

SEQUENCE LISTING

<110> BRISTOL-MYERS SQUIBB COMPANY

<120> MINIATURIZED DYSTROPHINS HAVING SPECTRIN FUSION DOMAINS AND USES THEREOF

<130> 13391-WO-PCT

<150> US 63/017148

<151> 2020-04-29

<160> 113

<170> PatentIn version 3.5

<210> 1

<211> 3685

<212> PRT

<213> Homo sapiens

<400> 1

Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
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Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
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Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
35 40 45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
50 55 60

Glu Lys Gly Ser Thr Arg Val His Ala Leu Asn Asn Val Asn Lys Ala
65 70 75 80

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
85 90 95

Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
100 105 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
115 120 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
130 135 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145 150 155 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
165 170 175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
180 185 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
195 200 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
210 215 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225 230 235 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu Met Leu Pro Arg
245 250 255

Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu His His Gln Met
260 265 270

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

Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala Tyr Thr Gln Ala
290 295 300

Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro Phe Pro Ser Gln
305 310 315 320

His Leu Glu Ala Pro Glu Asp Lys Ser Phe Gly Ser Ser Leu Met Glu
325 330 335

Ser Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu

340

345

350

Ser Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile
 355 360 365

Ser Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly
 370 375 380

Tyr Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu
 385 390 395 400

Gln Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu
 405 410 415

Glu Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu
 420 425 430

Cys Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His Arg Val
 435 440 445

Leu Met Asp Leu Gln Asn Gln Lys Leu Lys Glu Leu Asn Asp Trp Leu
 450 455 460

Thr Lys Thr Glu Glu Arg Thr Arg Lys Met Glu Glu Glu Pro Leu Gly
 465 470 475 480

Pro Asp Leu Glu Asp Leu Lys Arg Gln Val Gln Gln His Lys Val Leu
 485 490 495

Gln Glu Asp Leu Glu Gln Glu Gln Val Arg Val Asn Ser Leu Thr His
 500 505 510

Met Val Val Val Val Asp Glu Ser Ser Gly Asp His Ala Thr Ala Ala
 515 520 525

Leu Glu Glu Gln Leu Lys Val Leu Gly Asp Arg Trp Ala Asn Ile Cys
 530 535 540

Arg Trp Thr Glu Asp Arg Trp Val Leu Leu Gln Asp Ile Leu Leu Lys
 545 550 555 560

Trp Gln Arg Leu Thr Glu Glu Gln Cys Leu Phe Ser Ala Trp Leu Ser
565 570 575

Glu Lys Glu Asp Ala Val Asn Lys Ile His Thr Thr Gly Phe Lys Asp
580 585 590

Gln Asn Glu Met Leu Ser Ser Leu Gln Lys Leu Ala Val Leu Lys Ala
595 600 605

Asp Leu Glu Lys Lys Lys Gln Ser Met Gly Lys Leu Tyr Ser Leu Lys
610 615 620

Gln Asp Leu Leu Ser Thr Leu Lys Asn Lys Ser Val Thr Gln Lys Thr
625 630 635 640

Glu Ala Trp Leu Asp Asn Phe Ala Arg Cys Trp Asp Asn Leu Val Gln
645 650 655

Lys Leu Glu Lys Ser Thr Ala Gln Ile Ser Gln Ala Val Thr Thr Thr
660 665 670

Gln Pro Ser Leu Thr Gln Thr Thr Val Met Glu Thr Val Thr Thr Val
675 680 685

Thr Thr Arg Glu Gln Ile Leu Val Lys His Ala Gln Glu Glu Leu Pro
690 695 700

Pro Pro Pro Pro Gln Lys Lys Arg Gln Ile Thr Val Asp Ser Glu Ile
705 710 715 720

Arg Lys Arg Leu Asp Val Asp Ile Thr Glu Leu His Ser Trp Ile Thr
725 730 735

Arg Ser Glu Ala Val Leu Gln Ser Pro Glu Phe Ala Ile Phe Arg Lys
740 745 750

Glu Gly Asn Phe Ser Asp Leu Lys Glu Lys Val Asn Ala Ile Glu Arg
755 760 765

Glu Lys Ala Glu Lys Phe Arg Lys Leu Gln Asp Ala Ser Arg Ser Ala

770

775

780

Gln Ala Leu Val Glu Gln Met Val Asn Glu Gly Val Asn Ala Asp Ser
 785 790 795 800

Ile Lys Gln Ala Ser Glu Gln Leu Asn Ser Arg Trp Ile Glu Phe Cys
 805 810 815

Gln Leu Leu Ser Glu Arg Leu Asn Trp Leu Glu Tyr Gln Asn Asn Ile
 820 825 830

Ile Ala Phe Tyr Asn Gln Leu Gln Gln Leu Glu Gln Met Thr Thr Thr
 835 840 845

Ala Glu Asn Trp Leu Lys Ile Gln Pro Thr Thr Pro Ser Glu Pro Thr
 850 855 860

Ala Ile Lys Ser Gln Leu Lys Ile Cys Lys Asp Glu Val Asn Arg Leu
 865 870 875 880

Ser Gly Leu Gln Pro Gln Ile Glu Arg Leu Lys Ile Gln Ser Ile Ala
 885 890 895

Leu Lys Glu Lys Gly Gln Gly Pro Met Phe Leu Asp Ala Asp Phe Val
 900 905 910

Ala Phe Thr Asn His Phe Lys Gln Val Phe Ser Asp Val Gln Ala Arg
 915 920 925

Glu Lys Glu Leu Gln Thr Ile Phe Asp Thr Leu Pro Pro Met Arg Tyr
 930 935 940

Gln Glu Thr Met Ser Ala Ile Arg Thr Trp Val Gln Gln Ser Glu Thr
 945 950 955 960

Lys Leu Ser Ile Pro Gln Leu Ser Val Thr Asp Tyr Glu Ile Met Glu
 965 970 975

Gln Arg Leu Gly Glu Leu Gln Ala Leu Gln Ser Ser Leu Gln Glu Gln
 980 985 990

Gln Ser Gly Leu Tyr Tyr Leu Ser Thr Thr Val Lys Glu Met Ser Lys
995 1000 1005

Lys Ala Pro Ser Glu Ile Ser Arg Lys Tyr Gln Ser Glu Phe Glu
1010 1015 1020

Glu Ile Glu Gly Arg Trp Lys Lys Leu Ser Ser Gln Leu Val Glu
1025 1030 1035

His Cys Gln Lys Leu Glu Glu Gln Met Asn Lys Leu Arg Lys Ile
1040 1045 1050

Gln Asn His Ile Gln Thr Leu Lys Lys Trp Met Ala Glu Val Asp
1055 1060 1065

Val Phe Leu Lys Glu Glu Trp Pro Ala Leu Gly Asp Ser Glu Ile
1070 1075 1080

Leu Lys Lys Gln Leu Lys Gln Cys Arg Leu Leu Val Ser Asp Ile
1085 1090 1095

Gln Thr Ile Gln Pro Ser Leu Asn Ser Val Asn Glu Gly Gly Gln
1100 1105 1110

Lys Ile Lys Asn Glu Ala Glu Pro Glu Phe Ala Ser Arg Leu Glu
1115 1120 1125

Thr Glu Leu Lys Glu Leu Asn Thr Gln Trp Asp His Met Cys Gln
1130 1135 1140

Gln Val Tyr Ala Arg Lys Glu Ala Leu Lys Gly Gly Leu Glu Lys
1145 1150 1155

Thr Val Ser Leu Gln Lys Asp Leu Ser Glu Met His Glu Trp Met
1160 1165 1170

Thr Gln Ala Glu Glu Glu Tyr Leu Glu Arg Asp Phe Glu Tyr Lys
1175 1180 1185

Thr Pro Asp Glu Leu Gln Lys Ala Val Glu Glu Met Lys Arg Ala

1190						1195						1200			
Lys	Glu	Glu	Ala	Gln	Gln	Lys	Glu	Ala	Lys	Val	Lys	Leu	Leu	Thr	
1205						1210					1215				
Glu	Ser	Val	Asn	Ser	Val	Ile	Ala	Gln	Ala	Pro	Pro	Val	Ala	Gln	
1220						1225					1230				
Glu	Ala	Leu	Lys	Lys	Glu	Leu	Glu	Thr	Leu	Thr	Thr	Asn	Tyr	Gln	
1235						1240					1245				
Trp	Leu	Cys	Thr	Arg	Leu	Asn	Gly	Lys	Cys	Lys	Thr	Leu	Glu	Glu	
1250						1255					1260				
Val	Trp	Ala	Cys	Trp	His	Glu	Leu	Leu	Ser	Tyr	Leu	Glu	Lys	Ala	
1265						1270					1275				
Asn	Lys	Trp	Leu	Asn	Glu	Val	Glu	Phe	Lys	Leu	Lys	Thr	Thr	Glu	
1280						1285					1290				
Asn	Ile	Pro	Gly	Gly	Ala	Glu	Glu	Ile	Ser	Glu	Val	Leu	Asp	Ser	
1295						1300					1305				
Leu	Glu	Asn	Leu	Met	Arg	His	Ser	Glu	Asp	Asn	Pro	Asn	Gln	Ile	
1310						1315					1320				
Arg	Ile	Leu	Ala	Gln	Thr	Leu	Thr	Asp	Gly	Gly	Val	Met	Asp	Glu	
1325						1330					1335				
Leu	Ile	Asn	Glu	Glu	Leu	Glu	Thr	Phe	Asn	Ser	Arg	Trp	Arg	Glu	
1340						1345					1350				
Leu	His	Glu	Glu	Ala	Val	Arg	Arg	Gln	Lys	Leu	Leu	Glu	Gln	Ser	
1355						1360					1365				
Ile	Gln	Ser	Ala	Gln	Glu	Thr	Glu	Lys	Ser	Leu	His	Leu	Ile	Gln	
1370						1375					1380				
Glu	Ser	Leu	Thr	Phe	Ile	Asp	Lys	Gln	Leu	Ala	Ala	Tyr	Ile	Ala	
1385						1390					1395				

