

SEQUENCE LISTING

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

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

 <130> 77794

 <150> US 62/696,362
 <151> 2018-07-11

 <160> 99

 <170> PatentIn version 3.5

 <210> 1
 <211> 555
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> ORIGINAL SIRPa-4-1BBL with C-terminal His Tag

<400> 1

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
 115 120 125

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

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

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
 165 170 175

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
 210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr Gly Ala Cys Pro Trp Ala Val Ser Gly
 340 345 350

Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly
 355 360 365

Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln
 370 375 380

Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly
 385 390 395 400

Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr
 405 410 415

Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys
 420 425 430

Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val
 435 440 445

Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro
 450 455 460

Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu
 465 470 475 480

Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly
 485 490 495

Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His
 500 505 510

Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr
 515 520 525

Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro
 530 535 540

Ser Pro Arg Ser Glu His His His His His His
 545 550 555

<210> 2
 <211> 343
 <212> PRT
 <213> Artificial sequence

<220>
 <223> ORIGINAL SIRPa DOMAIN

<400> 2

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
 115 120 125

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

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

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
 165 170 175

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
 210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr
 340

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

<220>
 <223> ORIGINAL 4-1BBL 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> 19
 <212> PRT
 <213> Artificial sequence

<220>
 <223> SIGNAL PEPTIDE

<400> 4

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

Val His Ser

<210> 5
 <211> 549
 <212> PRT
 <213> Artificial sequence

<220>

<223> ORIGINAL SIRPa-4-1BBL without His Tag

<400> 5

Glu	Glu	Glu	Leu	Gln	Val	Ile	Gln	Pro	Asp	Lys	Ser	Val	Leu	Val	Ala
1				5					10				15		

Ala	Gly	Glu	Thr	Ala	Thr	Leu	Arg	Cys	Thr	Ala	Thr	Ser	Leu	Ile	Pro
			20					25					30		

Val	Gly	Pro	Ile	Gln	Trp	Phe	Arg	Gly	Ala	Gly	Pro	Gly	Arg	Glu	Leu
		35					40					45			

Ile	Tyr	Asn	Gln	Lys	Glu	Gly	His	Phe	Pro	Arg	Val	Thr	Thr	Val	Ser
	50					55					60				

Asp	Leu	Thr	Lys	Arg	Asn	Asn	Met	Asp	Phe	Ser	Ile	Arg	Ile	Gly	Asn
65					70					75					80

Ile	Thr	Pro	Ala	Asp	Ala	Gly	Thr	Tyr	Tyr	Cys	Val	Lys	Phe	Arg	Lys
				85					90					95	

Gly	Ser	Pro	Asp	Asp	Val	Glu	Phe	Lys	Ser	Gly	Ala	Gly	Thr	Glu	Leu
			100					105					110		

Ser	Val	Arg	Ala	Lys	Pro	Ser	Ala	Pro	Val	Val	Ser	Gly	Pro	Ala	Ala
		115					120					125			

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

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

Leu	Ser	Asp	Phe	Gln	Thr	Asn	Val	Asp	Pro	Val	Gly	Glu	Ser	Val	Ser
				165					170					175	

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
 210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr Gly Ala Cys Pro Trp Ala Val Ser Gly
 340 345 350

Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly
 355 360 365

Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln
 370 375 380

Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly
 385 390 395 400

Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr
 405 410 415

Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys
 420 425 430

Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val
 435 440 445

Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro
 450 455 460

Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu
 465 470 475 480

Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly
 485 490 495

Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His
 500 505 510

Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr
 515 520 525

Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro
 530 535 540

Ser Pro Arg Ser Glu
 545

<210> 6
 <211> 14
 <212> PRT
 <213> Artificial sequence

<220>

<223> partial sequence of the n-terminal of 4-1BBL domain

<400> 6

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

<210> 7

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> partial sequence of the n-terminal of 4-1BBL domain

<400> 7

Ala	Cys	Pro	Trp	Ala	Val
1				5	

<210> 8

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> partial sequence of the C-terminal of SIRP-alpha

<400> 8

Thr	Glu	Leu	Ser	Val	Arg	Ala	Lys	Pro	Ser
1				5				10	

<210> 9

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> partial sequence of SIRP-alpha

<400> 9

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

Thr Gly Ser Asn Glu Arg Asn Ile Tyr
 20 25

<210> 10
 <211> 30
 <212> PRT
 <213> Artificial sequence

<220>
 <223> partial sequence of the 4-1BB-L

<400> 10

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> 11
 <211> 543
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP107_var1 without His Tag

<400> 11

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
115 120 125

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

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

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
165 170 175

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr Gly Ser Gly Ala Arg Ala Ser Pro Gly
 340 345 350

Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
 355 360 365

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
 370 375 380

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
 385 390 395 400

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
 405 410 415

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
 420 425 430

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
 435 440 445

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
 450 455 460

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

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
 485 490 495

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
 500 505 510

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
 515 520 525

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 530 535 540

<210> 12
 <211> 549
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP107_var1 with His Tag

<400> 12

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
115 120 125

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

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

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
165 170 175

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr Gly Ser Gly Ala Arg Ala Ser Pro Gly
 340 345 350

Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
 355 360 365

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
 370 375 380

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
 385 390 395 400

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
 405 410 415

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
 420 425 430

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
 435 440 445

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
 450 455 460

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

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
 485 490 495

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
 500 505 510

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
 515 520 525

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu His
 530 535 540

His His His His His
 545

<210> 13
 <211> 535
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP107_var2 without His Tag

<400> 13

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
 115 120 125

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

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

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
 165 170 175

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
 210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr Gly Ser Ala Ala Ser Pro Arg Leu Arg
 340 345 350

Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu
 355 360 365

Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile
 370 375 380

Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser
 385 390 395 400

Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val
 405 410 415

Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg
 420 425 430

Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu
 435 440 445

Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val
 450 455 460

Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe
 465 470 475 480

Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His
485 490 495

Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly
500 505 510

Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly
515 520 525

Leu Pro Ser Pro Arg Ser Glu
530 535

$\langle 210 \rangle$	14
$\langle 211 \rangle$	541
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial sequence

<220>
<223> DSP107_var2 with His Tag

<400> 14

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
20 25 30

Val	Gly	Pro	Ile	Gln	Trp	Phe	Arg	Gly	Ala	Gly	Pro	Gly	Arg	Glu	Leu
		35					40					45			

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
 115 120 125

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

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

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
 165 170 175

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
 210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr Gly Ser Ala Ala Ser Pro Arg Leu Arg
 340 345 350

Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu
 355 360 365

Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile
 370 375 380

Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser
 385 390 395 400

Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val
 405 410 415

Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg
 420 425 430

Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu
 435 440 445

Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val
 450 455 460

Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe
 465 470 475 480

Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His
 485 490 495

Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly
 500 505 510

Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly
 515 520 525

Leu Pro Ser Pro Arg Ser Glu His His His His His His
 530 535 540

<210> 15
 <211> 322
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP107_var3 without His Tag

<400> 15

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Gly Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala
 115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

Ser Glu

<210> 16
 <211> 316
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP107_var3.1 without His Tag

<400> 16

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Gly Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala
 115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

<210> 17

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> DSP107_var3.1 with His Tag

<400> 17

Glu	Glu	Glu	Leu	Gln	Val	Ile	Gln	Pro	Asp	Lys	Ser	Val	Leu	Val	Ala
1				5					10					15	

Ala	Gly	Glu	Thr	Ala	Thr	Leu	Arg	Cys	Thr	Ala	Thr	Ser	Leu	Ile	Pro
			20					25					30		

Val	Gly	Pro	Ile	Gln	Trp	Phe	Arg	Gly	Ala	Gly	Pro	Gly	Arg	Glu	Leu
		35					40					45			

Ile	Tyr	Asn	Gln	Lys	Glu	Gly	His	Phe	Pro	Arg	Val	Thr	Thr	Val	Ser
	50					55					60				

Asp	Leu	Thr	Lys	Arg	Asn	Asn	Met	Asp	Phe	Ser	Ile	Arg	Ile	Gly	Asn
65					70					75					80

Ile	Thr	Pro	Ala	Asp	Ala	Gly	Thr	Tyr	Tyr	Cys	Val	Lys	Phe	Arg	Lys
				85					90					95	

Gly	Ser	Pro	Asp	Asp	Val	Glu	Phe	Lys	Ser	Gly	Ala	Gly	Thr	Glu	Leu
			100					105					110		

Ser	Val	Arg	Ala	Gly	Ser	Gly	Ala	Arg	Ala	Ser	Pro	Gly	Ser	Ala	Ala
		115					120					125			

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

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

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

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

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

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

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

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

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

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

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

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

His His

<210> 18
 <211> 543
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP107_Var1Mut without His Tag

<400> 18

Glu Glu Glu Ile Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ile Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Val Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Ile Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
 115 120 125

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

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

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
 165 170 175

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
 210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr Gly Ser Gly Ala Arg Ala Ser Pro Gly
 340 345 350

Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
 355 360 365

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
 370 375 380

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
 385 390 395 400

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
 405 410 415

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
 420 425 430

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
 435 440 445

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
 450 455 460

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

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
 485 490 495

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
 500 505 510

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
 515 520 525

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 530 535 540

<210> 19
 <211> 535
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP107_Var2Mut without His Tag

<400> 19

Glu Glu Glu Ile Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ile Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Val Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Ile Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
 115 120 125

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

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

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
 165 170 175

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
 210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr Gly Ser Ala Ala Ser Pro Arg Leu Arg
 340 345 350

Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu
 355 360 365

Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile
 370 375 380

Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser
 385 390 395 400

Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val
 405 410 415

Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg
 420 425 430

Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu
 435 440 445

Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val
 450 455 460

Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe
 465 470 475 480

Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His
 485 490 495

Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly
 500 505 510

Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly
 515 520 525

Leu Pro Ser Pro Arg Ser Glu
 530 535

<210> 20

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> DSP107_Var3Mut without His Tag

<400> 20

Glu Glu Glu Ile Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ile Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Val Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Ile Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Gly Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala
 115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

Ser Glu

$\langle 210 \rangle$	21
$\langle 211 \rangle$	315
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial sequence

<220>
<223> DSP170_Var3.1Mut without His tag

<400> 21

Glu Glu Glu Ile Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ile Thr Ser Leu Ile Pro
20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Val Leu
35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Ile Lys Phe Arg Lys
85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
100 105 110

Ser Val Arg Ala Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser
115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

<210> 22

<211> 199

<212> PRT

<213> Artificial sequence

<220>

<223> 199 amino acid sequence of 4-1BBL segment

<400> 22

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> 23
 <211> 191
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 191 amino acid sequence of 4-1BBL segment

<400> 23

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> 24

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> 116 amino acid sequence of SIRPa segment

<400> 24

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala
 115

<210> 25

<211> 343

<212> PRT

<213> Artificial sequence

<220>

<223> 343 amino acids sequence of SIRPa with 4 point mutations

<400> 25

Glu Glu Glu Ile Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ile Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Val Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Ile Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
 115 120 125

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

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

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
 165 170 175

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
 210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr
 340

<210> 26

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> 116 amino acids sequence of SIRPa with 4 point mutations

<400> 26

Glu Glu Glu Ile Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ile Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Val Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Ile Lys Phe Arg Lys
85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
100 105 110

Ser Val Arg Ala
115

<210> 27

<211> 197

<212> PRT

<213> Artificial sequence

<220>

<223> 197 amino acid sequence of 4-1BBL segment

<400> 27

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

$\langle 210 \rangle$	28
$\langle 211 \rangle$	185
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial sequence

<220>
<223> 185 amino acid sequence of 4-1BBL segment

<400> 28

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> 29

<211> 504

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence of full length SIRP

<400> 29

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
 1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
 20 25 30

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
 50 55 60

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
 65 70 75 80

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

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
 100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 115 120 125

