc tggtagagcg atcctggact tgctggcggt 660
 agcctgactg gcggcctgag ctacaaagag gacaccaaag aactggtggt ggccaaggcc 720
 ggcgtgtact acgtgttctt tcagctggaa ctgcggagag tggtagccgg cgaaggatct 780
 ggatctgtgt ctctggctct gcatctgcag cctctgagat ctgctgtggt tgctgtgct 840
 ctggccctga cagttgatct gcctcctgcc tctagcgagg ccagaaactc cgcctttggc 900
 ttccaaggca gactgctgca cctgagcgct ggacagagac tgggagtcca tctgcacaca 960

gaagccagag ctagacacgc ctggcagctg acacaaggcg ctacagtgct gggcctgttc 1020

agagtgaccc ctgagattcc agccggcctg ccatctccta gatctgag 1068

<210> 113

<211> 330

<212> PRT

<213> Artificial sequence

<220>

<223> DSP105 var23 amino acid sequence

<400> 113

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Ser Ala Ala Ser Pro

130

135

140

Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
 145 150 155 160

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
 165 170 175

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
 180 185 190

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
 195 200 205

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
 210 215 220

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
 225 230 235 240

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
 245 250 255

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
 260 265 270

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
 275 280 285

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
 290 295 300

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
 305 310 315 320

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 325 330

125

<210> 114
 <211> 990
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DSP105 var23 nucleic acid sequence

<400> 114
 gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
 gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
 aactgggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
 agatctcagc caggccagga ctgtcggttc agagtgaccc agctgcctaa cggcagagac 240
 ttccacatgt ccgtcgtgcg ggccagaaga aacgactctg gcacctatct gtgcggcgcc 300
 atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
 gaaagacgag ctgagggtgcc caccgctcat ccctcacctt ctccaagacc tgctggatct 420
 gccgcttctc ctagactgag agagggccct gagctgtctc ctgatgatcc tgctggactg 480
 ctggacctga gacagggcat gtttgctcag ctgggtggccc agaacgtgct gctgattgat 540
 ggccctctgt cctgggtactc tgatcctgga ttggctggcg tgtccctgac tggcggcctg 600
 tcttacaaag aggacaccaa agaactgggtg gtcgccaagg ccggcgtgta ctacgtgttc 660
 tttcagctgg aactgcggag agtgggtggct ggccaaggat ctggatctgt gtctctggcc 720
 ctgcatctgc agcctctgag aagtgtgca ggcgctgctg cactggctct gacagttgat 780
 ctgcctcctg cctcctccga ggccagaaac tccgcctttg gcttccaagg cagactgctg 840
 catctgtctg ccggacagag actgggagtg cacctccata cagaggccag agctagacac 900
 gcttggcagt tgacacaggg cgctacagtg ctgggcctgt ttagagtgac acctgagatc 960
 ccagccggcc tgccatctcc aagatctgaa 990

<210> 115
 <211> 136
 <212> PRT

<213> Artificial sequence

<220>

<223> PD1 variant amino acid sequence

<400> 115

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg
130 135

<210> 116

<211> 408

<212> DNA

<213> Artificial sequence

<220>

<223> PD1 variant nucleic acid sequence

<400> 116

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gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc      60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg      120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac      180
agatctcagc caggccagga ctgtcggttc agagttaccc agctgcctaa cggccggggac      240
ttccacatgt ctgttggtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc      300
atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca      360
gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaaga      408
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<210> 117

<211> 145

<212> PRT

<213> Artificial sequence

<220>

<223> PD1 variant amino acid sequence

<400> 117

```
Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1           5           10           15
```

```
Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
20           25           30
```

```
Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35           40           45
```

```
Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50           55           60
```

```
Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65           70           75           80
```

```
Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
```

85

90

95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
 100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
 115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
 130 135 140

Gln
 145

<210> 118
 <211> 435
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PD1 variant nucleic acid sequence

<400> 118
 cccggctggt ttctggactc tccagacaga ccttggaacc ctccaacctt ctctcccgt 60
 ctgctggtgg ttaccgaggg cgacaatgcc accttcacct gttccttcag caacacctcc 120
 gagtccttcg tgctgaactg gtacagaatg tcccctagca accagaccga caagctggcc 180
 gcctttcctg aggacagatc tcagccaggc caggactgtc ggttcagagt taccagctg 240
 cctaacggcc gggacttcca catgtctgtt gtgcgggcca gacggaacga ctctggcaca 300
 tatctgtgcg gcgccatctc tctggctccc aaggctcaga tcaaagagtc tctgcgggcc 360
 gagctgagag tgacagaaag acgagctgag gtgcccaccg ctcattccctc accttctcca 420
 agacctgctg gccag 435

<210> 119
 <211> 143
 <212> PRT
 <213> Artificial sequence

<220>

<223> PD1 variant amino acid sequence

<400> 119

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala
130 135 140

<210> 120

<211> 429

<212> DNA

<213> Artificial sequence

<220>

<223> PD1 variant nucleic acid sequence

<400> 120
 cccggctggg ttctggactc tccagacaga ccttggaacc ctccaacctt ctctcccgt 60
 ctgctgggtg ttaccgaggg cgacaatgcc accttcacct gttccttcag caacacctcc 120
 gagtccttcg tgctgaactg gtacagaatg tcccctagca accagaccga caagctggcc 180
 gcctttcctg aggacagatc tcagccaggc caggactgtc gggttcagagt taccagctg 240
 cctaacggcc gggacttcca catgtctgtt gtgcgggcca gacggaacga ctctggcaca 300
 tatctgtgcg gcgccatctc tctggctccc aaggctcaga tcaaagagtc tctgcgggcc 360
 gagctgagag tgacagaaag acgagctgag gtgcccaccg ctcatccctc accttctcca 420
 agacctgct 429