Asp Lys Val Asp Ala Ala Gln Met Pro Gln Glu Ala Gln Lys Ile
1400 1405 1410

Gln Ser Asp Leu Thr Ser His Glu Ile Ser Leu Glu Glu Met Lys
1415 1420 1425

Lys His Asn Gln Gly Lys Glu Ala Ala Gln Arg Val Leu Ser Gln
1430 1435 1440

Ile Asp Val Ala Gln Lys Lys Leu Gln Asp Val Ser Met Lys Phe
1445 1450 1455

Arg Leu Phe Gln Lys Pro Ala Asn Phe Glu Gln Arg Leu Gln Glu
1460 1465 1470

Ser Lys Met Ile Leu Asp Glu Val Lys Met His Leu Pro Ala Leu
1475 1480 1485

Glu Thr Lys Ser Val Glu Gln Glu Val Val Gln Ser Gln Leu Asn
1490 1495 1500

His Cys Val Asn Leu Tyr Lys Ser Leu Ser Glu Val Lys Ser Glu
1505 1510 1515

Val Glu Met Val Ile Lys Thr Gly Arg Gln Ile Val Gln Lys Lys
1520 1525 1530

Gln Thr Glu Asn Pro Lys Glu Leu Asp Glu Arg Val Thr Ala Leu
1535 1540 1545

Lys Leu His Tyr Asn Glu Leu Gly Ala Lys Val Thr Glu Arg Lys
1550 1555 1560

Gln Gln Leu Glu Lys Cys Leu Lys Leu Ser Arg Lys Met Arg Lys
1565 1570 1575

Glu Met Asn Val Leu Thr Glu Trp Leu Ala Ala Thr Asp Met Glu
1580 1585 1590

Leu Thr Lys Arg Ser Ala Val Glu Gly Met Pro Ser Asn Leu Asp

1595

1600

1605

Ser Glu Val Ala Trp Gly Lys Ala Thr Gln Lys Glu Ile Glu Lys
1610 1615 1620

Gln Lys Val His Leu Lys Ser Ile Thr Glu Val Gly Glu Ala Leu
1625 1630 1635

Lys Thr Val Leu Gly Lys Lys Glu Thr Leu Val Glu Asp Lys Leu
1640 1645 1650

Ser Leu Leu Asn Ser Asn Trp Ile Ala Val Thr Ser Arg Ala Glu
1655 1660 1665

Glu Trp Leu Asn Leu Leu Leu Glu Tyr Gln Lys His Met Glu Thr
1670 1675 1680

Phe Asp Gln Asn Val Asp His Ile Thr Lys Trp Ile Ile Gln Ala
1685 1690 1695

Asp Thr Leu Leu Asp Glu Ser Glu Lys Lys Lys Pro Gln Gln Lys
1700 1705 1710

Glu Asp Val Leu Lys Arg Leu Lys Ala Glu Leu Asn Asp Ile Arg
1715 1720 1725

Pro Lys Val Asp Ser Thr Arg Asp Gln Ala Ala Asn Leu Met Ala
1730 1735 1740

Asn Arg Gly Asp His Cys Arg Lys Leu Val Glu Pro Gln Ile Ser
1745 1750 1755

Glu Leu Asn His Arg Phe Ala Ala Ile Ser His Arg Ile Lys Thr
1760 1765 1770

Gly Lys Ala Ser Ile Pro Leu Lys Glu Leu Glu Gln Phe Asn Ser
1775 1780 1785

Asp Ile Gln Lys Leu Leu Glu Pro Leu Glu Ala Glu Ile Gln Gln
1790 1795 1800

Gly	Val	Asn	Leu	Lys	Glu	Glu	Asp	Phe	Asn	Lys	Asp	Met	Asn	Glu
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Asp	Asn	Glu	Gly	Thr	Val	Lys	Glu	Leu	Leu	Gln	Arg	Gly	Asp	Asn
1820						1825					1830			
Leu	Gln	Gln	Arg	Ile	Thr	Asp	Glu	Arg	Lys	Arg	Glu	Glu	Ile	Lys
1835						1840					1845			
Ile	Lys	Gln	Gln	Leu	Leu	Gln	Thr	Lys	His	Asn	Ala	Leu	Lys	Asp
1850						1855					1860			
Leu	Arg	Ser	Gln	Arg	Arg	Lys	Lys	Ala	Leu	Glu	Ile	Ser	His	Gln
1865						1870					1875			
Trp	Tyr	Gln	Tyr	Lys	Arg	Gln	Ala	Asp	Asp	Leu	Leu	Lys	Cys	Leu
1880						1885					1890			
Asp	Asp	Ile	Glu	Lys	Lys	Leu	Ala	Ser	Leu	Pro	Glu	Pro	Arg	Asp
1895						1900					1905			
Glu	Arg	Lys	Ile	Lys	Glu	Ile	Asp	Arg	Glu	Leu	Gln	Lys	Lys	Lys
1910						1915					1920			
Glu	Glu	Leu	Asn	Ala	Val	Arg	Arg	Gln	Ala	Glu	Gly	Leu	Ser	Glu
1925						1930					1935			
Asp	Gly	Ala	Ala	Met	Ala	Val	Glu	Pro	Thr	Gln	Ile	Gln	Leu	Ser
1940						1945					1950			
Lys	Arg	Trp	Arg	Glu	Ile	Glu	Ser	Lys	Phe	Ala	Gln	Phe	Arg	Arg
1955						1960					1965			
Leu	Asn	Phe	Ala	Gln	Ile	His	Thr	Val	Arg	Glu	Glu	Thr	Met	Met
1970						1975					1980			
Val	Met	Thr	Glu	Asp	Met	Pro	Leu	Glu	Ile	Ser	Tyr	Val	Pro	Ser
1985						1990					1995			
Thr	Tyr	Leu	Thr	Glu	Ile	Thr	His	Val	Ser	Gln	Ala	Leu	Leu	Glu

2000	2005	2010
Val Glu Gln Leu Leu Asn Ala 2015 2020	Pro Asp Leu Cys	Ala Lys Asp Phe 2025
Glu Asp Leu Phe Lys Gln 2030 2035	Glu Ser Leu Lys	Asn Ile Lys Asp 2040
Ser Leu Gln Gln Ser Ser 2045 2050	Gly Arg Ile Asp Ile	Ile His Ser Lys 2055
Lys Thr Ala Ala Leu Gln 2060 2065	Ser Ala Thr Pro Val	Glu Arg Val Lys 2070
Leu Gln Glu Ala Leu Ser 2075 2080	Gln Leu Asp Phe Gln	Trp Glu Lys Val 2085
Asn Lys Met Tyr Lys Asp 2090 2095	Arg Gln Gly Arg Phe	Asp Arg Ser Val 2100
Glu Lys Trp Arg Arg Phe 2105 2110	His Tyr Asp Ile Lys	Ile Phe Asn Gln 2115
Trp Leu Thr Glu Ala Glu 2120 2125	Gln Phe Leu Arg Lys	Thr Gln Ile Pro 2130
Glu Asn Trp Glu His Ala 2135 2140	Lys Tyr Lys Trp Tyr	Leu Lys Glu Leu 2145
Gln Asp Gly Ile Gly Gln 2150 2155	Arg Gln Thr Val Val	Arg Thr Leu Asn 2160
Ala Thr Gly Glu Glu Ile 2165 2170	Ile Gln Gln Ser Ser	Lys Thr Asp Ala 2175
Ser Ile Leu Gln Glu Lys 2180 2185	Leu Gly Ser Leu Asn	Leu Arg Trp Gln 2190
Glu Val Cys Lys Gln Leu 2195 2200	Ser Asp Arg Lys Lys	Arg Leu Glu Glu 2205