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

Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
 145 150 155 160

Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
 165 170 175

Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
 180 185 190

Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
 195 200 205

Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
 210 215 220

Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
 225 230 235 240

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

Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
 260 265 270

Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
 275 280 285

Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
 290 295 300

Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
 305 310 315 320

Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
 325 330 335

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

Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
 355 360 365

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

Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys
 385 390 395 400

Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
 405 410 415

Ala Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu
 420 425 430

Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn
 435 440 445

Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser
 450 455 460

Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg
 465 470 475 480

Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr
 485 490 495

Ala Ser Val Gln Val Pro Arg Lys
 500

<210> 30

<211> 1512

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence of full length SIRP

<400> 30

atggagcccc cccgccccggc ccccggccgc ctccggccgc tgctctgcct gctgctcgcc 60

gcgtcctgcg cctggtcagg agtggcgggt gaggaggagc tgcaggatgat tcagcctgac 120

aagtccgtat cagttgcagc tggagagtcg gccattctgc actgcactgt gacctccctg 180

atccctgtgg ggcccatcca gtggttcaga ggagctggac cagcccggga attaacttac 240

aatcaaaaag aaggccactt cccccgggta acaactgttt cagagtccac aaagagagaa 300

aacatggact tttccatcag catcagtaac atcacccag cagatgccgg cacctactac 360

tgtgtgaagt tccggaaagg gagccctgac acggagttaa agtctggagc aggcactgag 420

ctgtctgtgc gtgcaaacc ctctgcccc gtggtatcgg gccctgcggc gagggccaca 480

```

cctcagcaca cagtgaagctt cacctgcgag tcccacggct tctcaccag agacatcacc      540
ctgaaatggt tcaaaaatgg gaatgagctc tcagacttcc agaccaacgt ggaccccgta      600
ggagagagcg tgtcctacag catccacagc acagccaagg tgggtgctgac ccgcgaggac      660
gttcactctc aagtcactctg cgaggtggcc cacgtcacct tgcaggggga ccctcttcgt      720
gggactgcca acttgtctga gaccatccga gttccacca ccttgagggt tactcaacag      780
cccgtgaggg cagagaacca ggtgaatgtc acctgccagg tgaggaagtt ctacccccag      840
agactacagc tgacctggtt ggagaatgga aacgtgtccc ggacagaaac ggcctcaacc      900
gttacagaga acaaggatgg tacctacaac tggatgagct ggctcctggt gaatgtatct      960
gcccacaggg atgatgtgaa gctcacctgc caggtggagc atgacgggca gccagcggtc     1020
agcaaaagcc atgacctgaa ggtctcagcc caccgaagg agcagggctc aaataccgcc     1080
gctgagaaca ctggatctaa tgaacggaac atctatattg tgggtgggtgt ggtgtgcacc     1140
ttgctggtgg ccctactgat ggcgccctc tacctcgtcc gaatcagaca gaagaaagcc     1200
cagggctcca cttcttctac aaggttgcac gagcccgaga agaatgccag agaaataaca     1260
caggacacaa atgatatcac atatgcagac ctgaacctgc ccaaggggaa gaagcctgct     1320
ccccaggctg cggagcccaa caaccacacg gagtatgcca gcattcagac cagcccgag      1380
cccgcgtcgg aggacaccct cacctatgct gacctggaca tggtcacact caaccggacc     1440
cccaagcagc cggcccccaa gcctgagccg tccttctcag agtacgccag cgtccaggtc     1500
ccgaggaagt ga                                                              1512

```

<210> 31

<211> 1029

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 2

<400> 31

```

gaggaggagc tgcaggatgat tcagcctgac aagtccttat cagttgcagc tggagagtcg      60

```

```

gccattctgc actgcactgt gacctccctg atccctgtgg ggcccatcca gtggttcaga      120

```

```

ggagctggac cagccccggga attaatctac aatcaaaaag aaggccactt cccccgggta      180
acaactgttt cagagtccac aaagagagaa aacatggact tttccatcag catcagtaac      240
atcaccccag cagatgccgg cacctactac tgtgtgaagt tccggaaagg gagccctgac      300
acggagttta agtctggagc aggcactgag ctgtctgtgc gtgccaaacc ctctgcccc      360
gtggtatcgg gccctgcggc gagggccaca cctcagcaca cagtgaagctt cacctgcgag      420
tcccacggct tctcacccag agacatcacc ctgaaatgggt tcaaaaatgg gaatgagctc      480
tcagacttcc agaccaacgt ggacccccgta ggagagagcg tgtcctacag catccacagc      540
acagccaagg tgggtgctgac ccgcgaggac gttcactctc aagtcactctg cgagggtggcc      600
cacgtcacct tgcagggggga ccctcttcgt gggactgccca acttgtctga gaccatccga      660
gttccaccca ccttggaggt tactcaacag cccgtgaggg cagagaacca ggtgaatgtc      720
acctgccagg tgaggaagtt ctacccccag agactacagc tgacctgggtt ggagaatgga      780
aacgtgtccc ggacagaaac ggcctcaacc gttacagaga acaaggatgg tacctacaac      840
tggatgagct ggctcctgggt gaatgtatct gcccacaggg atgatgtgaa gctcacctgc      900
cagggtggagc atgacgggca gccagcggtc agcaaaaagcc atgacctgaa ggtctcagcc      960
cacccgaagg agcagggctc aaataccgcc gctgagaaca ctggatctaa tgaacggaac     1020
atctatatatt                                                                1029

```

```

<210> 32
<211> 227
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> THE DELETED PART OF SEQ ID NO: 2 FOR GENERATION OF THE 116 AA
      VARIANT

```

```

<400> 32

```

```

Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr Pro
1           5           10          15

```

```

Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro Arg

```

20

25

30

Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp Phe
 35 40 45

Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile His
 50 55 60

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

Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg Gly
 85 90 95

Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu Val
 100 105 110

Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys Gln
 115 120 125

Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu Asn
 130 135 140

Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn Lys
 145 150 155 160

Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser Ala
 165 170 175

His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly Gln
 180 185 190

Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro Lys
 195 200 205

Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu Arg
 210 215 220

Asn Ile Tyr
225

<210> 33
<211> 348
<212> DNA
<213> Artificial sequence

<220>
<223> nucleic acid sequence encoding SEQ ID NO: 24

<400> 33
gaagaggaac tgcaagtgat ccagcctgac aagtccgtgc tggtaggctgc tggcgaaacc 60
gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggtttaga 120
ggcgctggac ctggcagaga gctgatctac aaccagaaag agggccactt tcctagagtg 180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac 240
atcacccctg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac 300
gacgtcgagt ttaaataccgg cgctggcacc gaactgtccg tgcgagct 348

<210> 34
<211> 348
<212> DNA
<213> Artificial sequence

<220>
<223> nucleic acid sequence encoding SEQ ID NO: 26

<400> 34
gaagaggaaa tccaagtgat ccagcctgac aagtccgtgc tggtaggctgc tggcgaaacc 60
gccacactga gatgtaccat cacctctctg atccctgtgg gccctatcca gtggtttaga 120
ggcgctggac ctggcagagt gctgatctac aaccagaaag agggccactt tcctagagtg 180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac 240
atcacccctg ctgatgccgg cacctactac tgcataaagt tccggaaggg ctcccctgac 300
gacgtcgagt ttaaataccgg cgctggcacc gaactgtccg tgcgagct 348

<210> 35

<211> 1029
 <212> DNA
 <213> Artificial sequence

<220>
 <223> nucleic acid sequence encoding SEQ ID NO: 25

<400> 35
 gaagaggaaa tccaagtgat ccagcctgac aagtccgtgc tggaggctgc tggcgaacc 60
 gccacactga gatgtaccat cacctctctg atccctgtgg gccctatcca gtggtttaga 120
 ggcgctggac ctggcagagt gctgatctac aaccagaaag agggccactt tcctagagtg 180
 accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac 240
 atcacccctg ctgatgccgg cacctactac tgcatacaagt tccggaaggg ctcccctgac 300
 gacgtcgagt ttaaataccgg cgctggcacc gaactgtccg tgcgagctaa accttctgct 360
 cccgtgggtgt ctggccctgc cgctagagct acacctcagc acaccgtgtc ttttacctgc 420
 gagtcccacg gcttcagccc tagagacatc accctgaagt ggttcaagaa cggcaacgag 480
 ctgtccgact tccagaccaa cgtggaccct gtgggagagt ccgtgtccta ctccatccac 540
 tctaccgcca aggtgggtgct gacccgagag gacgtgcaca gccaagtgat ctgtgaagtg 600
 gccacgtga ccctccaggg cgatcctttg agaggcaccg ccaacctgtc cgagacaatc 660
 agagtgcctc ctacactgga agtgaccag cagcctgtgc gggccgagaa tcaagtgaac 720
 gtgacctgcc aagtgcggaa gttctaccct cagagactgc agctgacctg gctggaaaac 780
 ggcaatgtgt ccagaaccga gacagcctcc accgtgaccg agaacaagga tggcacctac 840
 aattggatgt cctggctgct cgtgaacgtg tccgctcaca gagatgacgt gaagctgaca 900
 tgccagggtg aacacgatgg ccagcctgcc gtgtctaagt cccacgacct gaaagtgtct 960
 gctcacccca aagagcaggg ctccaatacc gccgctgaga acaccggctc caacgagaga 1020
 aacatctac 1029

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

<220>

<223> amino acid sequence of full length 4-1BBL

<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 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> nucleic acid sequence of full length 4-1BBL

<400> 37
 atggaatacg cctctgacgc ttacttgac cccgaagccc cgtggcctcc cgcgccccgc 60
 gctcgcgcct gccgcgtact gccttgggcc ctggtcgcgg ggctgctgct gctgctgctg 120
 ctcgctgccg cctgcgccgt cttcctcgcc tgccccctggg ccgtgtccgg ggctcgcgcc 180
 tcgcccggct ccgcggccag cccgagactc cgcgagggtc ccgagctttc gcccgcacgat 240
 cccgccggcc tcttggacct gcggcagggc atgtttgcgc agctggtggc ccaaaatggt 300
 ctgctgatcg atgggccccct gagctggtag 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 gaggctcgga actcggcctt cggtttccag 600
 ggccgcttgc tgcacctgag tgccggccag cgcctgggag tccatcttca cactgaggcc 660

agggcacgcc atgcctggca gcttaccacag ggcgccacag tcttgggact cttccgggtg 720
 acccccgaaa tcccagccgg actcccttca ccgaggtcgg aataa 765

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

<220>
 <223> nucleic acid sequence encoding SEQ ID NO: 3

<400> 38
 gcctgccccct gggccgtgtc cggggctcgc gcctcgcccg gctccgcggc cagccccgaga 60
 ctccgcgagg gtcccagact ttgccccgac gatccccgcg gcctcttgga cctgcggcag 120
 ggcatgtttg cgcagctggg gggccaaaat gttctgctga tcgatgggcc cctgagctgg 180
 tacagtgacc caggcctggc aggcgtgtcc ctgacggggg gcctgagcta caaagaggac 240
 acgaaggagc tgggtggtggc caaggctgga gtctactatg tcttctttca actagagctg 300
 cggcgctgtg tggccggcga gggctcaggc tccgtttcac ttgcgctgca cctgcagcca 360
 ctgcgctctg ctgctggggc cgccgccctg gctttgaccg tggacctgcc acccgccctc 420
 tccgaggctc ggaactcggc cttcggtttc cagggccgct tgctgcacct gaggccggc 480
 cagcgccctg gcgtccatct tcacactgag gccagggcac gccatgcctg gcagcttacc 540
 cagggcgcca cagtcttggg actcttccgg gtgacccccg aaatcccagc cggactccct 600
 tcaccgaggt cgga 615