<210> 121
 <211> 14
 <212> PRT
 <213> Artificial sequence

<220>
 <223> linker amino acid sequence

<400> 121

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10

<210> 122
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> linker amino acid sequence

<400> 122

Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5

<210> 123
 <211> 184

<212> PRT
<213> Artificial sequence

<220>
<223> 4-1BBL variant amino acid sequence

<400> 123

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

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

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala

165

170

175

Gly Leu Pro Ser Pro Arg Ser Glu
180

<210> 124

<211> 552

<212> DNA

<213> Artificial sequence

<220>

<223> 4-1BBL variant nucleic acid sequence

<400> 124

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agagagggcc ctgagctgtc tcctgatgat cctgctggac tgctggacct gagacagggc      60
atgtttgctc agctgggtggc ccagaacgtg ctgctgattg atggccctct gtcctggtac      120
tctgatcctg gattggctgg cgtgtccctg actggcggcc tgtcttacaag agaggacacc      180
aaagaactgg tggtcgcca ggccggcgtg tactacgtgt tctttcagct ggaactgcgg      240
agagtgggtg ctggcgaagg atctggatct gtgtctcttg ccctgcatct gcagcctctg      300
agaagtgctg caggcgctgc tgcactggct ctgacagttg atctgcctcc tgcctcctcc      360
gaggccagaa actccgcctt tggcttccaa ggcagactgc tgcattctgtc tgccggacag      420
agactgggag tgcacctcca tacagaggcc agagctagac acgcttggca gttgacacag      480
ggcgctacag tgctgggcct gtttagagtg acacctgaga tcccagccgg cctgccatct      540
ccaagatctg aa                                                                552

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<210> 125

<211> 182

<212> PRT

<213> Artificial sequence

<220>

<223> 4-1BBL variant amino acid sequence

<400> 125

Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg
1 5 10 15

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
20 25 30

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
35 40 45

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
50 55 60

Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val
65 70 75 80

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
85 90 95

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
100 105 110

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
115 120 125

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
130 135 140

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
145 150 155 160

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
165 170 175

Pro Ser Pro Arg Ser Glu
180

<210> 126
<211> 546
<212> DNA

<213> Artificial sequence

<220>

<223> 4-1BBL variant nucleic acid sequence

<400> 126

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ggccctgagc tgtctcctga tgatcctgct ggactgctgg acctgagaca gggcatgttt      60
gctcagctgg tggcccagaa cgtgctgctg attgatggcc ctctgtcctg gtactctgat      120
cctggattgg ctggcgtgtc cctgactggc ggccctgtctt acaaagagga caccaaagaa      180
ctggctggctg ccaaggccgg cgtgtactac gtgttctttc agctggaact gcggagagtg      240
gtggctggcg aaggatctgg atctgtgtct ctggccctgc atctgcagcc tctgagaagt      300
gctgcaggcg ctgctgcact ggctctgaca gttgatctgc ctctgcctc ctccgaggcc      360
agaaactccg cctttggctt ccaaggcaga ctgctgcatc tgtctgccgg acagagactg      420
ggagtgcacc tccatacaga ggccagagct agacacgctt ggcagttgac acagggcgct      480
acagtgtggt gcctgttttag agtgacacct gagatcccag ccggcctgcc atctccaaga      540
tctgaa                                         546
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<210> 127

<211> 183

<212> PRT

<213> Artificial sequence

<220>

<223> 4-1BBL variant amino acid sequence

<400> 127

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Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
1           5           10          15
Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
20          25          30
Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
35          40          45
```

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
50 55 60

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

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
85 90 95

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
100 105 110

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
115 120 125

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
130 135 140

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
145 150 155 160

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
165 170 175

Val Thr Pro Glu Ile Pro Ala
180

<210> 128
<211> 551
<212> DNA
<213> Artificial sequence

<220>
<223> 4-1BBL variant nucleic acid sequence

<400> 128
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gactgctgga cctgagacag ggcatgtttg ctcagctggg gggccagaac gtgctgctga 120

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ttgatggccc tctgtcctgg tactctgatc ctggattggc tggcgtgtcc ctgactggcg      180
gcctgtctta caaagaggac accaaagaac tgggtggcgc caaggccggc gtgtactacg      240
tggttctttca gctggaactg cggagagtgg tggctggcga aggatctgga tctgtgtctc      300
tggccctgca tctgcagcct ctgagaagtg ctgcaggcgc tgctgcactg gctctgacag      360
ttgatctgcc tcctgcctcc tccgaggcca gaaactccgc ctttggcttc caaggcagac      420
tgctgcatct gtctgccgga cagagactgg gagtgcacct ccatacagag gccagagcta      480
gacacgcttg gcagttgaca cagggcgcta cagtgtctggg cctgtttaga gtgacacctg      540
agatcccagc c                                                                551

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<210> 129
 <211> 176
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 4-1BBL variant amino acid sequence

<400> 129

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Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1           5           10           15