Gln Lys Asn Ile Leu Ser Glu Phe Gln Arg Asp Leu Asn Glu Phe
2210 2215 2220

Val Leu Trp Leu Glu Glu Ala Asp Asn Ile Ala Ser Ile Pro Leu
2225 2230 2235

Glu Pro Gly Lys Glu Gln Gln Leu Lys Glu Lys Leu Glu Gln Val
2240 2245 2250

Lys Leu Leu Val Glu Glu Leu Pro Leu Arg Gln Gly Ile Leu Lys
2255 2260 2265

Gln Leu Asn Glu Thr Gly Gly Pro Val Leu Val Ser Ala Pro Ile
2270 2275 2280

Ser Pro Glu Glu Gln Asp Lys Leu Glu Asn Lys Leu Lys Gln Thr
2285 2290 2295

Asn Leu Gln Trp Ile Lys Val Ser Arg Ala Leu Pro Glu Lys Gln
2300 2305 2310

Gly Glu Ile Glu Ala Gln Ile Lys Asp Leu Gly Gln Leu Glu Lys
2315 2320 2325

Lys Leu Glu Asp Leu Glu Glu Gln Leu Asn His Leu Leu Leu Trp
2330 2335 2340

Leu Ser Pro Ile Arg Asn Gln Leu Glu Ile Tyr Asn Gln Pro Asn
2345 2350 2355

Gln Glu Gly Pro Phe Asp Val Gln Glu Thr Glu Ile Ala Val Gln
2360 2365 2370

Ala Lys Gln Pro Asp Val Glu Glu Ile Leu Ser Lys Gly Gln His
2375 2380 2385

Leu Tyr Lys Glu Lys Pro Ala Thr Gln Pro Val Lys Arg Lys Leu
2390 2395 2400

Glu Asp Leu Ser Ser Glu Trp Lys Ala Val Asn Arg Leu Leu Gln

2405

2410

2415

Glu Leu Arg Ala Lys Gln Pro Asp Leu Ala Pro Gly Leu Thr Thr
 2420 2425 2430

Ile Gly Ala Ser Pro Thr Gln Thr Val Thr Leu Val Thr Gln Pro
 2435 2440 2445

Val Val Thr Lys Glu Thr Ala Ile Ser Lys Leu Glu Met Pro Ser
 2450 2455 2460

Ser Leu Met Leu Glu Val Pro Ala Leu Ala Asp Phe Asn Arg Ala
 2465 2470 2475

Trp Thr Glu Leu Thr Asp Trp Leu Ser Leu Leu Asp Gln Val Ile
 2480 2485 2490

Lys Ser Gln Arg Val Met Val Gly Asp Leu Glu Asp Ile Asn Glu
 2495 2500 2505

Met Ile Ile Lys Gln Lys Ala Thr Met Gln Asp Leu Glu Gln Arg
 2510 2515 2520

Arg Pro Gln Leu Glu Glu Leu Ile Thr Ala Ala Gln Asn Leu Lys
 2525 2530 2535

Asn Lys Thr Ser Asn Gln Glu Ala Arg Thr Ile Ile Thr Asp Arg
 2540 2545 2550

Ile Glu Arg Ile Gln Asn Gln Trp Asp Glu Val Gln Glu His Leu
 2555 2560 2565

Gln Asn Arg Arg Gln Gln Leu Asn Glu Met Leu Lys Asp Ser Thr
 2570 2575 2580

Gln Trp Leu Glu Ala Lys Glu Glu Ala Glu Gln Val Leu Gly Gln
 2585 2590 2595

Ala Arg Ala Lys Leu Glu Ser Trp Lys Glu Gly Pro Tyr Thr Val
 2600 2605 2610

Asp Ala Ile Gln Lys Lys Ile Thr Glu Thr Lys Gln Leu Ala Lys
2615 2620 2625

Asp Leu Arg Gln Trp Gln Thr Asn Val Asp Val Ala Asn Asp Leu
2630 2635 2640

Ala Leu Lys Leu Leu Arg Asp Tyr Ser Ala Asp Asp Thr Arg Lys
2645 2650 2655

Val His Met Ile Thr Glu Asn Ile Asn Ala Ser Trp Arg Ser Ile
2660 2665 2670

His Lys Arg Val Ser Glu Arg Glu Ala Ala Leu Glu Glu Thr His
2675 2680 2685

Arg Leu Leu Gln Gln Phe Pro Leu Asp Leu Glu Lys Phe Leu Ala
2690 2695 2700

Trp Leu Thr Glu Ala Glu Thr Thr Ala Asn Val Leu Gln Asp Ala
2705 2710 2715

Thr Arg Lys Glu Arg Leu Leu Glu Asp Ser Lys Gly Val Lys Glu
2720 2725 2730

Leu Met Lys Gln Trp Gln Asp Leu Gln Gly Glu Ile Glu Ala His
2735 2740 2745

Thr Asp Val Tyr His Asn Leu Asp Glu Asn Ser Gln Lys Ile Leu
2750 2755 2760

Arg Ser Leu Glu Gly Ser Asp Asp Ala Val Leu Leu Gln Arg Arg
2765 2770 2775

Leu Asp Asn Met Asn Phe Lys Trp Ser Glu Leu Arg Lys Lys Ser
2780 2785 2790

Leu Asn Ile Arg Ser His Leu Glu Ala Ser Ser Asp Gln Trp Lys
2795 2800 2805

Arg Leu His Leu Ser Leu Gln Glu Leu Leu Val Trp Leu Gln Leu

2810

2815

2820

Lys Asp Asp Glu Leu Ser Arg Gln Ala Pro Ile Gly Gly Asp Phe
 2825 2830 2835

Pro Ala Val Gln Lys Gln Asn Asp Val His Arg Ala Phe Lys Arg
 2840 2845 2850

Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser Thr Leu Glu Thr
 2855 2860 2865

Val Arg Ile Phe Leu Thr Glu Gln Pro Leu Glu Gly Leu Glu Lys
 2870 2875 2880

Leu Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg Ala Gln
 2885 2890 2895

Asn Val Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn Thr
 2900 2905 2910

Glu Trp Glu Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys
 2915 2920 2925

Ile Asp Glu Thr Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr
 2930 2935 2940

Asp Glu Leu Asp Leu Lys Leu Arg Gln Ala Glu Val Ile Lys Gly
 2945 2950 2955

Ser Trp Gln Pro Val Gly Asp Leu Leu Ile Asp Ser Leu Gln Asp
 2960 2965 2970

His Leu Glu Lys Val Lys Ala Leu Arg Gly Glu Ile Ala Pro Leu
 2975 2980 2985

Lys Glu Asn Val Ser His Val Asn Asp Leu Ala Arg Gln Leu Thr
 2990 2995 3000

Thr Leu Gly Ile Gln Leu Ser Pro Tyr Asn Leu Ser Thr Leu Glu
 3005 3010 3015

Asp Leu Asn Thr Arg Trp Lys Leu Leu Gln Val Ala Val Glu Asp
3020 3025 3030

Arg Val Arg Gln Leu His Glu Ala His Arg Asp Phe Gly Pro Ala
3035 3040 3045

Ser Gln His Phe Leu Ser Thr Ser Val Gln Gly Pro Trp Glu Arg
3050 3055 3060

Ala Ile Ser Pro Asn Lys Val Pro Tyr Tyr Ile Asn His Glu Thr
3065 3070 3075

Gln Thr Thr Cys Trp Asp His Pro Lys Met Thr Glu Leu Tyr Gln
3080 3085 3090

Ser Leu Ala Asp Leu Asn Asn Val Arg Phe Ser Ala Tyr Arg Thr
3095 3100 3105

Ala Met Lys Leu Arg Arg Leu Gln Lys Ala Leu Cys Leu Asp Leu
3110 3115 3120

Leu Ser Leu Ser Ala Ala Cys Asp Ala Leu Asp Gln His Asn Leu
3125 3130 3135

Lys Gln Asn Asp Gln Pro Met Asp Ile Leu Gln Ile Ile Asn Cys
3140 3145 3150

Leu Thr Thr Ile Tyr Asp Arg Leu Glu Gln Glu His Asn Asn Leu
3155 3160 3165

Val Asn Val Pro Leu Cys Val Asp Met Cys Leu Asn Trp Leu Leu
3170 3175 3180

Asn Val Tyr Asp Thr Gly Arg Thr Gly Arg Ile Arg Val Leu Ser
3185 3190 3195

Phe Lys Thr Gly Ile Ile Ser Leu Cys Lys Ala His Leu Glu Asp
3200 3205 3210

Lys Tyr Arg Tyr Leu Phe Lys Gln Val Ala Ser Ser Thr Gly Phe

3215						3220						3225			
Cys	Asp	Gln	Arg	Arg	Leu	Gly	Leu	Leu	Leu	His	Asp	Ser	Ile	Gln	
	3230					3235					3240				
Ile	Pro	Arg	Gln	Leu	Gly	Glu	Val	Ala	Ser	Phe	Gly	Gly	Ser	Asn	
	3245					3250					3255				
Ile	Glu	Pro	Ser	Val	Arg	Ser	Cys	Phe	Gln	Phe	Ala	Asn	Asn	Lys	
	3260					3265					3270				
Pro	Glu	Ile	Glu	Ala	Ala	Leu	Phe	Leu	Asp	Trp	Met	Arg	Leu	Glu	
	3275					3280					3285				
Pro	Gln	Ser	Met	Val	Trp	Leu	Pro	Val	Leu	His	Arg	Val	Ala	Ala	
	3290					3295					3300				
Ala	Glu	Thr	Ala	Lys	His	Gln	Ala	Lys	Cys	Asn	Ile	Cys	Lys	Glu	
	3305					3310					3315				
Cys	Pro	Ile	Ile	Gly	Phe	Arg	Tyr	Arg	Ser	Leu	Lys	His	Phe	Asn	
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Tyr	Asp	Ile	Cys	Gln	Ser	Cys	Phe	Phe	Ser	Gly	Arg	Val	Ala	Lys	
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Gly	His	Lys	Met	His	Tyr	Pro	Met	Val	Glu	Tyr	Cys	Thr	Pro	Thr	
	3350					3355					3360				
Thr	Ser	Gly	Glu	Asp	Val	Arg	Asp	Phe	Ala	Lys	Val	Leu	Lys	Asn	
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Lys	Phe	Arg	Thr	Lys	Arg	Tyr	Phe	Ala	Lys	His	Pro	Arg	Met	Gly	
	3380					3385					3390				
Tyr	Leu	Pro	Val	Gln	Thr	Val	Leu	Glu	Gly	Asp	Asn	Met	Glu	Thr	
	3395					3400					3405				
Pro	Val	Thr	Leu	Ile	Asn	Phe	Trp	Pro	Val	Asp	Ser	Ala	Pro	Ala	
	3410					3415					3420				

Ser Ser Pro Gln Leu Ser His Asp Asp Thr His Ser Arg Ile Glu
3425 3430 3435

His Tyr Ala Ser Arg Leu Ala Glu Met Glu Asn Ser Asn Gly Ser
3440 3445 3450

Tyr Leu Asn Asp Ser Ile Ser Pro Asn Glu Ser Ile Asp Asp Glu
3455 3460 3465

His Leu Leu Ile Gln His Tyr Cys Gln Ser Leu Asn Gln Asp Ser
3470 3475 3480

Pro Leu Ser Gln Pro Arg Ser Pro Ala Gln Ile Leu Ile Ser Leu
3485 3490 3495

Glu Ser Glu Glu Arg Gly Glu Leu Glu Arg Ile Leu Ala Asp Leu
3500 3505 3510

Glu Glu Glu Asn Arg Asn Leu Gln Ala Glu Tyr Asp Arg Leu Lys
3515 3520 3525

Gln Gln His Glu His Lys Gly Leu Ser Pro Leu Pro Ser Pro Pro
3530 3535 3540

Glu Met Met Pro Thr Ser Pro Gln Ser Pro Arg Asp Ala Glu Leu
3545 3550 3555

Ile Ala Glu Ala Lys Leu Leu Arg Gln His Lys Gly Arg Leu Glu
3560 3565 3570

Ala Arg Met Gln Ile Leu Glu Asp His Asn Lys Gln Leu Glu Ser
3575 3580 3585

Gln Leu His Arg Leu Arg Gln Leu Leu Glu Gln Pro Gln Ala Glu
3590 3595 3600

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gttttgtcca ttattaataa ttaattaatt aacatcaaac acggcttctc atgctatttc	13200
tacctcactt tggttttggg gtgttcctga taattgtgca cacctgagtt cacagcttca	13260
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gtttttcttt tagacacatt agctctggag tgagtctgtc ataatatattg aacaaaaatt	13620
gagagcttta ttgctgcatt ttaagcataa ttaatttgga cattatttcg tgttgtgttc	13680
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gttttaacac caacactgta acatttacga attatttttt taaacttcag ttttactgca	13860