<210> 39
 <211> 624
 <212> DNA
 <213> Artificial sequence

<220>
 <223> nucleic acid sequence encoding SEQ ID NO: 22

<400> 39
 atctacggcg cctgtccttg ggctgtgtct ggcgctagag catctcctgg ctctgctgcc 60
 tctcctagac tgagagaggg acctgagctg tctcctgatg atcctgctgg cctgctggat 120

ctgagacagg gcatgtttgc tcagctgggtg gcccagaacg tgctgctgat tgatggccct 180
 ctgtcctgggt actctgatcc tggattggct ggcgtgtccc tgactggcgg cctgtcttac 240
 aaagaggaca ccaaagaact ggtgggtggcc aaggccggcg tgtactacgt gttctttcag 300
 ctggaactgc ggagagtgggt ggccggcgaa ggatctggat ctgtgtctctt ggcaactgcat 360
 ctgcagcccc tgagatctgc tgcaggcgct gctgctctgg ctctgacagt tgatctgcct 420
 cctgcctcct ccgaggccag aaactccgcc tttggcttcc aaggcagact gctgcatctg 480
 tctgccggcc agagactggg agtccatctg catacagagg ctagagccag gcacgcctgg 540
 cagttgacac aagggtgctac agtgctgggc ctgttcagag tgaccccaga gattccagcc 600
 ggccctgcctt ctccaagatc cgag 624

<210> 40
 <211> 573
 <212> DNA
 <213> Artificial sequence

<220>
 <223> nucleic acid sequence encoding SEQ ID NO: 23

<400> 40
 tctgctgcct ctcttagact gagagagggga cctgagctgt ctctgatga tcctgctggc 60
 ctgctggatc tgagacaggg catgtttgct cagctgggtg cccagaacgt gctgctgatt 120
 gatggccctc tgtcctggta ctctgacatc ggattggctg gcgtgtccct gactggcggc 180
 ctgtcttaca aagaggacac caaagaactg gtgggtggcca aggccggcgt gtactacgtg 240
 ttctttcagc tggaactgcg gagagtgggtg gccggcgaag gatctggatc tgtgtctctg 300
 gcactgcatc tgcagccccct gagatctgct gcaggcgctg ctgctctggc tctgacagtt 360
 gatctgcctc ctgcctcctc cgaggccaga aactccgcct ttggcttcca aggcagactg 420
 ctgcatctgt ctgccggcca gagactggga gtccatctgc atacagaggc tagagccagg 480
 cacgcctggc agttgacaca aggtgctaca gtgctgggcc tggttcagagt gaccccagag 540
 attccagccg gcctgccttc tccaagatcc gag 573

<210> 41

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

<220>
 <223> nucleic acid sequence encoding SEQ ID NO: 27

<400> 41
 gctagagcat ctcctggctc tgctgcctct cctagactga gagagggacc tgagctgtct 60
 cctgatgata ctgctggcct gctggatctg agacagggca tgtttgctca gctgggtggcc 120
 cagaacgtgc tgctgattga tggccctctg tcctgggtact ctgatcctgg attggctggc 180
 gtgtccctga ctggcggcct gtcttacaaa gaggacacca aagaactggg ggtggccaag 240
 gccggcgtgt actacgtgtt ctttcagctg gaactgcgga gactgggtggc cggcgaagga 300
 tctggatctg tgtctctggc actgcatctg cagcccctga gatctgctgc aggcgctgct 360
 gctctggctc tgacagttga tctgcctcct gcctcctccg aggccagaaa ctccgccttt 420
 ggcttccaag gcagactgct gcatctgtct gccggccaga gactgggagt ccatctgcat 480
 acagaggcta gagccaggca cgcctggcag ttgacacaag gtgctacagt gctgggcctg 540
 ttcagagtga cccagagat tccagccggc ctgccttctc caagatccga g 591

<210> 42
 <211> 555
 <212> DNA
 <213> Artificial sequence

<220>
 <223> nucleic acid sequence encoding SEQ ID NO: 28

<400> 42
 ctgagagagg gacctgagct gtctcctgat gatcctgctg gcctgctgga tctgagacag 60
 ggcatgtttg ctcagctggg gggccagaac gtgctgctga ttgatggccc tctgtcctgg 120
 tactctgata ctggattggc tggcgtgtcc ctgactggcg gcctgtctta caaagaggac 180
 accaaagaac tgggtgtggc caaggccggc gtgtactacg tgttctttca gctggaactg 240
 cggagagtgg tggccggcga aggatctgga tctgtgtctc tggcactgca tctgcagccc 300
 ctgagatctg ctgcaggcgc tgctgctctg gctctgacag ttgatctgcc tcctgcctcc 360

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tccgaggcca gaaactccgc ctttggcttc caaggcagac tgctgcatct gtctgccggc      420
cagagactgg gagtccatct gcatacagag gctagagcca ggcacgcctg gcagttgaca      480
caaggtgcta cagtgtctggg cctgttcaga gtgaccccag agattccagc cggcctgcct      540
tctccaagat ccgag                                                                555

```

```

<210> 43
<211> 574
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> ORIGINAL SIRPa-4-1BBL with signal peptide and C-term His Tag

```

```

<400> 43

```

```

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

```

```

Val His Ser Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val
          20          25          30

```

```

Leu Val Ala Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser
          35          40          45

```

```

Leu Ile Pro Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly
          50          55          60

```

```

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

```

```

Thr Val Ser Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg
          85          90          95

```