```

```

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
          20           25           30

```

```

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

```

```

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
          50           55           60

```

```

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65           70           75           80

```

```

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
          85           90           95

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Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

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

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

<210> 130
<211> 528
<212> DNA
<213> Artificial sequence

<220>
<223> 4-1BBL variant nucleic acid sequence

<400> 130
agagaggggcc ctgagctgtc tcctgatgat cctgctggac tgctggacct gagacagggc 60
atgtttgctc agctggtggc ccagaacgtg ctgctgattg atggccctct gtcctggtac 120
tctgatcctg gattggctgg cgtgtccctg actggcggcc tgtcttacaag agaggacacc 180
aaagaactgg tggctgcctc ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240
agagtgggtg ctggcgaagg atctggatct gtgtctctgg ccctgcatct gcagcctctg 300
agaagtgctg caggcgctgc tgcactggct ctgacagttg atctgcctcc tgcctcctcc 360
gaggccagaa actccgcctt tggcttccaa ggcagactgc tgcattctgtc tgccggacag 420
agactgggag tgcacctcca tacagaggcc agagctagac acgcttggca gttgacacag 480
ggcgctacag tgctgggcct gtttagagt acacctgaga tcccagcc 528

<210> 131
<211> 601
<212> PRT
<213> Artificial sequence

<220>
<223> sc3x4-1BBL -14-0 amino acids sequence

<400> 131

Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
1 5 10 15

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
20 25 30

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
35 40 45

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
50 55 60

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

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
85 90 95

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
100 105 110

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
115 120 125

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
130 135 140

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
145 150 155 160

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
165 170 175

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly
180 185 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala
195 200 205

Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala
210 215 220

Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln
225 230 235 240

Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly
245 250 255

Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr
260 265 270

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln
275 280 285

Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser
290 295 300

Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala
305 310 315 320

Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn
325 330 335

Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln
340 345 350

Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp
 355 360 365

Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro
 370 375 380

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ser Pro Arg
 405 410 415

Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
 420 425 430

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu
 435 440 445

Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly
 450 455 460

Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu
 465 470 475 480

Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu
 485 490 495

Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu
 500 505 510

His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu
 515 520 525

Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe
 530 535 540

Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly
 545 550 555 560

Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr
 565 570 575

Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro
 580 585 590

Ala Gly Leu Pro Ser Pro Arg Ser Glu
 595 600

<210> 132
 <211> 1803
 <212> DNA
 <213> Artificial sequence

<220>
 <223> sc3x4-1BBL -14-0 nucleic acid sequence

<400> 132
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 ctgctggacc tgaggcaggg aatgttcgca cagctgggtgg cccagaacgt gctgctgac 120
 gacggccctc tgtcctggta ctctgatcca ggcttgccg gcgtgtccct gacaggaggc 180
 ctgtcttata aggaggatac caaggagctg gtggtggcaa aggcaggcgt gtactacgtg 240
 ttcttccagc tggagctgag gagagtgggtg gcaggagagg gcagcggctc cgtgtctctg 300
 gccctgcacc tccagcctct gcggagcgcc gccggcgccg ccgccctggc cctgaccgtg 360
 gatctgcctc cagccagctc cgaggccagg aatagcgctt tcggctttca gggccgcctg 420
 ctgcacctgt ccgccggcca gcggctggga gtgcacctgc acacagaggc cagagcccgg 480
 cacgcatggc agctgacaca gggagcaacc gtgctggggc tgttccgcgt gacccctgag 540
 atcccagccg gcctgccaag cccccgtcc gagggcgggc gcggctctgg cggaggaggc 600
 agcggaggcg gcggctctgc cgccagcccc aggtgctgcg agggacccga gctgtcccca 660
 gacgatcctg ccggcctgct ggacctgcgc cagggaatgt ttgccagct ggtggctcaa 720

aacgtgctgt taatcgacgg ccctctgagc tggctactctg atcctggcct ggccggcgtg	780
agcctgaccg gcggcctgtc ctacaaagag gatactaaag agctgggtggc cgccaaagcc	840
ggcgtgtact acgtgttctt ccaactggag ctgaggaggg tcgtcgccgg cgaaggcagc	900
ggctccgtgt ctctggccct gcacctccag ccgctgagga gcgccgccgg cgccgccgcc	960
ctggccctga cgggtggacct gccacctgcc tctagcgagg caagaaattc tgccttcggc	1020
ttccagggca ggctgctgca cctgagcgcc ggccagcgcc tgggcgtcca cctgcatacc	1080
gaagccagag cccggcatgc ctggcagctg acccagggcg ccaccgtgct gggcctgttc	1140
agagtgaccc cagagatccc cgccggcctg cctagcccaa ggtccgaagg cggcggcggc	1200
tccggcggcg gaggctctgg aggagggggc tctgccgcca gcccaaggct gcgcgaggga	1260
cccgagctgt cgctgacga tccagccggc ctgctggacc tgcgtcaggg catgttcgcc	1320
cagctgggtgg ctcaaacgt gctgttaatc gacggcccac tgtcttggtta ttctgatccc	1380
ggcctggccg gcgtgtctct gacaggaggc ctgagctaca aagaggatac aaaagagctg	1440
gtggtcgcta aagctggcgt gtactacgtg ttcttccaac tggagctgcg cagggtcgtc	1500