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<210> 3

<211> 252

<212> PRT

<213> Homo sapiens

<400> 3

Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
1 5 10 15

Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
20 25 30

Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
35 40 45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
50 55 60

Glu Lys Gly Ser Thr Arg Val His Ala Leu Asn Asn Val Asn Lys Ala
65 70 75 80

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
85 90 95

Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
100 105 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
115 120 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
130 135 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145 150 155 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His

165

170

175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
 180 185 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
 195 200 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
 210 215 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
 225 230 235 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu
 245 250

<210> 4
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Leu Pro Arg Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu
 1 5 10 15

His His Gln Met His Tyr Ser Gln Gln Ile Thr Val Ser Leu Ala Gln
 20 25 30

Gly Tyr Glu Arg Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala
 35 40 45

Tyr Thr Gln Ala Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro
 50 55 60

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

Ser Leu Met Glu Ser
 85

<210> 5
<211> 109
<212> PRT
<213> Homo sapiens

<400> 5

Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu Ser
1 5 10 15

Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile Ser
20 25 30

Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly Tyr
35 40 45

Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu Gln
50 55 60

Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu Glu
65 70 75 80

Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu Cys
85 90 95

Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His
100 105

<210> 6
<211> 111
<212> PRT
<213> Homo sapiens

<400> 6

Arg Val Leu Met Asp Leu Gln Asn Gln Lys Leu Lys Glu Leu Asn Asp
1 5 10 15

Trp Leu Thr Lys Thr Glu Glu Arg Thr Arg Lys Met Glu Glu Glu Pro
20 25 30

Leu Gly Pro Asp Leu Glu Asp Leu Lys Arg Gln Val Gln Gln His Lys
35 40 45

Val Leu Gln Glu Asp Leu Glu Gln Glu Gln Val Arg Val Asn Ser Leu
50 55 60

Thr His Met Val Val Val Val Asp Glu Ser Ser Gly Asp His Ala Thr
65 70 75 80

Ala Ala Leu Glu Glu Gln Leu Lys Val Leu Gly Asp Arg Trp Ala Asn
85 90 95

Ile Cys Arg Trp Thr Glu Asp Arg Trp Val Leu Leu Gln Asp Ile
100 105 110

<210> 7
<211> 111
<212> PRT
<213> Homo sapiens

<400> 7

Leu Leu Lys Trp Gln Arg Leu Thr Glu Glu Gln Cys Leu Phe Ser Ala
1 5 10 15

Trp Leu Ser Glu Lys Glu Asp Ala Val Asn Lys Ile His Thr Thr Gly
20 25 30

Phe Lys Asp Gln Asn Glu Met Leu Ser Ser Leu Gln Lys Leu Ala Val
35 40 45

Leu Lys Ala Asp Leu Glu Lys Lys Lys Gln Ser Met Gly Lys Leu Tyr
50 55 60

Ser Leu Lys Gln Asp Leu Leu Ser Thr Leu Lys Asn Lys Ser Val Thr
65 70 75 80

Gln Lys Thr Glu Ala Trp Leu Asp Asn Phe Ala Arg Cys Trp Asp Asn
85 90 95

Leu Val Gln Lys Leu Glu Lys Ser Thr Ala Gln Ile Ser Gln Ala
100 105 110

<210> 8
<211> 49
<212> PRT

<213> Homo sapiens

<400> 8

Val Thr Thr Thr Gln Pro Ser Leu Thr Gln Thr Thr Val Met Glu Thr
1 5 10 15

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

Glu Glu Leu Pro Pro Pro Pro Pro Gln Lys Lys Arg Gln Ile Thr Val
35 40 45

Asp

<210> 9

<211> 111

<212> PRT

<213> Homo sapiens

<400> 9

Ser Glu Ile Arg Lys Arg Leu Asp Val Asp Ile Thr Glu Leu His Ser
1 5 10 15

Trp Ile Thr Arg Ser Glu Ala Val Leu Gln Ser Pro Glu Phe Ala Ile
20 25 30

Phe Arg Lys Glu Gly Asn Phe Ser Asp Leu Lys Glu Lys Val Asn Ala
35 40 45

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

Arg Ser Ala Gln Ala Leu Val Glu Gln Met Val Asn Glu Gly Val Asn
65 70 75 80

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

Glu Phe Cys Gln Leu Leu Ser Glu Arg Leu Asn Trp Leu Glu Tyr
100 105 110

<210> 10
<211> 109
<212> PRT
<213> Homo sapiens

<400> 10

Gln Asn Asn Ile Ile Ala Phe Tyr Asn Gln Leu Gln Gln Leu Glu Gln
1 5 10 15

Met Thr Thr Thr Ala Glu Asn Trp Leu Lys Ile Gln Pro Thr Thr Pro
20 25 30

Ser Glu Pro Thr Ala Ile Lys Ser Gln Leu Lys Ile Cys Lys Asp Glu
35 40 45

Val Asn Arg Leu Ser Gly Leu Gln Pro Gln Ile Glu Arg Leu Lys Ile
50 55 60

Gln Ser Ile Ala Leu Lys Glu Lys Gly Gln Gly Pro Met Phe Leu Asp
65 70 75 80

Ala Asp Phe Val Ala Phe Thr Asn His Phe Lys Gln Val Phe Ser Asp
85 90 95

Val Gln Ala Arg Glu Lys Glu Leu Gln Thr Ile Phe Asp
100 105

<210> 11
<211> 109
<212> PRT
<213> Homo sapiens

<400> 11

Thr Leu Pro Pro Met Arg Tyr Gln Glu Thr Met Ser Ala Ile Arg Thr
1 5 10 15

Trp Val Gln Gln Ser Glu Thr Lys Leu Ser Ile Pro Gln Leu Ser Val
20 25 30

Thr Asp Tyr Glu Ile Met Glu Gln Arg Leu Gly Glu Leu Gln Ala Leu
35 40 45

Gln Ser Ser Leu Gln Glu Gln Gln Ser Gly Leu Tyr Tyr Leu Ser Thr
50 55 60

Thr Val Lys Glu Met Ser Lys Lys Ala Pro Ser Glu Ile Ser Arg Lys
65 70 75 80

Tyr Gln Ser Glu Phe Glu Glu Ile Glu Gly Arg Trp Lys Lys Leu Ser
85 90 95

Ser Gln Leu Val Glu His Cys Gln Lys Leu Glu Glu Gln
100 105

<210> 12
<211> 109
<212> PRT
<213> Homo sapiens

<400> 12

Met Asn Lys Leu Arg Lys Ile Gln Asn His Ile Gln Thr Leu Lys Lys
1 5 10 15

Trp Met Ala Glu Val Asp Val Phe Leu Lys Glu Glu Trp Pro Ala Leu
20 25 30

Gly Asp Ser Glu Ile Leu Lys Lys Gln Leu Lys Gln Cys Arg Leu Leu
35 40 45

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

Gly Gly Gln Lys Ile Lys Asn Glu Ala Glu Pro Glu Phe Ala Ser Arg
65 70 75 80

Leu Glu Thr Glu Leu Lys Glu Leu Asn Thr Gln Trp Asp His Met Cys
85 90 95

Gln Gln Val Tyr Ala Arg Lys Glu Ala Leu Lys Gly Gly
100 105

<210> 13
<211> 109

<212> PRT
<213> Homo sapiens

<400> 13

Leu Glu Lys Thr Val Ser Leu Gln Lys Asp Leu Ser Glu Met His Glu
1 5 10 15

Trp Met Thr Gln Ala Glu Glu Glu Tyr Leu Glu Arg Asp Phe Glu Tyr
20 25 30

Lys Thr Pro Asp Glu Leu Gln Lys Ala Val Glu Glu Met Lys Arg Ala
35 40 45

Lys Glu Glu Ala Gln Gln Lys Glu Ala Lys Val Lys Leu Leu Thr Glu
50 55 60

Ser Val Asn Ser Val Ile Ala Gln Ala Pro Pro Val Ala Gln Glu Ala
65 70 75 80

Leu Lys Lys Glu Leu Glu Thr Leu Thr Thr Asn Tyr Gln Trp Leu Cys
85 90 95

Thr Arg Leu Asn Gly Lys Cys Lys Thr Leu Glu Glu Val
100 105

<210> 14
<211> 104
<212> PRT
<213> Homo sapiens

<400> 14

Trp Ala Cys Trp His Glu Leu Leu Ser Tyr Leu Glu Lys Ala Asn Lys
1 5 10 15

Trp Leu Asn Glu Val Glu Phe Lys Leu Lys Thr Thr Glu Asn Ile Pro
20 25 30

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

Met Arg His Ser Glu Asp Asn Pro Asn Gln Ile Arg Ile Leu Ala Gln
50 55 60

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

Glu Thr Phe Asn Ser Arg Trp Arg Glu Leu His Glu Glu Ala Val Arg
85 90 95

Arg Gln Lys Leu Leu Glu Gln Ser
100

<210> 15
<211> 92
<212> PRT
<213> Homo sapiens

<400> 15

Ile Gln Ser Ala Gln Glu Thr Glu Lys Ser Leu His Leu Ile Gln Glu
1 5 10 15

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

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

Leu Thr Ser His Glu Ile Ser Leu Glu Glu Met Lys Lys His Asn Gln
50 55 60

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