```

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

```

```

Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly
          115         120         125

```

Thr Glu Leu Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly
 130 135 140

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

Ser His Gly Phe Ser Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn
 165 170 175

Gly Asn Glu Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu
 180 185 190

Ser Val Ser Tyr Ser Ile His Ser Thr Ala Lys Val Val Leu Thr Arg
 195 200 205

Glu Asp Val His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu
 210 215 220

Gln Gly Asp Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg
 225 230 235 240

Val Pro Pro Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn
 245 250 255

Gln Val Asn Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu
 260 265 270

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

Ser Thr Val Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp
 290 295 300

Leu Leu Val Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys
 305 310 315 320

Gln Val Glu His Asp Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu

325

330

335

Lys Val Ser Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu
 340 345 350

Asn Thr Gly Ser Asn Glu Arg Asn Ile Tyr Gly Ala Cys Pro Trp Ala
 355 360 365

Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu
 370 375 380

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
 385 390 395 400

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
 405 410 415

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

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
 435 440 445

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
 450 455 460

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
 465 470 475 480

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
 485 490 495

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
 500 505 510

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
 515 520 525

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
 530 535 540

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
 545 550 555 560

Gly Leu Pro Ser Pro Arg Ser Glu His His His His His
 565 570

<210> 44

<211> 555

<212> PRT

<213> Artificial sequence

<220>

<223> ORIGINAL SIRPa-4-1BBL with signal peptide and N-terminal His Tag

<400> 44

His His His His His His Glu Glu Glu Leu Gln Val Ile Gln Pro Asp
 1 5 10 15

Lys Ser Val Leu Val Ala Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr
 20 25 30

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

Gly Pro Gly Arg Glu Leu Ile Tyr Asn Gln Lys Glu Gly His Phe Pro
 50 55 60

Arg Val Thr Thr Val Ser Asp Leu Thr Lys Arg Asn Asn Met Asp Phe
 65 70 75 80

Ser Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr
 85 90 95

Cys Val Lys Phe Arg Lys Gly Ser Pro Asp Asp Val Glu Phe Lys Ser
 100 105 110

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

Val Ser Gly Pro Ala Ala Arg Ala Thr Pro Gln His Thr Val Ser Phe
 130 135 140

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

Phe Lys Asn Gly Asn Glu Leu Ser Asp Phe Gln Thr Asn Val Asp Pro
 165 170 175

Val Gly Glu Ser Val Ser Tyr Ser Ile His Ser Thr Ala Lys Val Val
 180 185 190

Leu Thr Arg Glu Asp Val His Ser Gln Val Ile Cys Glu Val Ala His
 195 200 205

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

Thr Ile Arg Val Pro Pro Thr Leu Glu Val Thr Gln Gln Pro Val Arg
 225 230 235 240

Ala Glu Asn Gln Val Asn Val Thr Cys Gln Val Arg Lys Phe Tyr Pro
 245 250 255

Gln Arg Leu Gln Leu Thr Trp Leu Glu Asn Gly Asn Val Ser Arg Thr
 260 265 270

Glu Thr Ala Ser Thr Val Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp
 275 280 285

Met Ser Trp Leu Leu Val Asn Val Ser Ala His Arg Asp Asp Val Lys
 290 295 300

Leu Thr Cys Gln Val Glu His Asp Gly Gln Pro Ala Val Ser Lys Ser

305		310		315		320
His Asp Leu Lys Val Ser Ala His Pro Lys Glu Gln Gly Ser Asn Thr						
		325		330		335
Ala Ala Glu Asn Thr Gly Ser Asn Glu Arg Asn Ile Tyr Gly Ala Cys						
		340		345		350
Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser						
		355		360		365
Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly						
		370		375		380
Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn						
385		390		395		400
Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu						
		405		410		415
Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys						
		420		425		430
Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu						
		435		440		445
Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu						
		450		455		460
Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu						
465		470		475		480
Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser						
		485		490		495
Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg						
		500		505		510

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
 515 520 525

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
 530 535 540

Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 545 550 555

<210> 45

<211> 541

<212> PRT

<213> Artificial sequence

<220>

<223> DSP107 Var. 4 [SIRP SEQ ID NO: 2 (343 amino acids), glycine linker, 4-1BBL SEQ ID NO: 27 (197 aa)]

<400> 45

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
 115 120 125

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

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

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
 165 170 175

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
 210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr Gly Ala Arg Ala Ser Pro Gly Ser Ala
 340 345 350

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
 355 360 365

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
 370 375 380

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
 385 390 395 400

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
 405 410 415

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
 420 425 430

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
 435 440 445

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
 450 455 460

Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
 465 470 475 480

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
 485 490 495

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
 500 505 510

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
 515 520 525

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 530 535 540

<210> 46
 <211> 529
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSP107 Var. 5: SIRP SEQ ID NO: 2 (343 amino acids), glycine
 linker, 4-1BBL SEQ ID NO: 28 (185 aa)

<400> 46

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala

115

120

125

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

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

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
 165 170 175

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
 210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

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

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 325 330 335

Ser Asn Glu Arg Asn Ile Tyr Gly Leu Arg Glu Gly Pro Glu Leu Ser
 340 345 350

Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala
 355 360 365

Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp
 370 375 380

Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser
 385 390 395 400

Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr
 405 410 415

Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly
 420 425 430

Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala
 435 440 445

Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser
 450 455 460

Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His
 465 470 475 480

Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg
 485 490 495

Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu
 500 505 510

Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser

515

520

525

Glu

<210> 47

<211> 308

<212> PRT

<213> Artificial sequence

<220>

<223> DSP107 Var 6: SIRP SEQ ID NO: 24 (116 amino acids), glycine linker, 4-1BBL SEQ ID NO: 23 (191 amino acids):]

<400> 47

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro
 115 120 125

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

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

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
 165 170 175

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

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

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
 210 215 220

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
 225 230 235 240

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
 245 250 255

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
 260 265 270

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

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

Pro Arg Ser Glu
 305

<210> 48
 <211> 314

<212> PRT

<213> Artificial sequence

<220>

<223> Var 7: SIRP SEQ ID NO: 24 (116 amino acids), glycine linker,
4-1BBL SEQ ID NO: 27 (197 aa)

<400> 48

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
100 105 110

Ser Val Arg Ala Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro
115 120 125

Arg 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> 49

<211> 302

<212> PRT

<213> Artificial sequence

<220>

<223> DSP107 Var 8: SIRP SEQ ID NO: 24 (116 amino acids), glycine linker, 4-1BBL SEQ ID NO: 28 (185 aa)

<400> 49

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 65 70 75 80

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
 85 90 95

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 100 105 110

Ser Val Arg Ala Gly Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
 115 120 125

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
 130 135 140

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
 145 150 155 160

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
 165 170 175

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
 180 185 190

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
 195 200 205

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
 210 215 220

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
 225 230 235 240

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
 245 250 255

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
 260 265 270

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
 275 280 285

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

<210> 50

<211> 1722

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 44

<400> 50

atgggctggg cctgcatcat cctgtttctg gtggctaccg ctaccggcgt gcactccac 60

caccaccatc accacgaaga ggaactgcaa gtgatccagc ctgacaagtc cgtgctggg 120

gctgctggcg aaaccgccac actgagatgt accgccacct ctctgatccc tgtgggccct 180

atccagtggg ttagaggcgc tggacctggc agagagctga tctacaacca gaaagagggc 240

cactttccta gagtgaccac cgtgtccgac ctgaccaagc ggaacaacat ggacttctcc 300

atccggatcg gcaacatcac ccctgctgat gccggcacct actactgcgt gaagttccgg 360

aagggctccc ctgacgacgt cgagtttaaa tccggcgctg gcaccgaact gtccgtgcga 420

gctaaacctt ctgctcccgt ggtgtctggc cctgccgcta gagctacacc tcagcacacc 480

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gtgtctttta cctgcgagtc ccacggcttc agccctagag acatcacctt gaagtggttc      540
aagaacggca acgagctgtc cgacttccag accaacgtgg accctgtggg agagtccgtg      600
tcctactcca tccactctac cgccaagggtg gtgctgaccc gagaggacgt gcacagccaa      660
gtgatctgtg aagtggccca cgtgaccctc cagggcgatc ctttgagagg caccgccaac      720
ctgtccgaga caatcagagt gcctcctaca ctggaagtga cccagcagcc tgtgcgggcc      780
gagaatcaag tgaacgtgac ctgccaagtg cggaagttct accctcagag actgcagctg      840
acctggctgg aaaacggcaa tgtgtccaga accgagacag cctccaccgt gaccgagaac      900
aaggatggca cctacaattg gatgtcctgg ctgctcgtga acgtgtccgc tcacagagat      960
gacgtgaagc tgacatgcca ggtggaacac gatggccagc ctgccgtgtc taagtcccac     1020
gacctgaaag tgtctgctca ccccaaagag cagggtcca ataccgccgc tgagaacacc     1080
ggctccaacg agagaaacat ctacggcgcc tgtccttggg ctgtgtctgg cgctagagca     1140
tctcctggct ctgctgcctc tcctagactg agagaggac ctgagctgtc tcctgatgat     1200
cctgctggcc tgctggatct gagacagggc atgtttgctc agctgggtggc ccagaacgtg     1260
ctgctgattg atggccctct gtcctggtac tctgatcctg gattggctgg cgtgtccctg     1320
actggcggcc tgtcttacaa agaggacacc aaagaactgg tggtaggcaa ggccggcgtg     1380
tactacgtgt tctttcagct ggaactgcgg agagtgggtg ccggcgaagg atctggatct     1440
gtgtctctgg cactgcatct gcagcccctg agatctgtct caggcgctgc tgctctggct     1500
ctgacagttg atctgcctcc tgcctcctcc gaggccagaa actccgcctt tggcttccaa     1560
ggcagactgc tgcattctgtc tgccggccag agactgggag tccatctgca tacagaggct     1620
agagccaggc acgcctggca gttgacacaa ggtgctacag tgctgggcct gttcagagtg     1680
acccagaga ttccagccgg cctgccttct ccaagatccg ag                               1722

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<210> 51

<211> 1749

<212> DNA

<213> Artificial sequence

<220>

<223> Cloned sequence of the C-terminal his-tagged (CH)-DSP-107

<400> 51

gaattcccg	cgccaccatg	ggctggctcct	gcatcatcct	gtttctgggtg	gctaccgcta	60
ccggcgtgca	ctccgaagag	gaactgcaag	tgatccagcc	tgacaagtcc	gtgctgggtg	120
ctgctggcga	aaccgccaca	ctgagatgta	ccgccacctc	tctgatccct	gtgggcccta	180
tccagtgggtt	tagaggcgct	ggacctggca	gagagctgat	ctacaaccag	aaagagggcc	240
actttcctag	agtgaccacc	gtgtccgacc	tgaccaagcg	gaacaacatg	gacttctcca	300
tccggatcgg	caacatcacc	cctgctgatg	ccggcaccta	ctactgcgtg	aagttccgga	360
agggtcccc	tgacgacgtc	gagtttaaat	ccggcgctgg	caccgaactg	tccgtgcgag	420
ctaaaccttc	tgctcccgtg	gtgtctggcc	ctgccgctag	agctacacct	cagcacaccg	480
tgtcttttac	ctgcgagtcc	cacggcttca	gccctagaga	catcaccctg	aagtggttca	540
agaacggcaa	cgagctgtcc	gacttccaga	ccaacgtgga	ccctgtggga	gagtccgtgt	600
cctactccat	ccactctacc	gccaagggtg	tgctgaccgg	agaggacgtg	cacagccaag	660
tgatctgtga	agtggcccac	gtgaccctcc	agggcgatcc	tttgagaggc	accgccaacc	720
tgtccgagac	aatcagagtg	cctcctacac	tggaagtga	ccagcagcct	gtgcgggccg	780
agaatcaagt	gaacgtgacc	tgccaagtgc	ggaagttcta	ccctcagaga	ctgcagctga	840
cctggctgga	aaacggcaat	gtgtccagaa	ccgagacagc	ctccaccgtg	accgagaaca	900
aggatggcac	ctacaattgg	atgtcctggc	tgctcgtgaa	cgtgtccgct	cacagagatg	960
acgtgaagct	gacatgccag	gtggaacacg	atggccagcc	tgccgtgtct	aagtcccacg	1020
acctgaaaagt	gtctgctcac	cccaaagagc	agggtccaa	taccgccgct	gagaacaccg	1080
gctccaacga	gagaaacatc	tacggcgcct	gtccttgggc	tgtgtctggc	gctagagcat	1140
ctcctggctc	tgctgcctct	cctagactga	gagagggacc	tgagctgtct	cctgatgatc	1200
ctgctggcct	gctggatctg	agacagggca	tgtttgctca	gctgggtggc	cagaacgtgc	1260
tgctgattga	tggccctctg	tcctgggtact	ctgatcctgg	attggctggc	gtgtccctga	1320
ctggcggcct	gtcttataaa	gaggacacca	aagaactgg	ggtggccaag	gccggcgtgt	1380
actacgtgtt	ctttcagctg	gaactgcgga	gagtgggtggc	cggcgaagga	tctggatctg	1440

tgtctctggc actgcatctg cagccccctga gatctgctgc aggcgctgct gctctggctc	1500
tgacagttga tctgcctcct gcctcctccg aggccagaaa ctccgccttt ggcttccaag	1560
gcagactgct gcatctgtct gccggccaga gactgggagt ccatctgcat acagaggcta	1620
gagccaggca cgcctggcag ttgacacaag gtgctacagt gctgggcctg ttcagagtga	1680
ccccagagat tccagccggc ctgccttctc caagatccga gcaccaccac catcaccact	1740
gataagctt	1749

<210> 52

<211> 1731

<212> DNA

<213> Artificial sequence

<220>

<223> Cloned sequence of the C-terminal his-tagged (CH)-V1 DSP-107

<400> 52

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ccggcgtgca ctccgaagag gaactgcaag tgatccagcc tgacaagtcc gtgctgggtgg	120
ctgctggcga aaccgccaca ctgagatgta ccgccacctc tctgatccct gtggggcccta	180
tccagtgggt tagaggcgct ggacctggca gagagctgat ctacaaccag aaagagggcc	240
actttcctag agtgaccacc gtgtccgacc tgaccaagcg gaacaacatg gacttctcca	300
tccggatcgg caacatcacc cctgctgatg ccggcaccta ctactgcgtg aagttccgga	360
agggtcccc tgacgacgtc gagtttaa at ccggcgctgg caccgaactg tccgtgcgag	420
ctaaaccttc tgctcccgtg gtgtctggcc ctgccgctag agctacacct cagcacaccg	480
tgtcttttac ctgcgagtcc cacggcttca gccctagaga catcaccctg aagtgggttca	540
agaacggcaa cgagctgtcc gacttccaga ccaacgtgga ccctgtggga gagtccgtgt	600
cctactccat ccactctacc gccaaagggtg tgctgacccg agaggacgtg cacagccaag	660
tgatctgtga agtggcccac gtgacctcc agggcgatcc tttgagaggc accgccaacc	720
tgtccgagac aatcagagtg cctcctacac tggaagtgtg ccagcagcct gtgcgggccc	780
agaatcaagt gaacgtgacc tgccaagtgc ggaagttcta ccctcagaga ctgcagctga	840

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cctggctgga aaacggcaat gtgtccagaa ccgagacagc ctccaccgtg accgagaaca      900
aggatggcac ctacaattgg atgtcctggc tgctcgtgaa cgtgtccgct cacagagatg      960
acgtgaagct gacatgccag gtggaacacg atggccagcc tgccgtgtct aagtcccacg     1020
acctgaaagt gtctgctcac cccaaagagc agggctccaa taccgccgct gagaacaccg     1080
gctccaacga gagaaacatc tacggctctg gcgctagggc ctctcctgga tctgctgctt     1140
ctcccagact gagagagggc cctgagctgt ctctgatga tcctgctgga ctgctggatc     1200
tgagacaggg catgtttgct cagctgggtg cccagaacgt gctgctgatt gatggccctc     1260
tgtcctggta ctctgatcct ggattggctg gcgtgtccct gactggcggc ctgtcttaca     1320
aagaggacac caaagaactg gtggtggcca aggccggcgt gtactacgtg ttctttcagc     1380
tggaactgcg gagagtgggt gccggcgaag gatctggatc tgtgtctctg gctctgcatc     1440
tgcagcccct gagatctgca gcaggcgctg cagctctggc actgacagtt gatctgcctc     1500
ctgcctcctc cgaggccaga aactccgcct ttggcttcca aggcagactg ctgcacctgt     1560
ctgctggaca gagactggga gtgcacctcc acacagaggc cagagctaga catgcctggc     1620
agttgacaca gggcgctaca gtgctgggcc tgttcagagt gacacctgag attccagccg     1680
gcctgccttc tccaagatcc gagcaccacc accatcacca ctgataagct t              1731

```

<210> 53

<211> 1707

<212> DNA

<213> Artificial sequence

<220>

<223> Cloned sequence of the C-terminal his-tagged (CH)-V2 DSP-107

<400> 53

```

gaattccgc cgccaccatg ggctggctcct gcatcatcct gtttctgggtg gctaccgcta      60
ccggcgtgca ctccgaagag gaactgcaag tgatccagcc tgacaagtcc gtgctgggtg     120
ctgctggcga aaccgccaca ctgagatgta ccgccacctc tctgatccct gtgggcccta     180
tccagtgggt tagaggcgct ggacctggca gagagctgat ctacaaccag aaagagggcc     240
actttcctag agtgaccacc gtgtccgacc tgaccaagcg gaacaacatg gactttctcca     300