gccggcgagg gcagcggctc cgtgtctctg gccctgcacc tccagccatt acggagcgcc	1560
gccggcgccg ccgccctggc cctgactgtg gacctgccac cagcctcctc tgaggcacgg	1620
aacagcgctt tcggcttcca aggcagactg ctgcacctgt ctgccggcca gaggctgggc	1680
gtccacctgc acaccgaagc cagagcccgg cacgcctggc agctgactca gggcgctacc	1740
gtgctgggcc tggtccgcgt aaccccagag atccctgccg gcctgcccag ccctcggtcc	1800
gag	1803

<210> 133
 <211> 321
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> DSP105 variant amino acid sequence

 <400> 133

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Gly Arg Glu Gly Pro Glu Leu Ser
130 135 140

Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala
145 150 155 160

Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp
165 170 175

Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser
180 185 190

Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr

195

200

205

Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly
 210 215 220

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

Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser
 245 250 255

Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His
 260 265 270

Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg
 275 280 285

Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu
 290 295 300

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

Glu

<210> 134
 <211> 963
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DSP105 variant nucleic acid sequence

<400> 134
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 gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
 aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180

agatctcagc caggccagga ctgtcggttc agagttaccc agctgcctaa cggccgggac 240
 ttccacatgt ctgttgtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc 300
 atctctctgg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
 gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagagg aagagagggc 420
 cctgagctgt ctctgatga tcctgctgga ctgctggacc tgagacaggg catgtttgct 480
 cagctgggtgg cccagaacgt gctgctgatt gatggccctc tgtcctggta ctctgacct 540
 ggattggctg gcgtgtccct gactggcggc ctgtcttaca aagaggacac caaagaactg 600
 gtggtcgcca aggccggcgt gtactacgtg ttctttcagc tggaactgcg gagagtgggtg 660
 gctggcgaag gatctggatc tgtgtctctg gccctgcac tgcagcctct gagaagtgct 720
 gcaggcgctg ctgcactggc tctgacagtt gatctgcctc ctgcctcctc cgaggccaga 780
 aactccgcct ttggcttcca aggcagactg ctgcatctgt ctgccggaca gagactggga 840
 gtgcacctcc atacagaggc cagagctaga cacgcttggc agttgacaca gggcgctaca 900
 gtgctggggc tgttttagagt gacacctgag atcccagccg gcctgccatc tccaagatct 960
 gaa 963

<210> 135
 <211> 319
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP105 variant amino acid sequence

<400> 135

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
 1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
 20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser

35

40

45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
 50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
 65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
 85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
 100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
 115 120 125

Ala His Pro Ser Pro Ser Pro Arg Gly Gly Pro Glu Leu Ser Pro Asp
 130 135 140

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
 145 150 155 160

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
 165 170 175

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
 180 185 190

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
 195 200 205

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
 210 215 220

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

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
245 250 255

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
260 265 270

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
275 280 285

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
290 295 300

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

<210> 136
<211> 957
<212> DNA
<213> Artificial sequence

<220>
<223> DSP105 variant nucleic acid sequence

<400> 136
gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
agatctcagc caggccagga ctgtcggttc agagttaccc agctgcctaa cggccgggac 240
ttccacatgt ctgttggtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc 300
atctctcttg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagagg aggccctgag 420
ctgtctcctg atgatcctgc tggactgctg gacctgagac agggcatggt tgctcagctg 480
gtggcccaga acgtgctgct gattgatggc cctctgtcct ggtactctga tcctggattg 540

gctggcgtgt ccctgactgg cggcctgtct tacaaagagg acaccaaaga actggtggtc 600
 gccaaaggccg gcgtgtacta cgtgttcttt cagctggaac tgcggagagt ggtggctggc 660
 gaaggatctg gatctgtgtc tctggccctg catctgcagc ctctgagaag tgctgcaggc 720
 gctgctgcac tggctctgac agttgatctg cctcctgcct cctccgaggc cagaaactcc 780
 gcctttggct tccaaggcag actgctgcat ctgtctgccg gacagagact gggagtgcac 840
 ctccatacag aggccagagc tagacacgct tggcagttga cacagggcgc tacagtgtg 900
 ggcctgttta gagtgcacc tgagatccca gccggcctgc catctccaag atctgaa 957

<210> 137
 <211> 329
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP105 variant amino acid sequence

<400> 137

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
 1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
 20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
 35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
 50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
 65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
 85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser
145 150 155 160

Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala
165 170 175

Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp
180 185 190

Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser
195 200 205

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

Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly
225 230 235 240

Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala
245 250 255

Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser
260 265 270

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

Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg

290

295

300

Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu
 305 310 315 320

Phe Arg Val Thr Pro Glu Ile Pro Ala
 325

<210> 138
 <211> 987
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DSP105 variant nucleic acid sequence

<400> 138
 cccggctggt ttctggactc tccagacaga ccttgggaacc ctccaacctt ctctcccgt 60
 ctgctggtgg ttaccgaggg cgacaatgcc accttcacct gttccttcag caacacctcc 120
 gagtccttcg tgctgaactg gtacagaatg tcccctagca accagaccga caagctggcc 180
 gcctttcctg aggacagatc tcagccaggc caggactgtc ggttcagagt taccagctg 240
 cctaacggcc gggacttcca catgtctgtt gtgcgggcca gacggaacga ctctggcaca 300
 tatctgtgcg gcgccatctc tctggctccc aaggctcaga tcaaagagtc tctgcgggcc 360
 gagctgagag tgacagaaag acgagctgag gtgcccaccg ctcatccctc accttctcca 420
 agacctgctg gccagggatc tgccgcttct cctagactga gagaggggccc tgagctgtct 480
 cctgatgatc ctgctggact gctggacctg agacagggca tgtttgctca gctggtggcc 540
 cagaacgtgc tgctgattga tggccctctg tcctgggtact ctgatcctgg attggctggc 600
 gtgtccctga ctggcggcct gtcttacaaa gaggacacca aagaactggt ggtcgccaag 660
 gccggcgtgt actacgtgtt ctttcagctg gaactgcgga gagtggtggc tggcgaagga 720
 tctggatctg tgtctctggc cctgcatctg cagcctctga gaagtgtgc aggcgtgct 780
 gcactggctc tgacagttga tctgcctcct gcctcctccg aggccagaaa ctccgccttt 840
 ggcttccaag gcagactgct gcatctgtct gccggacaga gactgggagt gcacctccat 900

acagaggcca gagctagaca cgcttggcag ttgacacagg gcgctacagt gctgggcctg 960
 ttttagagtga cacctgagat cccagcc 987

<210> 139
 <211> 320
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP105 variant amino acid sequence

<400> 139

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
 1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
 20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
 35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
 50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
 65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
 85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
 100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
 115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly

130

135

140

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
 145 150 155 160

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
 165 170 175

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
 180 185 190

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
 195 200 205

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
 210 215 220

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
 225 230 235 240

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
 245 250 255

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
 260 265 270

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
 275 280 285

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
 290 295 300

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
 305 310 315 320

<210> 140

<211> 960

<212> DNA
<213> Artificial sequence

<220>
<223> DSP105 variant nucleic acid sequence

<400> 140
cccggctggt ttctggactc tccagacaga ccttgggaacc ctccaacctt ctctcccgt 60
ctgctgggtg ttaccgaggg cgacaatgcc accttcacct gttccttcag caacacctcc 120
gagtccttcg tgctgaactg gtacagaatg tcccctagca accagaccga caagctggcc 180
gcctttcctg aggacagatc tcagccaggc caggactgtc ggttcagagt taccagctg 240
cctaacggcc gggacttcca catgtctgtt gtgcgggcca gacggaacga ctctggcaca 300
tatctgtgcg gcgccatctc tctggctccc aaggctcaga tcaaagagtc tctgcgggcc 360
gagctgagag tgacagaaag acgagctgag gtgcccaccg ctcatccctc accttctcca 420
agacctgctg gaagagaggg ccctgagctg tctcctgatg atcctgctgg actgctggac 480
ctgagacagg gcatgtttgc tcagctgggtg gcccagaacg tgctgctgat tgatggccct 540
ctgtcctggt actctgatcc tggattggct ggcgtgtccc tgactggcgg cctgtcttac 600
aaagaggaca ccaaagaact ggtggtcgcc aaggccggcg tgtactacgt gttctttcag 660
ctggaactgc ggagagtggg ggctggcgaa ggatctggat ctgtgtctct ggccctgcat 720
ctgcagcctc tgagaagtgc tgcaggcgct gctgcactgg ctctgacagt tgatctgcct 780
cctgcctcct ccgaggccag aaactccgcc tttggcttcc aaggcagact gctgcatctg 840
tctgccggac agagactggg agtgcacctc catacagagg ccagagctag acacgcttgg 900
cagttgacac agggcgctac agtgctgggc ctgttttagag tgacacctga gatcccagcc 960

<210> 141
<211> 346
<212> PRT
<213> Artificial sequence

<220>
<223> DSP105 variant amino acid sequence

<400> 141

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Gly Ala Cys Pro
130 135 140

Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro
145 150 155 160

Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
165 170 175

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

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
195 200 205

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

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
225 230 235 240

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

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
260 265 270

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
275 280 285

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
290 295 300

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
305 310 315 320

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
325 330 335

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
340 345

<210> 142
<211> 1038
<212> DNA
<213> Artificial sequence

<220>
<223> DSP105 variant nucleic acid sequence

<400> 142

gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc	60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg	120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac	180
agatctcagc caggccagga ctgtcggttc agagttaccc agctgcctaa cggccgggac	240
ttccacatgt ctgttgtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc	300
atctctctgg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca	360
gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagacc tgctggccag	420