Lys Lys Leu Gln Asp Val Ser Met Lys Phe Arg Leu
85 90

<210> 16
<211> 109
<212> PRT
<213> Homo sapiens

<400> 16

Phe Gln Lys Pro Ala Asn Phe Glu Gln Arg Leu Gln Glu Ser Lys Met
1 5 10 15

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

Val Glu Gln Glu Val Val Gln Ser Gln Leu Asn His Cys Val Asn Leu
35 40 45

Tyr Lys Ser Leu Ser Glu Val Lys Ser Glu Val Glu Met Val Ile Lys
50 55 60

Thr Gly Arg Gln Ile Val Gln Lys Lys Gln Thr Glu Asn Pro Lys Glu
65 70 75 80

Leu Asp Glu Arg Val Thr Ala Leu Lys Leu His Tyr Asn Glu Leu Gly
85 90 95

Ala Lys Val Thr Glu Arg Lys Gln Gln Leu Glu Lys Cys
100 105

<210> 17
<211> 108
<212> PRT
<213> Homo sapiens

<400> 17

Leu Lys Leu Ser Arg Lys Met Arg Lys Glu Met Asn Val Leu Thr Glu
1 5 10 15

Trp Leu Ala Ala Thr Asp Met Glu Leu Thr Lys Arg Ser Ala Val Glu
20 25 30

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

Gln Lys Glu Ile Glu Lys Gln Lys Val His Leu Lys Ser Ile Thr Glu
50 55 60

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

Glu Asp Lys Leu Ser Leu Leu Asn Ser Asn Trp Ile Ala Val Thr Ser

85

90

95

Arg Ala Glu Glu Trp Leu Asn Leu Leu Leu Glu Tyr
 100 105

<210> 18
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 18

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

Trp Ile Ile Gln Ala Asp Thr Leu Leu Asp Glu Ser Glu Lys Lys Lys
 20 25 30

Pro Gln Gln Lys Glu Asp Val Leu Lys Arg Leu Lys Ala Glu Leu Asn
 35 40 45

Asp Ile Arg Pro Lys Val Asp Ser Thr Arg Asp Gln Ala Ala Asn Leu
 50 55 60

Met Ala Asn Arg Gly Asp His Cys Arg Lys Leu Val Glu Pro Gln Ile
 65 70 75 80

Ser Glu Leu Asn His Arg Phe Ala Ala Ile Ser His Arg Ile Lys Thr
 85 90 95

Gly Lys Ala Ser Ile Pro Leu Lys
 100

<210> 19
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 19

Glu Leu Glu Gln Phe Asn Ser Asp Ile Gln Lys Leu Leu Glu Pro Leu
 1 5 10 15

Glu Ala Glu Ile Gln Gln Gly Val Asn Leu Lys Glu Glu Asp Phe Asn

20

25

30

Lys Asp Met Asn Glu Asp Asn Glu Gly Thr Val Lys Glu Leu Leu Gln
 35 40 45

Arg Gly Asp Asn Leu Gln Gln Arg Ile Thr Asp Glu Arg Lys Arg Glu
 50 55 60

Glu Ile Lys Ile Lys Gln Gln Leu Leu Gln Thr Lys His Asn Ala Leu
 65 70 75 80

Lys Asp Leu Arg Ser Gln Arg Arg Lys Lys Ala Leu Glu Ile
 85 90

<210> 20

<211> 98

<212> PRT

<213> Homo sapiens

<400> 20

Ser His Gln Trp Tyr Gln Tyr Lys Arg Gln Ala Asp Asp Leu Leu Lys
 1 5 10 15

Cys Leu Asp Asp Ile Glu Lys Lys Leu Ala Ser Leu Pro Glu Pro Arg
 20 25 30

Asp Glu Arg Lys Ile Lys Glu Ile Asp Arg Glu Leu Gln Lys Lys Lys
 35 40 45

Glu Glu Leu Asn Ala Val Arg Arg Gln Ala Glu Gly Leu Ser Glu Asp
 50 55 60

Gly Ala Ala Met Ala Val Glu Pro Thr Gln Ile Gln Leu Ser Lys Arg
 65 70 75 80

Trp Arg Glu Ile Glu Ser Lys Phe Ala Gln Phe Arg Arg Leu Asn Phe
 85 90 95

Ala Gln

<210> 21
<211> 20
<212> PRT
<213> Homo sapiens

<400> 21

Ile His Thr Val Arg Glu Glu Thr Met Met Val Met Thr Glu Asp Met
1 5 10 15

Pro Leu Glu Ile
20

<210> 22
<211> 109
<212> PRT
<213> Homo sapiens

<400> 22

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

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

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

Lys Asp Ser Leu Gln Gln Ser Ser Gly Arg Ile Asp Ile Ile His Ser
50 55 60

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

Leu Gln Glu Ala Leu Ser Gln Leu Asp Phe Gln Trp Glu Lys Val Asn
85 90 95

Lys Met Tyr Lys Asp Arg Gln Gly Arg Phe Asp Arg Ser
100 105

<210> 23
<211> 107
<212> PRT
<213> Homo sapiens

<400> 23

Val Glu Lys Trp Arg Arg Phe His Tyr Asp Ile Lys Ile Phe Asn Gln
1 5 10 15

Trp Leu Thr Glu Ala Glu Gln Phe Leu Arg Lys Thr Gln Ile Pro Glu
20 25 30

Asn Trp Glu His Ala Lys Tyr Lys Trp Tyr Leu Lys Glu Leu Gln Asp
35 40 45

Gly Ile Gly Gln Arg Gln Thr Val Val Arg Thr Leu Asn Ala Thr Gly
50 55 60

Glu Glu Ile Ile Gln Gln Ser Ser Lys Thr Asp Ala Ser Ile Leu Gln
65 70 75 80

Glu Lys Leu Gly Ser Leu Asn Leu Arg Trp Gln Glu Val Cys Lys Gln
85 90 95

Leu Ser Asp Arg Lys Lys Arg Leu Glu Glu Gln
100 105

<210> 24

<211> 117

<212> PRT

<213> Homo sapiens

<400> 24

Lys Asn Ile Leu Ser Glu Phe Gln Arg Asp Leu Asn Glu Phe Val Leu
1 5 10 15

Trp Leu Glu Glu Ala Asp Asn Ile Ala Ser Ile Pro Leu Glu Pro Gly
20 25 30

Lys Glu Gln Gln Leu Lys Glu Lys Leu Glu Gln Val Lys Leu Leu Val
35 40 45

Glu Glu Leu Pro Leu Arg Gln Gly Ile Leu Lys Gln Leu Asn Glu Thr
50 55 60

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

Lys Leu Glu Asn Lys Leu Lys Gln Thr Asn Leu Gln Trp Ile Lys Val
85 90 95

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

Asp Leu Gly Gln Leu
115

<210> 25
<211> 101
<212> PRT
<213> Homo sapiens

<400> 25

Glu Lys Lys Leu Glu Asp Leu Glu Glu Gln Leu Asn His Leu Leu Leu
1 5 10 15

Trp Leu Ser Pro Ile Arg Asn Gln Leu Glu Ile Tyr Asn Gln Pro Asn
20 25 30

Gln Glu Gly Pro Phe Asp Val Gln Glu Thr Glu Ile Ala Val Gln Ala
35 40 45

Lys Gln Pro Asp Val Glu Glu Ile Leu Ser Lys Gly Gln His Leu Tyr
50 55 60

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

Ser Ser Glu Trp Lys Ala Val Asn Arg Leu Leu Gln Glu Leu Arg Ala
85 90 95

Lys Gln Pro Asp Leu
100

<210> 26
<211> 41
<212> PRT

<213> Homo sapiens

<400> 26

Ala Pro Gly Leu Thr Thr Ile Gly Ala Ser Pro Thr Gln Thr Val Thr
1 5 10 15

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

Glu Met Pro Ser Ser Leu Met Leu Glu
35 40

<210> 27

<211> 110

<212> PRT

<213> Homo sapiens

<400> 27

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

Trp Leu Ser Leu Leu Asp Gln Val Ile Lys Ser Gln Arg Val Met Val
20 25 30

Gly Asp Leu Glu Asp Ile Asn Glu Met Ile Ile Lys Gln Lys Ala Thr
35 40 45

Met Gln Asp Leu Glu Gln Arg Arg Pro Gln Leu Glu Glu Leu Ile Thr
50 55 60

Ala Ala Gln Asn Leu Lys Asn Lys Thr Ser Asn Gln Glu Ala Arg Thr
65 70 75 80

Ile Ile Thr Asp Arg Ile Glu Arg Ile Gln Asn Gln Trp Asp Glu Val
85 90 95

Gln Glu His Leu Gln Asn Arg Arg Gln Gln Leu Asn Glu Met
100 105 110

<210> 28

<211> 109

<212> PRT

<213> Homo sapiens

<400> 28

Leu Lys Asp Ser Thr Gln Trp Leu Glu Ala Lys Glu Glu Ala Glu Gln
1 5 10 15

Val Leu Gly Gln Ala Arg Ala Lys Leu Glu Ser Trp Lys Glu Gly Pro
20 25 30

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

Ala Lys Asp Leu Arg Gln Trp Gln Thr Asn Val Asp Val Ala Asn Asp
50 55 60

Leu Ala Leu Lys Leu Leu Arg Asp Tyr Ser Ala Asp Asp Thr Arg Lys
65 70 75 80

Val His Met Ile Thr Glu Asn Ile Asn Ala Ser Trp Arg Ser Ile His
85 90 95

Lys Arg Val Ser Glu Arg Glu Ala Ala Leu Glu Glu Thr
100 105

<210> 29

<211> 116

<212> PRT

<213> Homo sapiens

<400> 29

His Arg Leu Leu Gln Gln Phe Pro Leu Asp Leu Glu Lys Phe Leu Ala
1 5 10 15

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

Arg Lys Glu Arg Leu Leu Glu Asp Ser Lys Gly Val Lys Glu Leu Met
35 40 45

Lys Gln Trp Gln Asp Leu Gln Gly Glu Ile Glu Ala His Thr Asp Val
50 55 60

Tyr His Asn Leu Asp Glu Asn Ser Gln Lys Ile Leu Arg Ser Leu Glu
65 70 75 80

Gly Ser Asp Asp Ala Val Leu Leu Gln Arg Arg Leu Asp Asn Met Asn
85 90 95

Phe Lys Trp Ser Glu Leu Arg Lys Lys Ser Leu Asn Ile Arg Ser His
100 105 110

Leu Glu Ala Ser
115

<210> 30
<211> 129
<212> PRT
<213> Homo sapiens

<400> 30

Ser Asp Gln Trp Lys Arg Leu His Leu Ser Leu Gln Glu Leu Leu Val
1 5 10 15

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

Gly Asp Phe Pro Ala Val Gln Lys Gln Asn Asp Val His Arg Ala Phe
35 40 45

Lys Arg Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser Thr Leu Glu
50 55 60