```

tccggatcgg caacatcacc cctgctgatg ccggcaccta ctactgcgtg aagttccgga	360
agggctcccc tgacgacgtc gagtttaaat ccggcgctgg caccgaactg tccgtgag	420
ctaaaccttc tgctcccgtg gtgtctggcc ctgccgctag agctacacct cagcacaccg	480
tgtcttttac ctgcgagtcc cacggcttca gccctagaga catcacctg aagtggttca	540
agaacggcaa cgagctgtcc gacttccaga ccaacgtgga ccctgtggga gagtccgtgt	600
cctactccat ccactctacc gccaaagggtg tgctgacccg agaggacgtg cacagccaag	660
tgatctgtga agtggcccac gtgaccttc agggcgatcc tttgagaggc accgccaacc	720
tgtccgagac aatcagagt cctcctacac tggaagtgc ccagcagcct gtgcgggccg	780
agaatcaagt gaacgtgacc tgccaagtgc ggaagtctta ccctcagaga ctgcagctga	840
cctggctgga aaacggcaat gtgtccagaa ccgagacagc ctccaccgtg accgagaaca	900
aggatggcac ctacaattgg atgtcctggc tgctcgtgaa cgtgtccgct cacagagatg	960
acgtgaagct gacatgccag gtggaacacg atggccagcc tgccgtgtct aagtcacacg	1020
acctgaaagt gtctgctcac cccaaagagc agggctccaa taccgccgct gagaacaccg	1080
gctccaacga gagaaacatc tacggctctg ccgcctctcc tagactgaga gagggacctg	1140
agctgtctcc tgatgatcct gctggcctgc tggatctgag acagggcagc tttgctcagc	1200
tgggtggcca gaacgtgctg ctgattgatg gccctctgtc ctggtactct gatcctggat	1260
tggctggcgt gtccctgact ggcggcctgt cttacaaaga ggacaccaa gaactgggtg	1320
tggccaaggc cggcgtgtac tacgtgttct ttcagctgga actgcggaga gtggtggccg	1380
gcgaaggatc tggatctgtg tctctggctc tgcatctgca gcccctgaga tctgctgcag	1440
gcgctgctgc tctggcactg acagttgatc tgcctcctgc ctctccgag gccagaaact	1500
ccgcctttgg cttccaaggc agactgctgc atctgtctgc cggccagaga ctgggagtcc	1560
atctgcatac agaggccaga gctagacacg cttggcagtt gacacagggc gctacagtgc	1620
tgggcctgtt cagagtgaca cctgagatcc cagccggcct gccttctcca agatctgagc	1680
accaccacca tcaccactga taagctt	1707

<210> 54
 <211> 1047
 <212> DNA
 <213> Artificial sequence

<220>

<223> Cloned sequence of the C-terminal his-tagged (CH)-V3.1 DSP-107

<400> 54

```

gaattcccg c gccaccatg ggctggctcct gcatcatcct gtttctgggtg gctaccgcta      60
ccggcgtgca ctccgaagag gaactgcaag tgatccagcc tgacaagtcc gtgctgggtgg      120
ctgctggcga aaccgccaca ctgagatgta ccgccacctc tctgatccct gtggggcccta      180
tccagtgggtt tagaggcgct ggacctggca gagagctgat ctacaaccag aaagagggcc      240
actttcctag agtgaccacc gtgtccgacc tgaccaagcg gaacaacatg gacttctcca      300
tccggatcgg caacatcacc cctgctgatg ccggcaccta ctactgcgtg aagttccgga      360
agggctcccc tgacgacgtc gagtttaa at ccggcgctgg caccgagctg tccgtcagag      420
cttctgggtgc tagagcctct cctggctctg ccgcttctcc tagactgaga gagggacctg      480
agctgtctcc tgatgatcct gctggcctgc tggatctgag acagggcatg tttgctcagc      540
tggtggccca gaacgtgctg ctgattgatg gccctctgtc ctggtactct gatcctggat      600
tggctggcgt gtccctgact ggcggcctgt cttacaaaga ggacaccaaa gaactgggtgg      660
tggccaaggc cggcgtgtac tacgtgttct ttcagctgga actgcggaga gtggtggccg      720
gcgaaggatc tggatctgtg tctctggcac tgcatctgca gcctctgaga tctgctgcag      780
gcgctgctgc tctggctctg acagttgatc tgccctctgc ctccctccgag gccagaaact      840
ccgcctttgg cttccaaggc agactgctgc atctgtctgc cggccagaga ctgggagtcc      900
atctgcatac agaggccaga gctagacacg cttggcagtt gacacagggc gctacagtgc      960
tgggcctgtt cagagtgaca cctgagatcc cagccggcct gccttctcca agatctgagc     1020
accaccacca tcaccactga taagctt                                           1047

```

<210> 55
 <211> 1629
 <212> DNA
 <213> Artificial sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 11 (DSP107_var1 without His Tag)

<400> 55

gaagaggaac tgcaagtgat ccagcctgac aagtccgtgc tggaggctgc tggcgaaacc	60
gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggtttaga	120
ggcgctggac ctggcagaga gctgatctac aaccagaaaag agggccactt tcctagagtg	180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac	240
atcacccctg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac	300
gacgtcgagt ttaaattccgg cgctggcacc gaactgtccg tgcgagctaa accttctgct	360
cccgtgggtg ctggccctgc cgctagagct acacctcagc acaccgtgtc ttttacctgc	420
gagtcccacg gcttcagccc tagagacatc accctgaagt ggttcaagaa cggcaacgag	480
ctgtccgact tccagaccaa cgtggaccct gtgggagagt ccgtgtccta ctccatccac	540
tctaccgcca aggtgggtgct gacccgagag gacgtgcaca gccaagtgat ctgtgaagtg	600
gcccacgtga ccctccaggg cgatcctttg agaggcaccg ccaacctgtc cgagacaatc	660
agagtgcctc ctacactgga agtgaccag cagcctgtgc gggccgagaa tcaagtgaac	720
gtgacctgcc aagtgcggaa gttctaccct cagagactgc agctgacctg gctggaaaac	780
ggcaatgtgt ccagaaccga gacagcctcc accgtgaccg agaacaagga tggcacctac	840
aattggatgt cctggctgct cgtgaacgtg tccgctcaca gagatgacgt gaagctgaca	900
tgccagggtg aacacgatgg ccagcctgcc gtgtctaagt cccacgacct gaaagtgtct	960
gctcacccca aagagcaggg ctccaatacc gccgctgaga acaccggctc caacgagaga	1020
aacatctacg gctctggcgc tagggcctct cctggatctg ctgcttctcc cagactgaga	1080
gagggccctg agctgtctcc tgatgatcct gctggactgc tggatctgag acagggcatg	1140
tttgctcagc tggaggccca gaacgtgctg ctgattgatg gccctctgtc ctggtactct	1200
gatcctggat tggctggcgt gtccctgact ggcggcctgt cttacaaaga ggacaccaaa	1260
gaactggtgg tggccaaggc cggcgtgtac tacgtgttct ttcagctgga actgcggaga	1320

```

gtggtggccg gcgaaggatc tggatctgtg tctctggctc tgcattctgca gcccctgaga      1380
tctgcagcag gcgctgcagc tctggcactg acagttgatc tgcctcctgc ctctccgag      1440
gccagaaact ccgccttttg cttccaaggc agactgctgc acctgtctgc tggacagaga      1500
ctgggagtg acctccacac agaggccaga gctagacatg cctggcagtt gacacagggc      1560
gctacagtgc tgggcctgtt cagagtgaca cctgagattc cagccggcct gccttctcca      1620
agatccgag      1629

```

<210> 56

<211> 1605

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 13 (DSP107_var2 without His Tag)

<400> 56

```

gaagaggaac tgcaagtgat ccagcctgac aagtccgtgc tggtagctgc tggcgaaacc      60
gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggtttaga      120
ggcgctggac ctggcagaga gctgatctac aaccagaaag agggccactt tcctagagtg      180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac      240
atcacccctg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac      300
gacgtcgagt ttaaataccg cgctggcacc gaactgtccg tgcgagctaa accttctgct      360
cccgtggtgt ctggccctgc cgctagagct acacctcagc acaccgtgtc ttttacctgc      420
gagtcccacg gcttcagccc tagagacatc accctgaagt ggttcaagaa cggcaacgag      480
ctgtccgact tccagaccaa cgtggaccct gtgggagagt ccgtgtccta ctccatccac      540
tctaccgcca aggtggtgct gacccgagag gacgtgcaca gccaagtgat ctgtgaagtg      600
gccacgtga ccctccaggg cgatcctttg agaggcaccg ccaacctgtc cgagacaatc      660
agagtgcctc ctacactgga agtgacctag cagcctgtgc gggccgagaa tcaagtgaac      720
gtgacctgcc aagtgcggaa gttctaccct cagagactgc agctgacctg gctggaaaac      780
ggcaatgtgt ccagaaccga gacagcctcc accgtgaccg agaacaagga tggcacctac      840

```

```

aattggatgt cctggctgct cgtgaacgtg tccgctcaca gagatgacgt gaagctgaca      900
tgccagggtgg aacacgatgg ccagcctgcc gtgtctaagt cccacgacct gaaagtgtct      960
gctcacccca aagagcaggg ctccaatacc gccgctgaga acaccggctc caacgagaga     1020
aacatctacg gctctgccgc ctctcctaga ctgagagagg gacctgagct gtctcctgat     1080
gatcctgctg gcctgctgga tctgagacag ggcatgtttg ctcagctggg ggcccagaac     1140
gtgctgctga ttgatggccc tctgtcctgg tactctgata ctggattggc tggcgtgtcc     1200
ctgactggcg gcctgtctta caaagaggac accaaagaac tgggtggcggc caaggccggc     1260
gtgtactacg tgttctttca gctggaactg cggagagtgg tggccggcga aggatctgga     1320
tctgtgtctc tggctctgca tctgcagccc ctgagatctg ctgcaggcgc tgctgctctg     1380
gcactgacag ttgatctgcc tcctgcctcc tccgaggcca gaaactccgc ctttggcttc     1440
caaggcagac tgctgcatct gtctgccggc cagagactgg gagtccatct gcatacagag     1500
gccagagcta gacacgcttg gcagttgaca cagggcgcta cagtgtctggg cctgttcaga     1560
gtgacacctg agatcccagc cggcctgcct tctccaagat ctgag                        1605

```

```

<210> 57
<211> 966
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> nucleic acid sequence encoding SEQ ID NO: 15 (DSP107_var3 without
      His Tag)

```

```

<400> 57
gaagaggaac tgcaagtgat ccagcctgac aagtccgtgc tggcggctgc tggcgaaacc      60
gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggttttaga     120
ggcgctggac ctggcagaga gctgatctac aaccagaaag agggccactt tcctagagtg     180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac     240
atcacccttg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac     300
gacgtcgagt ttaaataccg cgctggcacc gaactgtccg tgcgagctgg cgctgtcct      360

```

tgggctgtgt ctggcgctag agcatctcct ggctctgctg cctctcctag actgagagag 420
 ggacctgagc tgtctcctga tgatcctgct ggcttgctgg atctgagaca gggcatgttt 480
 gctcagctgg tggcccagaa cgtgctgctg attgatggcc ctctgtcctg gtactctgat 540
 cctggattgg ctggcgtgtc cctgactggc ggctgtctt acaaagagga caccaaagaa 600
 ctggtggtgg ccaaggccgg cgtgtactac gtgttctttc agctggaact gcggagagtg 660
 gtggccggcg aaggatctgg atctgtgtct ctggcactgc atctgcagcc cctgagatct 720
 gctgcaggcg ctgctgctct ggctctgaca gttgatctgc ctctgcctc ctccgaggcc 780
 agaaactccg cctttggctt ccaaggcaga ctgctgcatc tgtctgccgg ccagagactg 840
 ggagtccatc tgcatacaga ggctagagcc aggcacgcct ggagttgac acaaggtgct 900
 acagtgtggt gcctgttcag agtgacccca gagattccag ccggcctgcc ttctccaaga 960
 tccgag 966

<210> 58

<211> 945

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 16: (DSP107_var3.1 without His Tag)