ggagcctgtc cttgggctgt gtctggcgct agagcatctc ctggctctgc tgcctctcct	480
agactgagag agggacctga gctgtctcct gatgatcctg ctggcctgct ggatctgaga	540
cagggcatgt ttgctcagct ggtggcccag aacgtgctgc tgattgatgg ccctctgtcc	600
tgggtactctg atcctggatt ggctggcgtg tccctgactg gcggcctgtc ttacaaagag	660
gacaccaaag aactggtggt ggccaaggcc ggcgtgtact acgtgttctt tcagctggaa	720
ctgcggagag tgggtggccgg cgaaggatct ggatctgtgt ctctggcact gcatctgcag	780
cccctgagat ctgctgcagg cgctgctgct ctggctctga cagttgatct gcctcctgcc	840
tcctccgagg ccagaaactc cgcctttggc ttccaaggca gactgctgca tctgtctgcc	900
ggccagagac tgggagtcca tctgcataca gaggctagag ccaggcacgc ctggcagttg	960
acacaaggtg ctacagtgct gggcctgttc agagtgaccc cagagattcc agccggcctg	1020
ccttctccaa gatccgag	1038

<210> 143
 <211> 350
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP105 variant amino acid sequence

<400> 143

Pro	Gly	Trp	Phe	Leu	Asp	Ser	Pro	Asp	Arg	Pro	Trp	Asn	Pro	Pro	Thr
1				5					10					15	

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Phe Gln Thr Leu Val Gly Ser Gly Ala Arg Ala Ser Pro Gly Ser
145 150 155 160

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
165 170 175

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
180 185 190

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
195 200 205

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
210 215 220

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
225 230 235 240

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

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
260 265 270

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
275 280 285

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
290 295 300

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
305 310 315 320

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
325 330 335

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
340 345 350

<210> 144
<211> 1092
<212> DNA
<213> Artificial sequence

<220>
<223> DSP105 variant nucleic acid sequence

<400> 144
cctggctggt ttctggacag ccccgacaga ccttgaacc ctctacatt cagccccgct 60
ctgctggtgg ttaccgaggg cgataatgcc accttcacct gtagcttcag caacaccagc 120

gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc 180
gcctttcctg aggatagatc tcagcccggc caggactgtc ggttcagagt tacacagctg 240
cccaacggcc gggacttcca catgtctgtc gtccggggcca gaagaaacga cagcggcaca 300
tatctgtgcg gcgccatttc tctggcccct aaggctcaga tcaaagagag cctgagagcc 360
gagctgagag tgacagaaaag acggggccgaa gtgcccacag ctcacccttc accttctcca 420
agacctgccg gccagtttca gacactcgtg ggagcttgct cttgggccgt ttctggcgct 480
agagcctctc ctggatctgg cgctagagcc tctcctggat ctgccgcttc tcccagactg 540
agagaggggac ctgagctgag ccctgatgat cctgctggac tgctggatct gagacagggc 600
atgtttgccc agctggtgcc ccagaatgtg ctgctgattg atggccctct gtcctggtac 660
agcgatcctg gacttgctgg cgttagcctg actggcggcc tgagctacaa agaggacacc 720
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 780
agagtgggtg ccggcgaagg atctggatct gtgtctctgg ctctgcatct gcagcctctg 840
agatctgctg ctggtgctgc tgctctggcc ctgacagttg atctgcctcc tgcctctagc 900
gaggccagaa actccgcctt tggcttccaa ggcagactgc tgcacctgag cgctggacag 960
agactgggag tccatctgca cacagaagcc agagctagac acgcctggca gctgacacaa 1020
ggcgctacag tgctgggcct gttcagagtg acccctgaga ttccagccgg cctgccatct 1080
cctagatctg ag 1092

<210> 145
<211> 365
<212> PRT
<213> Artificial sequence

<220>
<223> DSP105 variant amino acid sequence

<400> 145

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Phe Gln Thr Leu Val Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
165 170 175

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
180 185 190

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
195 200 205

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
210 215 220

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
225 230 235 240

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
245 250 255

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
260 265 270

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
275 280 285

Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
290 295 300

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
305 310 315 320

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
325 330 335

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
340 345 350

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
355 360 365

<210> 146
<211> 1095
<212> DNA
<213> Artificial sequence

<220>
<223> DSP105 variant nucleic acid sequence

<400> 146

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ctgctggtgg ttaccgaggg cgataatgcc accttcacct gtagcttcag caacaccagc	120
gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc	180
gcctttcctg aggatagatc tcagcccggc caggactgtc ggttcagagt tacacagctg	240
cccaacggcc gggacttcca catgtctgtc gtccgggcca gaagaaacga cagcggcaca	300
tatctgtgcg gcgccatttc tctggcccct aaggctcaga tcaaagagag cctgagagcc	360
gagctgagag tgacagaaag acgggcccga gtgcccacag ctcacccttc accttctcca	420
agacctgccg gccagtttca gacactcgtg ggaggaggag gatccggagg aggaggatcc	480
gcctgtcctt gggctgtgtc tggcgctaga gcatctcctg gctctgtgc ctctcctaga	540
ctgagagagg gacctgagct gtctcctgat gatcctgtg gcctgctgga tctgagacag	600
ggcatgtttg ctcagctggt ggcccagaac gtgctgtga ttgatggccc tctgtcctgg	660
tactctgatc ctggattggc tggcgtgtcc ctgactggcg gcctgtctta caaagaggac	720
accaaagaac tgggtggtggc caaggccggc gtgtactacg tggtctttca gctggaactg	780
cggagagtgg tggccggcga aggatctgga tctgtgtctc tggcactgca tctgcagccc	840
ctgagatctg ctgcaggcgc tgctgctctg gctctgacag ttgatctgcc tcctgcctcc	900
tccgaggcca gaaactccgc ctttggcttc caaggcagac tgctgcatct gtctgccggc	960
cagagactgg gagtccatct gcatacagag gctagagcca ggcacgcctg gcagttgaca	1020
caaggtgcta cagtgtctggg cctgttcaga gtgaccccag agattccagc cggcctgcct	1080
tctccaagat ccgag	1095

<210> 147

<211> 750

<212> PRT

<213> Artificial sequence

<220>

<223> DSP105 variant amino acid sequence

<400> 147

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser
20 25 30

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro
145 150 155 160