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

Leu Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg Ala Gln Asn
85 90 95

Val Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn Thr Glu Trp
100 105 110

Glu Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys Ile Asp Glu
115 120 125

Thr

<210> 31
<211> 108
<212> PRT
<213> Homo sapiens

<400> 31

Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr Asp Glu Leu Asp Leu
1 5 10 15

Lys Leu Arg Gln Ala Glu Val Ile Lys Gly Ser Trp Gln Pro Val Gly
20 25 30

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

Leu Arg Gly Glu Ile Ala Pro Leu Lys Glu Asn Val Ser His Val Asn
50 55 60

Asp Leu Ala Arg Gln Leu Thr Thr Leu Gly Ile Gln Leu Ser Pro Tyr
65 70 75 80

Asn Leu Ser Thr Leu Glu Asp Leu Asn Thr Arg Trp Lys Leu Leu Gln
85 90 95

Val Ala Val Glu Asp Arg Val Arg Gln Leu His Glu
100 105

<210> 32
<211> 72
<212> PRT
<213> Homo sapiens

<400> 32

Ala His Arg Asp Phe Gly Pro Ala Ser Gln His Phe Leu Ser Thr Ser
1 5 10 15

Val Gln Gly Pro Trp Glu Arg Ala Ile Ser Pro Asn Lys Val Pro Tyr
20 25 30

Tyr Ile Asn His Glu Thr Gln Thr Thr Cys Trp Asp His Pro Lys Met
35 40 45

Thr Glu Leu Tyr Gln Ser Leu Ala Asp Leu Asn Asn Val Arg Phe Ser
50 55 60

Ala Tyr Arg Thr Ala Met Lys Leu
65 70

<210> 33
<211> 296
<212> PRT
<213> Homo sapiens

<400> 33

Arg Arg Leu Gln Lys Ala Leu Cys Leu Asp Leu Leu Ser Leu Ser Ala
1 5 10 15

Ala Cys Asp Ala Leu Asp Gln His Asn Leu Lys Gln Asn Asp Gln Pro
20 25 30

Met Asp Ile Leu Gln Ile Ile Asn Cys Leu Thr Thr Ile Tyr Asp Arg
35 40 45

Leu Glu Gln Glu His Asn Asn Leu Val Asn Val Pro Leu Cys Val Asp
50 55 60

Met Cys Leu Asn Trp Leu Leu Asn Val Tyr Asp Thr Gly Arg Thr Gly
65 70 75 80

Arg Ile Arg Val Leu Ser Phe Lys Thr Gly Ile Ile Ser Leu Cys Lys
85 90 95

Ala His Leu Glu Asp Lys Tyr Arg Tyr Leu Phe Lys Gln Val Ala Ser
100 105 110

Ser Thr Gly Phe Cys Asp Gln Arg Arg Leu Gly Leu Leu Leu His Asp
115 120 125

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

130

135

140

Ser Asn Ile Glu Pro Ser Val Arg Ser Cys Phe Gln Phe Ala Asn Asn
 145 150 155 160

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

Pro Gln Ser Met Val Trp Leu Pro Val Leu His Arg Val Ala Ala Ala
 180 185 190

Glu Thr Ala Lys His Gln Ala Lys Cys Asn Ile Cys Lys Glu Cys Pro
 195 200 205

Ile Ile Gly Phe Arg Tyr Arg Ser Leu Lys His Phe Asn Tyr Asp Ile
 210 215 220

Cys Gln Ser Cys Phe Phe Ser Gly Arg Val Ala Lys Gly His Lys Met
 225 230 235 240

His Tyr Pro Met Val Glu Tyr Cys Thr Pro Thr Thr Ser Gly Glu Asp
 245 250 255

Val Arg Asp Phe Ala Lys Val Leu Lys Asn Lys Phe Arg Thr Lys Arg
 260 265 270

Tyr Phe Ala Lys His Pro Arg Met Gly Tyr Leu Pro Val Gln Thr Val
 275 280 285

Leu Glu Gly Asp Asn Met Glu Thr
 290 295

<210> 34
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 34

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

Ser Pro Gln Leu Ser His Asp Asp Thr His Ser Arg Ile Glu His Tyr
20 25 30

Ala Ser Arg Leu Ala Glu Met Glu Asn Ser Asn Gly Ser Tyr Leu Asn
35 40 45

Asp Ser Ile Ser Pro Asn Glu Ser Ile Asp Asp Glu His Leu Leu Ile
50 55 60

Gln His Tyr Cys Gln Ser Leu Asn Gln Asp Ser Pro Leu Ser Gln Pro
65 70 75 80

Arg Ser Pro Ala Gln Ile Leu Ile Ser Leu Glu Ser Glu Glu Arg Gly
85 90 95

Glu Leu Glu Arg Ile Leu Ala Asp Leu Glu Glu Glu Asn Arg Asn Leu
100 105 110

Gln Ala Glu Tyr Asp Arg Leu Lys Gln Gln His Glu His Lys Gly Leu
115 120 125

Ser Pro Leu Pro Ser Pro Pro Glu Met Met Pro Thr Ser Pro Gln Ser
130 135 140

Pro Arg Asp Ala Glu Leu Ile Ala Glu Ala Lys Leu Leu Arg Gln His
145 150 155 160

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

Gln Leu Glu Ser Gln Leu His Arg Leu Arg Gln Leu Leu Glu Gln Pro
180 185 190

Gln Ala Glu Ala Lys Val Asn Gly Thr Thr Val Ser Ser Pro Ser Thr
195 200 205

Ser Leu Gln Arg Ser Asp Ser Ser Gln Pro Met Leu Leu Arg Val Val
210 215 220

Gly Ser Gln Thr Ser Asp Ser Met Gly Glu Glu Asp Leu Leu Ser Pro
225 230 235 240

Pro Gln Asp Thr Ser Thr Gly Leu Glu Glu Val Met Glu Gln Leu Asn
245 250 255

Asn Ser Phe Pro Ser Ser Arg Gly Arg Asn Thr Pro Gly Lys Pro Met
260 265 270

Arg Glu Asp Thr Met
275

<210> 35
<211> 208
<212> DNA
<213> Homo sapiens

<400> 35
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aaacgaatag gaaaaactga agtggttactt tttttaaaagc tgctgaagtt tgttggtttc 120
tcattgtttt taagcctact ggagcaataa agtttgaaga actttttacca ggtttttttt 180
atcgctgcct tgatatacac ttttcaaa 208

<210> 36
<211> 756
<212> DNA
<213> Homo sapiens

<400> 36
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ttcagtgacc tacaggatgg gaggcgcctc ctagacctcc tcgaaggcct gacagggcaa 180
aaactgccaa aagaaaaagg atccacaaga gttcatgccc tgaacaatgt caacaaggca 240
ctgcggggtt tgcaagaaca taatgttgat ttagtgaata ttggaagtac tgacatcgta 300
gatggaaatc ataaactgac tcttggtttg atttggaata taatcctcca ctggcaggtc 360
aaaaatgtaa tgaaaaatat catggctgga ttgcaacaaa ccaacagtga aaagattctc 420
ctgagctggg tccgacaatc aactcgtaat tatccacagg ttaatgtaat caacttcacc 480
accagctggg ctgatggcct ggctttgaat gctctcatcc atagtcatag gccagacctc 540
tttgactgga atagtgtggt ttgccagcag tcagccacac aacgactgga acatgcattc 600

aacatcgcca gatatcaatt aggcatagag aaactactcg atcctgaaga tgttgatacc	660
acctatccag ataagaagtc catcttaatg tacatcacat cactcttcca agttttgcct	720
caacaagtga gcattgaagc catccaggaa gtggaa	756

<210> 37
 <211> 255
 <212> DNA
 <213> Homo sapiens

<400> 37	
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cactattctc aacagatcac ggtcagtcta gcacagggat atgagagaac ttctttccct	120
aagcctcgat tcaagagcta tgcctacaca caggctgctt atgtcaccac ctctgaccct	180
acacggagcc catttccttc acagcatttg gaagctcctg aagacaagtc atttggcagt	240
tcattgatgg agagt	255

<210> 38
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 38	
gaagtaaacc tggaccgtta tcaaacagct ttagaagaag tattatcgtg gcttctttct	60
gctgaggaca cattgcaagc acaaggagag atttctaagc atgtggaagt ggtgaaagac	120
cagtttcata ctcatgaggg gtacatgatg gatttgacag cccatcaggg ccgggttggt	180
aatattctac aattgggaag taagctgatt ggaacaggaa aattatcaga agatgaagaa	240
actgaagtac aagagcagat gaatctccta aattcaagat gggaatgcct cagggtagct	300
agcatggaaa aacaaagcaa ttacat	327

<210> 39
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 39	
agagttttaa tggatctcca gaatcagaaa ctgaaagagt tgaatgactg gctaacaaaa	60
acagaagaaa gaacaaggaa aatggaggaa gagcctcttg gacctgatct tgaagaccta	120

aaacgccaag tacaacaaca taaggtgctt caagaagatc tagaacaaga acaagtcagg	180
gtcaattctc tcactcacat ggtgggtgga gttgatgaat ctagtggaga tcacgcaact	240
gctgctttgg aagaacaact taaggtattg ggagatcgat gggcaaacat ctgtagatgg	300
acagaagacc gctgggttct tttaacaagac atc	333

<210> 40
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 40	
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aaagaagatg cagtgaacaa gattcacaca actggcttta aagatcaaaa tgaaatgtta	120
tcaagtcttc aaaaactggc cgttttaaaa gcggatctag aaaagaaaaa gcaatccatg	180
ggcaaaactgt attcactcaa acaagatctt ctttcaacac tgaagaataa gtcagtgacc	240
cagaagacgg aagcatggct ggataacttt gcccggtgtt gggataattt agtccaaaaa	300
cttgaaaaga gtacagcaca gatttcacag gct	333