<400> 58

gaagaggaac tgcaagtgat ccagcctgac aagtccgtgc tgggtggctgc tggcgaaacc 60
 gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggttttaga 120
 ggcgctggac ctggcagaga gctgatctac aaccagaaag agggccactt tcctagagtg 180
 accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac 240
 atcacccttg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac 300
 gacgtcgagt ttaaattccgg cgctggcacc gagctgtccg tcagagcttc tgggtgctaga 360
 gcctctcctg gctctgccgc ttctcctaga ctgagagagg gacctgagct gtctcctgat 420
 gatcctgctg gcctgttgga tctgagacag ggcatgtttg ctgagctggg ggcccagaac 480
 gtgctgctga ttgatggccc tctgtcctgg tactctgatc ctggattggc tggcgtgtcc 540

```

ctgactggcg gcctgtctta caaagaggac accaaagaac tgggtggcgc caaggccggc      600
gtgtactacg tgttctttca gctggaactg cggagagtgg tggccggcga aggatctgga      660
tctgtgtctc tggcactgca tctgcagcct ctgagatctg ctgcaggcgc tgctgctctg      720
gctctgacag ttgatctgcc tcctgcctcc tccgaggcca gaaactccgc ctttggcttc      780
caaggcagac tgctgcatct gtctgccggc cagagactgg gagtccatct gcatacagag      840
gccagagcta gacacgcttg gcagttgaca cagggcgcta cagtgtctggg cctgttcaga      900
gtgacacctg agatcccagc cggcctgcct tctccaagat ctgag                        945

```

<210> 59

<211> 1629

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 18 (DSP107_Var1Mut
without His Tag)

<400> 59

```

gaagaggaaa tccaagtgat ccagcctgac aagtccgtgc tggcggctgc tggcgaaacc      60
gccacactga gatgtaccat cacctctctg atccctgtgg gccctatcca gtggtttaga      120
ggcgctggac ctggcagaat gctgatctac aaccagaaag aggccactt tcctagagtg      180
accaccgtgt ccgacctgac caagcggaac aacatcgact tctccatccg gatcggcaac      240
atcacccctg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac      300
gacgtcgagt ttaaataccg cgctggcacc gaactgtccg tgcgagctaa accttctgct      360
cccgtgggtg ctggccctgc cgctagagct acacctcagc acaccgtgtc ttttacctgc      420
gagtcccacg gcttcagccc tagagacatc accctgaagt ggttcaagaa cggcaacgag      480
ctgtccgact tccagaccaa cgtggaccct gtgggagagt ccgtgtccta ctccatccac      540
tctaccgcca aggtgggtgct gacccgagag gacgtgcaca gccaaagtgat ctgtgaagtg      600
gcccacgtga ccctccaggg cgatcctttg agaggcaccg ccaacctgtc cgagacaatc      660
agagtgcctc ctacactgga agtgacccag cagcctgtgc gggccgagaa tcaagtgaac      720

```

```

gtgacctgcc aagtgcggaa gttctaccct cagagactgc agctgacctg gctggaaaac      780
ggcaatgtgt ccagaaccga gacagcctcc accgtgaccg agaacaagga tggcacctac      840
aattggatgt cctggctgct cgtgaacgtg tccgctcaca gagatgacgt gaagctgaca      900
tgccaggtgg aacacgatgg ccagcctgcc gtgtctaagt cccacgacct gaaagtgtct      960
gctcacccca aagagcaggg ctccaatacc gccgctgaga acaccggctc caacgagaga     1020
aacatctacg gctctggcgc tagggcctct cctggatctg ctgcttctcc cagactgaga     1080
gagggccctg agctgtctcc tgatgatcct gctggactgc tggatctgag acagggcatg     1140
tttgctcagc tgggtggcca gaacgtgctg ctgattgatg gccctctgtc ctggtactct     1200
gatcctggat tggctggcgt gtccctgact ggcggcctgt cttacaaaga ggacaccaaa     1260
gaactggtgg tggccaaggc cggcgtgtac tacgtgttct ttcagctgga actgcggaga     1320
gtggtggccg gcgaaggatc tggatctgtg tctctggctc tgcattctgca gcccctgaga     1380
tctgcagcag gcgctgcagc tctggcactg acagttgatc tgcctcctgc ctctccgag     1440
gccagaaaact cgccttttgg cttccaaggc agactgctgc acctgtctgc tggacagaga     1500
ctgggagtg c acctccacac agaggccaga gctagacatg cctggcagtt gacacagggc     1560
gctacagtgc tgggcctgtt cagagtgaca cctgagattc cagccggcct gccttctcca     1620
agatccgag                                     1629

```

<210> 60

<211> 1605

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 19: (DSP107_Var2Mut without His Tag)

<400> 60

```

gaagaggaaa tccaagtgat ccagcctgac aagtccgtgc tgggtggctgc tggcgaaacc      60
gccacactga gatgtaccat cacctctctg atccctgtgg gccctatcca gtggtttaga     120
ggcgtctggac ctggcagaat gctgatctac aaccagaaaag agggccactt tcctagagtg     180
accaccgtgt ccgacctgac caagcggaac aacatcgact tctccatccg gatcggcaac     240

```

atcacccctg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac 300
 gacgtcgagt ttaaataccgg cgctggcacc gaactgtccg tgcgagctaa accttctgct 360
 cccgtgggtgt ctggccctgc cgctagagct acacctcagc acaccgtgtc ttttacctgc 420
 gagtcccacg gcttcagccc tagagacatc accctgaagt ggttcaagaa cggcaacgag 480
 ctgtccgact tccagaccaa cgtggaccct gtgggagagt ccgtgtccta ctccatccac 540
 tctaccgcca aggtgggtgct gacccgagag gacgtgcaca gccaagtgat ctgtgaagtg 600
 gcccacgtga ccctccaggg cgatcctttg agaggcaccg ccaacctgtc cgagacaatc 660
 agagtgcctc ctacactgga agtgaccag cagcctgtgc gggccgagaa tcaagtgaac 720
 gtgacctgcc aagtgcggaa gttctaccct cagagactgc agctgacctg gctggaaaac 780
 ggcaatgtgt ccagaaccga gacagcctcc accgtgaccg agaacaagga tggcacctac 840
 aattggatgt cctggctgct cgtgaacgtg tccgctcaca gagatgacgt gaagctgaca 900
 tgccaggtgg aacacgatgg ccagcctgcc gtgtctaagt cccacgacct gaaagtgtct 960
 gctcacccca aagagcaggg ctccaatacc gccgctgaga acaccggctc caacgagaga 1020
 aacatctacg gctctgccgc ctctcctaga ctgagagagg gacctgagct gtctcctgat 1080
 gatcctgctg gcctgtgga tctgagacag ggcatgtttg ctcagctggt ggcccagaac 1140
 gtgctgctga ttgatggccc tctgtcctgg tactctgac ctggattggc tggcgtgtcc 1200
 ctgactggcg gcctgtctta caaagaggac accaaagaac tgggtggtggc caaggccggc 1260
 gtgtactacg tgttctttca gctggaactg cggagagtgg tggccggcga aggatctgga 1320
 tctgtgtctc tggctctgca tctgcagccc ctgagatctg ctgcaggcgc tgctgctctg 1380
 gcactgacag ttgatctgcc tcctgcctcc tccgaggcca gaaactccgc ctttggcttc 1440
 caaggcagac tgctgcatct gtctgccggc cagagactgg gagtccatct gcatacagag 1500
 gccagagcta gacacgcttg gcagttgaca cagggcgcta cagtgtctggg cctgttcaga 1560
 gtgacacctg agatcccagc cggcctgcct tctccaagat ctgag 1605

<210> 61

<211> 966

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 20 (DSP107_Var3Mut without His Tag)

<400> 61

```

gaagaggaaa tccaagtgat ccagcctgac aagtccgtgc tggaggctgc tggcgaacc      60
gccacactga gatgtaccat cacctctctg atccctgtgg gccctatcca gtggtttaga      120
ggcgctggac ctggcagagt gctgatctac aaccagaaag agggccactt tcctagagtg      180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac      240
atcacccctg ctgatgccgg cacctactac tgcatacaagt tccggaaggg ctcccctgac      300
gacgtcgagt ttaaataccgg cgctggcacc gaactgtccg tgcgagctgg cgctgtcct      360
tgggctgtgt ctggcgctag agcatctcct ggctctgctg cctctcctag actgagagag      420
ggacctgagc tgtctcctga tgatcctgct ggctgtctgg atctgagaca gggcatgttt      480
gctcagctgg tggcccagaa cgtgctgctg attgatggcc ctctgtcctg gtactctgat      540
cctggattgg ctggcgtgtc cctgactggc ggctgtcttt acaaagagga caccaaagaa      600
ctgggtgggg ccaaggccgg cgtgtactac gtgttctttc agctggaact gcggagagtg      660
gtggccggcg aaggatctgg atctgtgtct ctggcactgc atctgcagcc cctgagatct      720
gctgcaggcg ctgtgtctct ggctctgaca gttgatctgc ctctgcctc ctccgaggcc      780
agaaactccg cttttggctt ccaaggcaga ctgtgtcatc tgtctgccgg ccagagactg      840
ggagtccatc tgcatacaga ggctagagcc aggcacgcct ggcagttgac acaaggtgct      900
acagtgtctg gcctgttcag agtgacccca gagattccag ccggcctgcc ttctccaaga      960
tccgag                                         966

```

<210> 62

<211> 1623

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 45 (Var 4)

<400> 62

gaagaggaac tgcaagtgat ccagcctgac aagtccgtgc tggaggctgc tggcgaaacc	60
gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggtttaga	120
ggcgctggac ctggcagaga gctgatctac aaccagaaag agggccactt tcctagagtg	180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac	240
atcacccctg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac	300
gacgtcgagt ttaaataccgg cgctggcacc gaactgtccg tgcgagctaa accttctgct	360
cccgtgggtg ctggccctgc cgctagagct acacctcagc acaccgtgtc ttttacctgc	420
gagtcccacg gcttcagccc tagagacatc accctgaagt ggttcaagaa cggcaacgag	480
ctgtccgact tccagaccaa cgtggaccct gtgggagagt ccgtgtccta ctccatccac	540
tctaccgcca aggtgggtgct gacccgagag gacgtgcaca gccaaagtgat ctgtgaagtg	600
gcccacgtga ccctccaggg cgatcctttg agaggcaccg ccaacctgtc cgagacaatc	660
agagtgcctc ctacactgga agtgacccag cagcctgtgc gggccgagaa tcaagtgaac	720
gtgacctgcc aagtgcggaa gttctaccct cagagactgc agctgacctg gctggaaaac	780
ggcaatgtgt ccagaaccga gacagcctcc accgtgaccg agaacaagga tggcacctac	840
aattggatgt cctggctgct cgtgaacgtg tccgctcaca gagatgacgt gaagctgaca	900
tgccaggtgg aacacgatgg ccagcctgcc gtgtctaagt cccacgacct gaaagtgtct	960
gctcacccca aagagcaggg ctccaatacc gccgctgaga acaccggctc caacgagaga	1020
aacatctacg gagctagagc atctcctggc tctgctgcct ctctagact gagagaggga	1080
cctgagctgt ctctgatga tcctgctggc ctgctggatc tgagacaggg catgtttgct	1140
cagctgggtg cccagaacgt gctgctgatt gatggccctc tgtcctggta ctctgacct	1200
ggattggctg gcgtgtccct gactggcggc ctgtcttaca aagaggacac caaagaactg	1260
gtgggtggcca aggccggcgt gtactacgtg ttctttcagc tggaactgcg gagagtgggtg	1320
gccggcgaag gatctggatc tgtgtctctg gcactgcatc tgcagcccct gagatctgct	1380
gcaggcgctg ctgctctggc tctgacagtt gatctgcctc ctgcctcctc cgaggccaga	1440

aactccgcct ttggcttcca aggcagactg ctgcatctgt ctgccggcca gagactggga	1500
gtccatctgc atacagaggc tagagccagg cacgcctggc agttgacaca aggtgctaca	1560
gtgctgggcc tgttcagagt gaccccagag attccagccg gcctgccttc tccaagatcc	1620
gag	1623