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
165 170 175

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
180 185 190

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly

195

200

205

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

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
 225 230 235 240

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
 245 250 255

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
 260 265 270

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
 275 280 285

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
 290 295 300

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
 305 310 315 320

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
 325 330 335

Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 340 345 350

Gly Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser
 355 360 365

Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala
 370 375 380

Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp
 385 390 395 400

Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser
405 410 415

Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr
420 425 430

Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly
435 440 445

Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala
450 455 460

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

Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His
485 490 495

Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg
500 505 510

Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu
515 520 525

Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser
530 535 540

Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
545 550 555 560

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
565 570 575

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
580 585 590

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
595 600 605

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
610 615 620

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
625 630 635 640

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
645 650 655

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
660 665 670

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
675 680 685

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
690 695 700

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
705 710 715 720

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
725 730 735

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
740 745 750

<210> 148
<211> 2250
<212> DNA
<213> Artificial sequence

<220>
<223> DSP105 variant nucleic acid sequence

<400> 148

gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc	60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg	120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac	180
agatctcagc caggccagga ctgtcggttc agagttaccc agctgcctaa cggccgggac	240
ttccacatgt ctgttggtgc ggccagacgg aacgactctg gcacatatct gtgcggcgcc	300
atctctcttg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca	360
gaaagacgag ctgagggtgcc caccgctcat ccctcacctt ctccaagacc tgctggccag	420
ggcggcgggc gctccggagg aggaggatct gccgccagcc ctaggctgcg cgagggaccc	480
gagctgagcc cagacgatcc cgccggcctg ctggacctga ggcagggaat gttcgcacag	540
ctgggtggccc agaacgtgct gctgatcgac ggccctctgt cctggtactc tgatccaggc	600
ctggccggcg tgtccctgac aggaggcctg tcttataagg aggataccaa ggagctggtg	660
gtggcaaagg caggcgtgta ctacgtgttc ttccagctgg agctgaggag agtggtggca	720
ggagagggca gcggctccgt gtctctggcc ctgcacctcc agcctctgcg gagcgccgcc	780
ggcgccgccg ccctggccct gaccgtggat ctgcctccag ccagctccga ggccaggaat	840
agcgcttctg gctttcaggg ccgcctgctg cacctgtccg ccggccagcg gctgggagtg	900
cacctgcaca cagaggccag agcccggcac gcatggcagc tgacacaggg agcaaccgtg	960
ctgggcctgt tccgcgtgac ccctgagatc ccagccggcc tgccaagccc ccggtccgag	1020
ggcggcgggc gctctggcgg aggaggcagc ggaggcggcg gctctgccgc cagccccagg	1080
ctgcgcgagg gacccgagct gtccccagac gatcctgccg gcctgctgga cctgcgccag	1140
ggaatgtttg cccagctggt ggctcaaaac gtgctgttaa tcgacggccc tctgagctgg	1200
tactctgatc ctggcctggc cggcgtgagc ctgaccggcg gcctgtccta caaagaggat	1260
actaaagagc tgggtggtcgc caaagccggc gtgtactacg tgttcttcca actggagctg	1320
aggagggctc tcgccggcga aggcagcggc tccgtgtctc tggccctgca cctccagccg	1380
ctgaggagcg ccgccggcgc cgccgccctg gccctgacgg tggacctgcc acctgcctct	1440

agcgaggcaa gaaattctgc cttcggcttc cagggcaggc tgctgcacct gagcgccggc	1500
cagcgcttgg gcggtccacct gcataccgaa gccagagccc ggcatgcctg gcagctgacc	1560
cagggcgcca ccgtgctggg cctgttcaga gtgaccccag agatccccgc cggcctgcct	1620
agcccaaggt ccgaaggcgg cggcggctcc ggcgggcggag gctctggagg agggggctct	1680
gccgccagcc caaggctgcg cgagggaccc gagctgtcgc ctgacgatcc agccggcctg	1740
ctggacctgc gtcagggcat gttcgcccag ctggtggctc agaacgtgct gttaatcgac	1800
ggcccactgt cttggtattc tgatcccggc ctggccggcg tgtctctgac aggaggcctg	1860
agctacaaag aggatacaaa agagctggtg gtcgctaaag ctggcgtgta ctacgtgttc	1920
ttccaactgg agctgcgcag ggtcgtcgcc ggcgagggca gcggctccgt gtctctggcc	1980
ctgcacctcc agccattacg gagcgccgcc ggcgccgccg ccctggccct gactgtggac	2040
ctgccaccag cctcctctga ggcacggaac agcgcttcg gcttccaagg cagactgctg	2100
cacctgtctg ccggccagag gctgggcgtc cacctgcaca ccgaagccag agcccggcac	2160
gcctggcagc tgactcaggg cgctaccgtg ctgggcctgt tccgcgtaac cccagagatc	2220
cctgccggcc tgcccagccc tcggtccgag	2250

<210> 149

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> linker amino acid sequence

<220>

<221> REPEAT

<222> (1)..(5)

<223> may repeat 1-4 times

<400> 149

Gly Gly Gly Gly Ser

1 5

<210> 150
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> linker amino acid sequence

<400> 150

Gly Gly Gly Gly Ser
1 5

<210> 151
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> linker amino acid sequence

<400> 151

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 152
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> linker amino acid sequence

<220>
<221> REPEAT
<222> (1)..(5)
<223> may repeat 1-3 times

<400> 152

Glu Ala Ala Ala Lys
1 5

<210> 153