<210> 41
 <211> 147
 <212> DNA
 <213> Homo sapiens

<400> 41	
gtcaccacca ctacgcatc actaacacag acaactgtta tggaacagtt aactacggtg	60
accacaaggg aacagatcct ggtaaagcat gctcaagagg aacttcacc accacctccc	120
caaaagaaga ggcagattac tgtggat	147

<210> 42
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 42	
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tcagaagctg tgttgagag tcctgaattt gcaatctttc ggaaggaagg caacttctca	120
gacttaaaaag aaaaagtcaa tgccatagag cgagaaaaag ctgagaagtt cagaaaactg	180
caagatgcca gcagatcagc tcaggccctg gtggaacaga tggatgaatga ggggtgttaat	240

gcagatagca tcaaacaagc ctcagaacaa ctgaacagcc ggtggatcga attctgccag	300
ttgctaagtg agagacttaa ctggctggag tat	333

<210> 43
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 43	
cagaacaaca tcatcgcttt ctataatcag ctacaacaat tggagcagat gacaactact	60
gctgaaaact ggttgaaaat ccaacccacc accccatcag agccaacagc aattaaaagt	120
cagttaaaaa tttgtaagga tgaagtcaac cggctatcag gtcttcaacc tcaaattgaa	180
cgattaaaaa ttcaaagcat agccctgaaa gagaaaggac aaggacccat gttcctggat	240
gcagactttg tggcctttac aaatcatttt aagcaagtct tttctgatgt gcaggccaga	300
gagaaagagc tacagacaat ttttgac	327

<210> 44
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 44	
actttgccac caatgcgcta tcaggagacc atgagtgcc a tcaggacatg ggtccagcag	60
tcagaaacca aactctccat acctcaactt agtgtcaccg actatgaaat catggagcag	120
agactcgggg aattgcaggc tttaaaagt tctctgcaag agcaacaaag tggcctatac	180
tatctcagca ccactgtgaa agagatgtcg aagaaagcgc cctctgaaat tagccgaaa	240
tatcaatcag aatttgaaga aattgaggga cgctggaaga agctctcctc ccagctggtt	300
gagcattgtc aaaagctaga ggagcaa	327

<210> 45
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 45	
atgaataaac tccgaaaaat tcagaatcac atacaaaccc tgaagaaatg gatggctgaa	60
gttgatgttt ttctgaagga ggaatggcct gcccttgggg attcagaaat tctaaaaaag	120

cagctgaaac agtgcagact tttagtcagt gatattcaga caattcagcc cagtctaaac	180
agtgtcaatg aaggtgggca gaagataaag aatgaagcag agccagagtt tgcttcgaga	240
cttgagacag aactcaaaga acttaacact cagtgggatc acatgtgcca acaggtctat	300
gccagaaagg aggccttgaa gggaggt	327

<210> 46
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 46	
ttggagaaaa ctgtaagcct ccagaaagat ctatcagaga tgcacgaatg gatgacacaa	60
gctgaagaag agtatcttga gagagatttt gaatataaaa ctccagatga attacagaaa	120
gcagttgaag agatgaagag agctaaagaa gaggcccaac aaaaagaagc gaaagtgaaa	180
ctccttactg agtctgtaaa tagtgtcata gctcaagctc cacctgtagc acaagaggcc	240
ttaaaaaagg aacttgaaac tctaaccacc aactaccagt ggctctgcac taggctgaat	300
gggaaatgca agactttgga agaagtt	327

<210> 47
 <211> 312
 <212> DNA
 <213> Homo sapiens

<400> 47	
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gtagaattta aacttaaaac cactgaaaac attcctggcg gagctgagga aatctctgag	120
gtgctagatt cacttgaaaa tttgatgcga cattcagagg ataaccctaaa tcagattcgc	180
atattggcac agaccctaac agatggcgga gtcattgatg agctaataca tgaggaactt	240
gagacattta attctcgttg gagggaaacta catgaagagg ctgtaaggag gcaaaagttg	300
cttgaacaga gc	312

<210> 48
 <211> 276
 <212> DNA
 <213> Homo sapiens

<400> 48	
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attgacaagc agttggcagc ttatatattgca gacaaggtgg acgcagctca aatgcctcag	120
gaagcccaga aaatccaatc tgattttgaca agtcatgaga tcagttttaga agaaatgaag	180
aaacataatc aggggaagga ggctgcccac agagtcctgt ctcagattga tgttgccacag	240
aaaaaattac aagatgtctc catgaagttt cgatta	276

<210> 49
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 49	
ttccagaaac cagccaattt tgagcagcgt ctacaagaaa gtaagatgat tttagatgaa	60
gtgaagatgc acttgcctgc attggaaaca aagagtgtgg aacaggaagt agtacagtca	120
cagctaaatc atttgttgaa cttgtataaa agtctgagtg aagtgaagtc tgaagtggaa	180
atggtgataa agactggacg tcagattgta cagaaaaagc agacggaaaa tcccaaagaa	240
cttgatgaaa gagtaacagc tttgaaattg cattataatg agctgggagc aaaggttaaca	300
gaaagaaagc aacagttgga gaaatgc	327

<210> 50
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 50	
ttgaaattgt cccgtaagat gcgaaaggaa atgaatgtct tgacagaatg gctggcagct	60
acagatatgg aattgacaaa gagatcagca gttgaaggaa tgcctagtaa tttggattct	120
gaagttgcct ggggaaaggc tactcaaaaa gagattgaga aacagaaggt gcacctgaag	180
agtatcacag aggtaggaga ggccttgaaa acagttttgg gcaagaagga gacgttggtg	240
gaagataaac tcagtcttct gaatagtaac tggatagctg tcacctcccg agcagaagag	300
tggttaaatac ttttggttga atac	324

<210> 51
 <211> 312
 <212> DNA
 <213> Homo sapiens

<400> 51

cagaaacaca tggaaacttt tgaccagaat gtggaccaca tcacaaagtg gatcattcag	60
gctgacacac ttttggatga atcagagaaa aagaaacccc agcaaaaaga agacgtgctt	120
aagcgtttta aggcagaact gaatgacata cgcccaaagg tggactctac acgtgaccaa	180
gcagcaaact tgatggcaaa ccgcggtgac cactgcagga aattagtaga gccccaaatc	240
tcagagctca accatcgatt tgcagccatt tcacacagaa ttaagactgg aaaggcctcc	300
attcctttga ag	312

<210> 52
 <211> 282
 <212> DNA
 <213> Homo sapiens

<400> 52	
gaattggagc agtttaactc agatatacaa aaattgcttg aaccactgga ggctgaaatt	60
cagcaggggg tgaatctgaa agaggaagac ttcaataaag atatgaatga agacaatgag	120
ggtactgtaa aagaattggt gcaaagagga gacaacttac aacaaagaat cacagatgag	180
agaaagagag aggaaataaa gataaaacag cagctgttac agacaaaaca taatgctctc	240
aaggatttga ggtctcaaag aagaaaaaag gctctagaaa tt	282

<210> 53
 <211> 294
 <212> DNA
 <213> Homo sapiens

<400> 53	
tctcatcagt ggtatcagta caagaggcag gctgatgatc tcctgaaatg cttggatgac	60
attgaaaaaa aattagccag cctacctgag cccagagatg aaaggaaaat aaaggaaatt	120
gatcgggaat tgcagaagaa gaaagaggag ctgaatgcag tgcgtaggca agctgagggc	180
ttgtctgagg atggggccgc aatggcagtg gagccaactc agatccagct cagcaagcgc	240
tggcgggaaa ttgagagcaa atttgctcag tttcgaagac tcaactttgc acaa	294

<210> 54
 <211> 60
 <212> DNA
 <213> Homo sapiens

<400> 54	
attcacactg tccgtgaaga aacgatgatg gtgatgactg aagacatgcc tttggaaatt	60

<210> 55
<211> 327
<212> DNA
<213> Homo sapiens

<400> 55
tcttatgtgc cttctactta ttgactgaa atcactcatg tctcacaagc cctattagaa 60
gtggaacaac ttctcaatgc tcctgacctc tgtgctaagg actttgaaga tctctttaag 120
caagaggagt ctctgaagaa tataaaagat agtctacaac aaagctcagg tcggattgac 180
attattcata gcaagaagac agcagcattg caaagtgcaa cgcctgtgga aagggtgaag 240
ctacaggaag ctctctccca gcttgatttc caatgggaaa aagttaacaa aatgtacaag 300
gaccgacaag ggcgatttga cagatct 327

<210> 56
<211> 321
<212> DNA
<213> Homo sapiens

<400> 56
gttgagaaat ggcggcgttt tcattatgat ataaagatat ttaatcagtg gctaacagaa 60
gctgaacagt ttctcagaaa gacacaaatt cctgagaatt gggaacatgc taaatacaaa 120
tggtatctta aggaactcca ggatggcatt gggcagcggc aaactgttgt cagaacattg 180
aatgcaactg gggaagaaat aattcagcaa tcctcaaaaa cagatgccag tattctacag 240
gaaaaattgg gaagcctgaa tctgcggtgg caggaggtct gcaaacagct gtcagacaga 300
aaaaagaggc tagaagaaca a 321

<210> 57
<211> 351
<212> DNA
<213> Homo sapiens

<400> 57
aagaatatct tgtcagaatt tcaaagagat ttaaatgaat ttgttttatg gttggaggaa 60
gcagataaca ttgctagtat ccacttgaa cctggaaaag agcagcaact aaaagaaaag 120
cttgagcaag tcaagttact ggtggaagag ttgccctgc gccagggaat tctcaaacaa 180
ttaaatgaaa ctggaggacc cgtgcttgta agtgctccca taagcccaga agagcaagat 240

aaacttgaaa ataagctcaa gcagacaaat ctccagtgga taaaggtttc cagagcttta	300
cctgagaaac aaggagaaat tgaagctcaa ataaaagacc ttgggcagct t	351

<210> 58
 <211> 303
 <212> DNA
 <213> Homo sapiens

<400> 58	
gaaaaaaagc ttgaagacct tgaagagcag ttaaatcatc tgctgctgtg gttatctcct	60
attaggaatc agttggaaat ttataaccaa ccaaaccaag aaggaccatt tgacgttcag	120
gaaactgaaa tagcagttca agctaaacaa ccggatgtgg aagagatttt gtctaaaggg	180
cagcatttgt acaaggaaaa accagccact cagccagtga agaggaagtt agaagatctg	240
agctctgagt ggaaggcggt aaaccgttta cttcaagagc tgagggcaaa gcagcctgac	300
cta	303