<210> 63
 <211> 1587
 <212> DNA
 <213> Artificial sequence

<220>
 <223> nucleic acid sequence encoding SEQ ID NO: 46 (Var 5)

<400> 63	
gaagaggaac tgcaagtgat ccagcctgac aagtccgtgc tgggtggctgc tggcgaaacc	60
gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggtttaga	120
ggcgctggac ctggcagaga gctgatctac aaccagaaag agggccactt tcctagagtg	180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac	240
atcacccctg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac	300
gacgtcgagt ttaaataccgg cgctggcacc gaactgtccg tgcgagctaa accttctgct	360
cccgtgggtg ctggccctgc cgctagagct acacctcagc acaccgtgtc ttttacctgc	420
gagtcccacg gcttcagccc tagagacatc accctgaagt ggttcaagaa cggcaacgag	480
ctgtccgact tccagaccaa cgtggaccct gtgggagagt ccgtgtccta ctccatccac	540
tctaccgcca aggtgggtgct gacccgagag gacgtgcaca gccaagtgat ctgtgaagtg	600
gcccacgtga ccctccaggg cgatcctttg agaggcaccg ccaacctgtc cgagacaatc	660
agagtgcctc ctacactgga agtgacccag cagcctgtgc gggccgagaa tcaagtgaac	720
gtgacctgcc aagtgcggaa gttctaccct cagagactgc agctgacctg gctggaaaac	780
ggcaatgtgt ccagaaccga gacagcctcc accgtgaccg agaacaagga tggcacctac	840
aattggatgt cctggctgct cgtgaacgtg tccgctcaca gagatgacgt gaagctgaca	900
tgccaggtgg aacacgatgg ccagcctgcc gtgtctaagt cccacgacct gaaagtgtct	960

gctcacccca aagagcaggg ctccaatacc gccgctgaga acaccggctc caacgagaga 1020
 aacatctacg gactgagaga gggacctgag ctgtctcctg atgacacctg tggcctgctg 1080
 gatctgagac agggcatgtt tgctcagctg gtggcccaga acgtgctgct gattgatggc 1140
 cctctgtcct ggtactctga tcctggattg gctggcgtgt ccctgactgg cggcctgtct 1200
 tacaaagagg acaccaaaga actggtggtg gccaaaggccg gcgtgtacta cgtgttcttt 1260
 cagctggaac tgcggagagt ggtggccggc gaaggatctg gatctgtgtc tctggcactg 1320
 catctgcagc ccctgagatc tgctgcaggc gctgctgctc tggctctgac agttgatctg 1380
 cctcctgcct cctccgaggc cagaaactcc gcctttggct tccaaggcag actgctgcat 1440
 ctgtctgccg gccagagact gggagtccat ctgcatacag aggctagagc caggcacgcc 1500
 tggcagttga cacaaggtgc tacagtgtg ggccgtgttca gaggtagcccc agagattcca 1560
 gccggcctgc cttctccaag atccgag 1587

<210> 64

<211> 924

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 47 (Var 6)

<400> 64

gaagaggaac tgcaagtgat ccagcctgac aagtccgtgc tggcggctgc tggcgaaacc 60
 gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggtttaga 120
 ggcgctggac ctggcagaga gctgatctac aaccagaaag agggccactt tcctagagtg 180
 accaccgtgt ccgacctgac caagcgggaa aacatggact tctccatccg gatcggcaac 240
 atcacccttg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac 300
 gacgtcgagt ttaaataccg cgctggcacc gaactgtccg tgcgagctgg atctgctgcc 360
 tctcctagac tgagagaggg acctgagctg tctcctgatg atcctgctgg cctgctggat 420
 ctgagacagg gcatgtttgc tcagctgggtg gcccagaacg tgctgctgat tgatggccct 480
 ctgtcctggt actctgatcc tggattggct ggcgtgtccc tgactggcgg cctgtcttac 540

```

aaagaggaca ccaaagaact ggtggtggcc aaggccggcg tgtactacgt gttctttcag      600
ctggaactgc ggagagtggg ggccggcgaa ggatctggat ctgtgtctct ggcaactgcat      660
ctgcagcccc tgagatctgc tgcaggcgct gctgctctgg ctctgacagt tgatctgcct      720
cctgcctcct ccgaggccag aaactccgcc tttggcttcc aaggcagact gctgcatctg      780
tctgccggcc agagactggg agtccatctg catacagagg ctagagccag gcacgcctgg      840
cagttgacac aaggtgctac agtgctgggc ctgttcagag tgaccccaga gattccagcc      900
ggcctgcctt ctccaagatc cgag                                           924

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

```

```

<220>
<223> nucleic acid sequence encoding SEQ ID NO: 48 (Var 7)

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```

<400> 65
gaagaggaaac tgcaagtgat ccagcctgac aagtccgtgc tggaggctgc tggcgaaacc      60
gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggtttaga      120
ggcgctggac ctggcagaga gctgatctac aaccagaaag agggccactt tcctagagtg      180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac      240
atcacccctg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac      300
gacgtcgagt ttaaataccg cgctggcacc gaactgtccg tgcgagctgg agctagagca      360
tctcctggct ctgctgcctc tcctagactg agagaggggac ctgagctgtc tcctgatgat      420
cctgctggcc tgctggatct gagacagggc atgtttgctc agctgggtggc ccagaacgtg      480
ctgctgattg atggccctct gtcctggtag tctgatcctg gattggctgg cgtgtccctg      540
actggcggcc tgtcttacaa agaggacacc aaagaactgg tggtaggcaa ggccggcgctg      600
tactacgtgt tctttcagct ggaactgcgg agagtggtag ccggcgaagg atctggatct      660
gtgtctctgg cactgcatct gcagcccctg agatctgtct caggcgctgc tgctctggct      720
ctgacagttg atctgcctcc tgcctcctcc gaggccagaa actccgcctt tggcttccaa      780

```

ggcagactgc tgcattctgtc tgccggccag agactgggag tccattctgca tacagaggct 840
 agagccaggc acgcctggca gttgacacaa ggtgctacag tgctgggcct gttcagagtg 900
 accccagaga ttccagccgg cctgccttct ccaagatccg ag 942

<210> 66
 <211> 906
 <212> DNA
 <213> Artificial sequence

<220>
 <223> nucleic acid sequence encoding SEQ ID NO: 49 (Var 8)

<400> 66
 gaagaggaac tgcaagtgat ccagcctgac aagtccgtgc tggaggctgc tggcgaaacc 60
 gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggtttaga 120
 ggcgctggac ctggcagaga gctgatctac aaccagaaag agggccactt tcctagagtg 180
 accaccgtgt ccgacctgac caagcggaaac aacatggact tctccatccg gatcggcaac 240
 atcacccctg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac 300
 gacgtcgagt ttaaattccgg cgctggcacc gaactgtccg tgcgagctgg actgagagag 360
 ggacctgagc tgtctcctga tgatcctgct ggctgtctgg atctgagaca gggcatgttt 420
 gctcagctgg tggcccagaa cgtgtgtctg attgatggcc ctctgtcctg gtactctgat 480
 cctggattgg ctggcgtgtc cctgactggc ggctgtctt acaaagagga caccaaagaa 540
 ctgggtgggtgg ccaaggccgg cgtgtactac gtgttctttc agctggaact gcggagagtg 600
 gtggccggcg aaggatctgg atctgtgtct ctggcactgc atctgcagcc cctgagatct 660
 gctgcaggcg ctgctgtctt ggctctgaca gttgatctgc ctctgcctc ctccgaggcc 720
 agaaactccg cctttggctt ccaaggcaga ctgctgcatac tgtctgccgg ccagagactg 780
 ggagtccatc tgcatacaga ggctagagcc aggcacgcct ggcagttgac acaaggtgct 840
 acagtgtgg gcctgttcag agtgacccca gagattccag ccggcctgcc ttctccaaga 900
 tccgag 906

<210> 67

<211> 1029
 <212> DNA
 <213> Artificial sequence

<220>

<223> alternative nucleic acid sequence encoding SEQ ID NO: 2 (original
 SIRP fragment)

<400> 67

gaagaggaac tgcaagtgat ccagcctgac aagtccgtgc tggaggctgc tggcgaaacc	60
gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggtttaga	120
ggcgctggac ctggcagaga gctgatctac aaccagaaag agggccactt tcctagagt	180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac	240
atcacccctg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac	300
gacgtcgagt ttaaataccgg cgctggcacc gaactgtccg tgcgagctaa accttctgct	360
cccgtgggtg ctggccctgc cgctagagct acacctcagc acaccgtgtc ttttacctgc	420
gagtcccacg gcttcagccc tagagacatc accctgaagt ggttcaagaa cggcaacgag	480
ctgtccgact tccagaccaa cgtggaccct gtgggagagt ccgtgtccta ctccatccac	540
tctaccgcca aggtgggtgct gacccgagag gacgtgcaca gccaagtgat ctgtgaagt	600
gcccacgtga ccctccaggg cgatcctttg agaggcaccg ccaacctgtc cgagacaatc	660
agagtgcctc ctacactgga agtgacctag cagcctgtgc gggccgagaa tcaagtgaac	720
gtgacctgcc aagtgcggaa gttctaccct cagagactgc agctgacctg gctggaaaac	780
ggcaatgtgt ccagaaccga gacagcctcc accgtgaccg agaacaagga tggcacctac	840
aattggatgt cctggctgct cgtgaacgtg tccgctcaca gagatgacgt gaagctgaca	900
tgccagggtg aacacgatgg ccagcctgcc gtgtctaagt cccacgacct gaaagtgtct	960
gctcacccca aagagcaggg ctccaatacc gccgctgaga acaccggctc caacgagaga	1020
aacatctac	1029

<210> 68
 <211> 945
 <212> DNA
 <213> Artificial sequence

<220>

<223> nucleic acid SEQUENCE FOR SEQ ID NO: 21

<400> 68

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gaagaggaaa tccaagtgat ccagcctgac aagtccgtgc tggaggctgc tggcgaaacc      60
gccacactga gatgtacat cactctctg atccctgtgg gccctatcca gtggtttaga      120
ggcgctggac ctggcagagt gctgatctac aaccagaaag agggccactt tcctagagtg      180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac      240
atcacccctg ctgatgccgg cacctactac tgcataaagt tccggaaggg ctcccctgac      300
gacgtcgagt ttaaataccg cgctggcacc gagctgtccg tcagagcttc tgggtgctaga      360
gcctctcctg gctctgccgc ttctcctaga ctgagagagg gacctgagct gtctcctgat      420
gatcctgctg gcctgctgga tctgagacag ggcatgtttg ctcagctggg gggccagaac      480
gtgctgctga ttgatggccc tctgtcctgg tactctgatc ctggattggc tggcgtgtcc      540
ctgactggcg gcctgtctta caaagaggac accaaagaac tggagggtgg caaggccggc      600
gtgtactacg tgttctttca gctggaactg cggagagtgg tggccggcga aggatctgga      660
tctgtgtctc tggcactgca tctgcagcct ctgagatctg ctgcaggcgc tgctgctctg      720
gctctgacag ttgatctgcc tcctgcctcc tccgaggcca gaaactccgc ctttggcttc      780
caaggcagac tgctgcatct gtctgccggc cagagactgg gaggccatct gcatacagag      840
gccagagcta gacacgcttg gcagttgaca cagggcgcta cagtgtctggg cctgttcaga      900
gtgacacctg agatcccagc cggcctgcct tctccaagat ctgag                      945

```

<210> 69

<211> 1749

<212> DNA

<213> Artificial sequence

<220>

<223> Cloned sequence of the N-terminal his-tagged (NH)-DSP-107

<400> 69

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gaattcccg cgcaccatg ggctggctct gcatcattct gtttctgggt gccacagcca      60
ccggcgtgca ctctacat catcaccacc atgaagagga actgcaagt atccagcctg      120