<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> linker amino acid sequence

<220>
<221> REPEAT
<222> (2)..(6)
<223> EAAAK

<220>
<221> REPEAT
<222> (2)..(6)
<223> repeat 2-5 times

<400> 153

Ala Glu Ala Ala Ala Lys Ala
1 5

<210> 154
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> linker amino acid sequence

<400> 154

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
1 5 10

<210> 155
<211> 46
<212> PRT
<213> Artificial sequence

<220>
<223> linker amino acid sequence

<400> 155

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys

1	5	10	15
Glu	Ala	Ala	Ala
	Lys	Ala	Leu
		Glu	Ala
		Glu	Ala
		Ala	Ala
		Lys	Glu
			Ala
	20	25	30

Ala	Ala	Lys	Glu	Ala	Ala	Ala	Lys	Glu	Ala	Ala	Ala	Lys	Ala
		35					40					45	

<210> 156
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> linker amino acid sequence

<400> 156

Pro	Ala	Pro	Ala	Pro
1			5	

<210> 157
 <211> 18
 <212> PRT
 <213> Artificial sequence

<220>
 <223> linker amino acid sequence

<400> 157

Lys	Glu	Ser	Gly	Ser	Val	Ser	Ser	Glu	Gln	Leu	Ala	Gln	Phe	Arg	Ser
1				5					10					15	

Leu Asp

<210> 158
 <211> 14
 <212> PRT
 <213> Artificial sequence

<220>

<223> linker amino acid sequence

<400> 158

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr
1 5 10

<210> 159

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> linker amino acid sequence

<400> 159

Gly Ser Ala Gly Ser Ala Ala Gly Ser Gly Glu Phe
1 5 10

<210> 160

<211> 229

<212> PRT

<213> Artificial sequence

<220>

<223> hIgG4 Fc linker

<400> 160

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser

65		70		75		80
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu						
		85		90		95
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser						
		100		105		110
Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro						
		115		120		125
Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln						
		130		135		140
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala						
145		150		155		160
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr						
		165		170		175
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu						
		180		185		190
Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser						
		195		200		205
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser						
		210		215		220
Leu Ser Leu Gly Lys						
225						

<210> 161

<400> 161
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<210> 162

<400> 162
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<210> 163
<211> 232
<212> PRT
<213> Artificial sequence

<220>
<223> hIgG4 Fc linker

<400> 163

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 164

<400> 164
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<210> 165

<400> 165
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<210> 166

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Linker amino acid sequence

<400> 166

Gly Leu Pro Ser Pro Arg Ser Glu
 1 5

<210> 167
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Linker amino acid sequence

<400> 167

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
1 5 10 15

Ala Ser Pro Arg Leu Arg Glu
20

<210> 168
<211> 331
<212> PRT
<213> Artificial sequence

<220>
<223> DSP105_V32 (4-1BBL-PD1 FUSION) amino acid sequence

<400> 168

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
1 5 10 15

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
20 25 30

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
35 40 45

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
50 55 60

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

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser

85

90

95

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
 100 105 110

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
 115 120 125

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
 130 135 140

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
 145 150 155 160

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
 165 170 175

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Asp
 180 185 190

Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu
 195 200 205

Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn
 210 215 220

Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn
 225 230 235 240

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

Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe
 260 265 270

His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu
 275 280 285

Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu
 290 295 300

Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala
 305 310 315 320

His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln
 325 330

<210> 169
 <211> 996
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DSP105_V32 (4-1BBL-PD1 FUSION) nucleic acid sequence

<400> 169
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 ctgctggatc tgcggcaggg catgtttgct cagttgggtgg cccagaacgt gctgctgac 120
 gatggccctc tgtcctggta ctctgatcca ggattggctg gcgtgtccct gactggcggc 180
 ctgtcttaca aagaggacac caaagaactg gtggtggcca aggccggcgt gtactacgtg 240
 ttctttcagc tggaactgcg gagagtgggtg gctggcgaag gatctggatc tgtgtctctg 300
 gccctgcatc tgcagcctct gagaagtgct gcaggcgctg ctgcactggc tctgacagtt 360
 gatctgcctc ctgcctcctc cgaggccaga aactccgcct ttggcttcca aggcagactg 420
 ctgcacctgt ccgctggaca gagactggga gtccatctgc acacagaggc cagagctaga 480
 cacgcttggc agttgacaca gggcgctaca gtgctgggcc tgttttagagt gaccctgag 540
 attccagccg gcctgccatc tcctagatct gagggcgact cccctgacag accttggaac 600
 cctccaacct tctctcccgc tctgctgggtg gttaccgagg gcgacaatgc caccttcacc 660
 tggttccttca gcaacacctc cgagtccttc gtgctgaact ggtacagaat gtcccctagc 720
 aaccagaccg acaagctggc cgcccttcct gaggacagat ctcagccagg ccaggactgc 780

cggttcagag ttaccagct gcctaacggc cgggacttcc acatgtctgt tgtgcgggcc	840
agacggaacg actctggcac atatctgtgc ggcgccatct ctctggctcc caaggctcag	900
atcaaagagt ctctgcgggc cgagctgaga gtgacagaaa gacgagctga ggtgcccacc	960
gctcatccct caccttctcc aagacctgcc ggccag	996