```

acaagagcgt gctggtggct gctggcgaaa cagccacact gagatgtacc gccacctctc	180
tgatccctgt gggccctatc cagtgggttta gaggcgctgg acctggcaga gagctgatct	240
acaaccagaa agaggggacac ttccccagag tgaccaccgt gtccgacctg accaagcgga	300
acaacatgga cttcagcatc cggatcggca acatcacccc tgccgatgcc ggcacctact	360
actgctgaa gttcagaaaag ggcagccccg acgacgtcga gtttaaaagc ggagccggca	420
cagagctgag cgtgcgggct aaaccttctg ctctgtgggt gtctggacct gccgctagag	480
ctacacctca gcacaccgtg tcttttacct gcgagagcca cggcttcagc cccagagata	540
tcaccctgaa gtggttcaag aacggcaacg agctgtccga cttccagacc aacgtggacc	600
ctgtgggaga gagcgtgtcc tacagcatcc acagcacagc caaggtgggtg ctgaccggg	660
aagatgtgca ctccaagtg atttgcgagg tggcccacgt taccctgcaa ggcgatcctc	720
tgagaggcac cgccaatctg agcgagacaa tccgggtgcc acctacactg gaagtgaccc	780
agcagcctgt gcgggcccag aatcaagtga acgtgacctg ccaagtgcgg aagttctacc	840
ctcagagact gcagctgacc tggctggaaa acggcaatgt gtccagaacc gagacagcca	900
gcaccgtgac cgagaacaag gatggcacct acaattggat gagctggctg ctctgtaatg	960
tgtctgcca ccgggacgat gtgaagctga catgccaggt ggaacacgat ggccagcctg	1020
ccgtgtctaa gagccacgac ctgaagggtg ccgctcatcc caaagagcag ggctctaata	1080
ctgccgccga gaacaccggc agcaacgaga gaaatatcta cggcgcttgt ccttgggccg	1140
tttctggcgc tagagcctct cctggatctg ccgcttctcc cagactgaga gagggacctg	1200
agctgagccc tgatgatcct gctggactgc tggatctgag acagggcatg tttgcccagc	1260
tggtggccca gaatgtgctg ctgattgatg gccctctgtc ctggtacagc gatcctggac	1320
ttgctggcgt tagcctgact ggcggcctga gctacaaaga ggacaccaaa gaactgggtg	1380
tggccaaggc cggcgtgtac tacgtgttct ttcagctgga actgcggaga gtggtggccg	1440
gcgaaggatc tggatctgtg tctctggctc tgcacttgca gcctctgaga tctgctgctg	1500
gtgctgctgc tctggccctg acagttgatc tgccctctgc ctctagcgag gccagaaact	1560
ccgcctttgg cttccaaggc agactgctgc acctgagcgc tggacagaga ctgggagtcc	1620

atctgcacac agaagccaga gctagacacg cctggcagct gacacaaggc gctacagtgc 1680
 tgggcctgtt cagagtgacc cctgagattc cagccggcct gccatctcct agatctgagt 1740
 gataagctt 1749

<210> 70
 <211> 184
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 4-1BBL -21-0 184 aa

<400> 70

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> 71
 <211> 552
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 70

<400> 71
 agagaggggcc ctgagctgtc tcctgatgat cctgctggac tgctggacct gagacagggc 60
 atgtttgctc agctggtggc ccagaacgtg ctgctgattg atggccctct gtcctggtac 120
 tctgatcctg gattggctgg cgtgtccctg actggcggcc tgtcttaca agaggacacc 180
 aaagaactgg tggctgccaa 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 tcccagccgg cctgccatct 540
 ccaagatctg aa 552

<210> 72
 <211> 182
 <212> PRT
 <213> Artificial sequence

<220>

<223> 4-1BBL -23-0 182 aa

<400> 72

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> 73
<211> 546
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO: 72

<400> 73
ggccctgagc tgtctcctga tgatcctgct ggactgctgg acctgagaca gggcatgttt 60
gctcagctgg tggcccagaa cgtgctgctg attgatggcc ctctgtcctg gtactctgat 120
cctggattgg ctggcgtgtc cctgactggc ggccctgtctt acaaagagga caccaaagaa 180
ctgggtggctc 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
acagtgtgg gcctgtttag agtgacacct gagatcccag ccggcctgcc atctccaaga 540
tctgaa 546

<210> 74
<211> 183
<212> PRT
<213> Artificial sequence

<220>
<223> 4-1BBL -14-8 183 aa

<400> 74

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> 75

<211> 551

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO: 74 551 bp

```

<400> 75
gatctgccgc ttctcctaga ctgagagagg gccctgagct gtctcctgat gatcctgctg      60
gactgctgga cctgagacag ggcatgtttg ctcagctggg gggccagaac gtgctgctga      120
ttgatggccc tctgtcctgg tactctgatc ctggattggc tggcgtgtcc ctgactggcg      180
gcctgtctta caaagaggac accaaagaac tgggtggcgc caaggccggc gtgtactacg      240
tgttctttca 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 cagtgtggg cctgtttaga gtgacacctg      540
agatcccagc c                                                                551

```

```

<210> 76
<211> 176
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> 4-1BBL -21-8 176 aa

```

```

<400> 76

```

```

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

<210> 77

<211> 528

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO: 76 528 bp

<400> 77

agagagggcc ctgagctgtc tcctgatgat cctgctggac tgctggacct gagacagggc 60

atgtttgctc agctgggtggc ccagaacgtg ctgctgattg atggccctct gtcctggtac 120

tctgatacctg gattggctgg cgtgtccctg actggcggcc tgtcttataa agaggacacc 180

aaagaactgg tggctgcca aa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtgggtg ctggcgaagg atctggatct gtgtctctgg ccctgcatct gcagcctctg 300

agaagtgctg caggcgctgc tgactggct ctgacagttg atctgcctcc tgcctcctcc 360

gaggccagaa actccgcctt tggcttccaa ggcagactgc tgcactctgtc tgccggacag 420

agactgggag tgcacctcca tacagaggcc agagctagac acgcttggca gttgacacag 480

ggcgctacag tgctgggcct gtttagagtg acacctgaga tcccagcc

528

<210> 78

<211> 601

<212> PRT

<213> Artificial sequence

<220>

<223> sc3x4-1BBL -14-0 601 aa

<400> 78

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> 79
 <211> 1803
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO: 78

<400> 79
 tctgccgcca gccctaggct gcgcgaggga cccgagctga gcccagacga tcccgccggc 60
 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 tgggtactctg atcctggcct ggccggcgtg 780

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agcctgaccg gcggcctgtc ctacaaagag gatactaaag agctgggtgt 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 gccaaggct gcgcgaggga     1260
cccgagctgt cgctgacga tccagccggc ctgctggacc tgcgtcaggg catgttcgcc     1320
cagctgggtg ctcagaacgt 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 tgttccgcgt aaccccagag atccctgccg gcctgcccag ccctcgggtcc     1800
gag                                                                           1803

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```

<210> 80
<211> 535
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> DSP107_Var2

```

```

<400> 80

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

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 195 200 205

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 210 215 220

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 225 230 235 240

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 245 250 255

Asp Leu Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn
 260 265 270

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys
 275 280 285

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu
 290 295 300

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
 305 310 315 320

Arg Ala Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly
 325 330 335

Phe Ser Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu
 340 345 350

Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser
 355 360 365

Tyr Ser Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val
 370 375 380

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 385 390 395 400

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

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 420 425 430

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 435 440 445

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 450 455 460

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 465 470 475 480

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 485 490 495

His Asp Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser
 500 505 510

Ala His Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly
 515 520 525

Ser Asn Glu Arg Asn Ile Tyr
 530 535

<210> 81
 <211> 699
 <212> DNA
 <213> Artificial sequence

<220>
 <223> NA sequence of SEQ ID NO: 80

<400> 81
 tctgctgcct ctcctagact gagagaggga cctgagctgt ctctgatga tcctgctggc 60
 ctgctggatc tgagacaggg catgtttgct cagctgggtgg ccagaaactg gctgctgatt 120
 gatggccctc tgtcctggta ctctgatacct ggattggctg gcgtgtccct gactggcggc 180
 ctgtcttaca aagaggacac caaagaactg gtggtggcca aggccggcgt gtactacgtg 240

```

ttctttcagc tggaactgcg gagagtgggt gccggcgaag gatctggatc tgtgtctctg      300
gcactgcatc tgcagcccct gagatctgct gcaggcgctg ctgctctggc tctgacagtt      360
gatctgcctc ctgcctcctc cgaggccaga aactccgcct ttggcttcca aggcagactg      420
ctgcatctgt ctgccggcca gagactggga gtccatctgc atacagaggc tagagccagg      480
cacgcctggc agttgacaca aggtgctaca gtgctgggcc tggtcagagt gaccccagag      540
attccagccg gcctgccttc tccaagatcc gagggcgaag aggaactgca agtgatccag      600
cctgacaagt cctgtctggt ggctgctggc gaaaccgcca cactgagatg taccgccacc      660
tctctgatcc ctgtgggccc tatccagtgg tttagaggc                               699

```

```

<210> 82
<211> 14
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> polypeptide linker

```

```

<400> 82

```

```

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1           5           10

```

```

<210> 83
<211> 9
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> polypeptide linker

```

```

<400> 83

```

```

Gly Gly Gly Gly Ser Gly Gly Gly Gly
1           5

```

```

<210> 84
<211> 5
<212> PRT
<213> Artificial sequence

```

<220>

<223> polypeptide linker

<220>

<221> REPEAT

<222> (1)..(5)

<223> may repeat 1-4 times

<400> 84

Gly Gly Gly Gly Ser
1 5

<210> 85

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> polypeptide linker

<400> 85

Gly Gly Gly Gly Ser
1 5

<210> 86

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> polypeptide linker

<400> 86

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 87

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> polypeptide linker

<220>

<221> REPEAT

<222> (1)..(5)

<223> may repeat 1-3 times

<400> 87

Glu Ala Ala Ala Lys

1 5

<210> 88

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> polypeptide linker

<220>

<221> REPEAT

<222> (2)..(6)

<223> repeat 2-5 times

<400> 88

Ala Glu Ala Ala Ala Lys Ala

1 5

<210> 89

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> polypeptide linker

<400> 89

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala

1 5 10

<210> 90

<211> 46

<212> PRT
 <213> Artificial sequence

<220>
 <223> polypeptide linker

<400> 90

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> 91
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> polypeptide linker

<400> 91

Pro Ala Pro Ala Pro
 1 5

<210> 92
 <211> 18
 <212> PRT
 <213> Artificial sequence

<220>
 <223> polypeptide linker

<400> 92

Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
 1 5 10 15

Leu Asp

<210> 93
 <211> 14
 <212> PRT
 <213> Artificial sequence

<220>
 <223> polypeptide linker

<400> 93

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr
 1 5 10

<210> 94
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
 <223> polypeptide linker

<400> 94

Gly Ser Ala Gly Ser Ala Ala Gly Ser Gly Glu Phe
 1 5 10

<210> 95
 <211> 229
 <212> PRT
 <213> Artificial sequence

<220>
 <223> polypeptide linker

<400> 95

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> 96
 <211> 232
 <212> PRT
 <213> Artificial sequence

<220>
 <223> polypeptide linker

<400> 96

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> 97
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> polypeptide linker

<400> 97

Gly Leu Pro Ser Pro Arg Ser Glu
 1 5

<210> 98
 <211> 23
 <212> PRT
 <213> Artificial sequence

<220>
 <223> polypeptide linker

<400> 98

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> 99
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> polypeptide linker

<400> 99

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

Val Leu Ser