<210> 59
 <211> 123
 <212> DNA
 <213> Homo sapiens

<400> 59	
gctcctggac tgaccactat tggagcctct cctactcaga ctgttactct ggtgacacaa	60
cctgtgggta ctaaggaaac tgccatctcc aaactagaaa tgccatcttc cttgatgttg	120
gag	123

<210> 60
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 60	
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cttgatcaag ttataaaatc acagagggtg atgggtgggtg accttgagga tatcaacgag	120
atgatcatca agcagaaggc aacaatgcag gatttggaaac agaggcgtcc ccagttggaa	180
gaactcatta ccgctgccca aaatttgaaa aacaagacca gcaatcaaga ggctagaaca	240
atcattacgg atcgaattga aagaattcag aatcagtggg atgaagtaca agaacacctt	300
cagaaccgga ggcaacagtt gaatgaaatg	330

<210> 61
<211> 327
<212> DNA
<213> Homo sapiens

<400> 61
ttaaaggatt caacacaatg gctggaagct aaggaagaag ctgagcaggt cttaggacag 60
gccagagcca agcttgagtc atggaaggag ggtccctata cagtagatgc aatccaaaag 120
aaaatcacag aaaccaagca gttggcctaaa gacctccgcc agtggcagac aaatgtagat 180
gtggcaaatg acttggccct gaaacttctc cgggattatt ctgcagatga taccagaaaa 240
gtccacatga taacagagaa tatcaatgcc tcttggagaa gcattcataa aagggtgagt 300
gagcgagagg ctgctttgga agaaact 327

<210> 62
<211> 348
<212> DNA
<213> Homo sapiens

<400> 62
catagattac tgcaacagtt ccccctggac ctggaaaagt ttcttgcttg gcttacagaa 60
gctgaaacaa ctgccaatgt cctacaggat gctacccgta aggaaaggct cctagaagac 120
tccaagggag taaaagagct gatgaaacaa tggcaagacc tccaaggtga aattgaagct 180
cacacagatg tttatcacia cctggatgaa aacagccaaa aaatcctgag atccctggaa 240
ggttccgatg atgcagtcct gttacaaaga cgtttggata acatgaactt caagtggagt 300
gaacttcgga aaaagtctct caacattagg tcccatttgg aagccagt 348

<210> 63
<211> 387
<212> DNA
<213> Homo sapiens

<400> 63
tctgaccagt ggaagcgtct gcacctttct ctgcaggaac ttctggtgtg gctacagctg 60
aaagatgatg aattaagccg gcaggcacct attggaggcg actttccagc agttcagaag 120
cagaacgatg tacatagggc cttcaagagg gaattgaaaa ctaaagaacc tgtaatcatg 180
agtactcttg agactgtacg aatatttctg acagagcagc ctttgaagg actagagaaa 240

ctctaccagg agcccagaga gctgcctcct gaggagagag cccagaatgt cactcggctt	300
ctacgaaagc aggctgagga ggtcaatact gagtgggaaa aattgaacct gcactccgct	360
gactggcaga gaaaaataga tgagacc	387

<210> 64
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 64	
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gctgaggtga tcaagggatc ctggcagccc gtgggcgatc tcctcattga ctctctccaa	120
gatcacctcg agaaagtcaa ggcacttcga ggagaaattg cgcctctgaa agagaacgtg	180
agccacgtca atgaccttgc tcgccagctt accactttgg gcattcagct ctcaccgtat	240
aacctcagca ctctggaaga cctgaacacc agatggaagc ttctgcaggt ggccgtcgag	300
gaccgagtca ggcagctgca tgaa	324

<210> 65
 <211> 216
 <212> DNA
 <213> Homo sapiens

<400> 65	
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tgggagagag ccatctcgcc aaacaaagtg ccctactata tcaaccacga gactcaaaca	120
acttgctggg accatcccaa aatgacagag ctctaccagt ctttagctga cctgaataat	180
gtcagattct cagcttatag gactgcatg aaactc	216

<210> 66
 <211> 888
 <212> DNA
 <213> Homo sapiens

<400> 66	
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ttggaccagc acaacctcaa gcaaaatgac cagcccatgg atatcctgca gattattaat	120
tgtttgacca ctatttatga cgcctggag caagagcaca acaatttggt caacgtccct	180
ctctgcgtgg atatgtgtct gaactggctg ctgaatgttt atgatacggg acgaacaggg	240

aggatccgtg tcctgtcttt taaaactggc atcatttccc tgtgtaaagc acatttggaa	300
gacaagtaca gatacctttt caagcaagtg gcaagttcaa caggattttg tgaccagcgc	360
aggctgggcc tccttctgca tgattctatc caaattccaa gacagttggg tgaagttgca	420
tcctttgggg gcagtaacat tgagccaagt gtccggagct gcttccaatt tgctaataat	480
aagccagaga tcgaagcggc cctcttccta gactggatga gactggaacc ccagtccatg	540
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tgtaacatct gcaaagagtg tccaatcatt ggattcaggt acaggagtct aaagcacttt	660
aattatgaca tctgccaaag ctgctttttt tctggtcgag ttgcaaaagg ccataaaatg	720
cactatccca tgggtggaata ttgcactccg actacatcag gagaagatgt tcgagacttt	780
gccaaggtac taaaaaaca atttcgaacc aaaaggtatt ttgcgaagca tccccgaatg	840
ggctacctgc cagtgcagac tgtcttagag ggggacaaca tggaaact	888

<210> 67
 <211> 834
 <212> DNA
 <213> Homo sapiens

<400> 67	
cccgttactc tgatcaactt ctggccagta gattctgcgc ctgcctcgtc ccctcagctt	60
tcacacgatg atactcattc acgcattgaa cattatgcta gcaggctagc agaaatggaa	120
aacagcaatg gatcttatct aaatgatagc atctctccta atgagagcat agatgatgaa	180
catttgtaa tccagcatta ctgccaaagt ttgaaccagg actccccct gagccagcct	240
cgtagtcctg cccagatctt gatttcctta gagagtgagg aaagagggga gctagagaga	300
atcctagcag atcttgagga agaaaacagg aatctgcaag cagaatatga ccgtctaaag	360
cagcagcacg aacataaagg cctgtcccca ctgccgtccc ctctgaaat gatgccacc	420
tctccccaga gtccccggga tgctgagctc attgctgagg ccaagctact gcgtcaacac	480
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cagttacaca ggctaaggca gctgctggag caaccccagg cagaggccaa agtgaatggc	600
acaacggtgt cctctccttc tacctctcta cagaggtccg acagcagtca gcctatgctg	660
ctccgagtgg ttggcagtca aacttcggac tccatgggtg aggaagatct tctcagtcct	720

ccccaggaca caagcacagg gttagaggag gtgatggagc aactcaacaa ctccttcctt 780

agttcaagag gaagaaatac ccctggaaag ccaatgagag aggacacaat gtag 834

<210> 68
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Spectrin-16 (junction J4V13)

<400> 68

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

<210> 69
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Spectrin-16 (junction J4V12)

<400> 69

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

<210> 70
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Spectrin-16 (junction J4V11)

<400> 70

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

<210> 71
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Spectrin-16 (junction J4V4)

<400> 71

Leu His Arg Val Leu Met Asp Leu Thr Tyr Leu Thr Glu Ile Thr His
1 5 10 15

<210> 72

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified Spectrin-16 (junction J4)

<400> 72

Met Glu Lys Gln Ser Asn Leu His Ser Tyr Val Pro Ser Thr Tyr Leu
1 5 10 15

<210> 73

<211> 252

<212> PRT

<213> Homo sapiens

<400> 73

Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
1 5 10 15

Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
20 25 30

Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
35 40 45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
50 55 60

Glu Lys Gly Ser Thr Arg Val His Ala Leu Asn Asn Val Asn Lys Ala
65 70 75 80

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
85 90 95

Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
100 105 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
115 120 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
130 135 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145 150 155 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
165 170 175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
180 185 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
195 200 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
210 215 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225 230 235 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu
245 250

<210> 74
<211> 85
<212> PRT
<213> Homo sapiens

<400> 74

Met Leu Pro Arg Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu
1 5 10 15

His His Gln Met His Tyr Ser Gln Gln Ile Thr Val Ser Leu Ala Gln
20 25 30

Gly Tyr Glu Arg Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala

35

40

45

Tyr Thr Gln Ala Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro
 50 55 60

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

Ser Leu Met Glu Ser
 85

<210> 75
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 75

Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu Ser
 1 5 10 15

Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile Ser
 20 25 30

Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly Tyr
 35 40 45

Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu Gln
 50 55 60

Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu Glu
 65 70 75 80

Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu Cys
 85 90 95

Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His
 100 105

<210> 76
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Modified Spectrin-16

<400> 76

Arg Val Leu Met Asp Leu Gln Asn Gln Lys Leu Thr Glu Ile Thr His
1 5 10 15

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

Leu Cys Ala Lys Asp Phe Glu Asp Leu Phe Lys Gln Glu Glu Ser Leu
35 40 45

Lys Asn Ile Lys Asp Ser Leu Gln Gln Ser Ser Gly Arg Ile Asp Ile
50 55 60

Ile His Ser Lys Lys Thr Ala Ala Leu Gln Ser Ala Thr Pro Val Glu
65 70 75 80

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

Lys Val Asn Lys Met Tyr Lys Asp Arg Gln Gly Arg Phe Asp Arg Ser
100 105 110

<210> 77

<211> 107

<212> PRT

<213> Homo sapiens

<400> 77

Val Glu Lys Trp Arg Arg Phe His Tyr Asp Ile Lys Ile Phe Asn Gln
1 5 10 15

Trp Leu Thr Glu Ala Glu Gln Phe Leu Arg Lys Thr Gln Ile Pro Glu
20 25 30

Asn Trp Glu His Ala Lys Tyr Lys Trp Tyr Leu Lys Glu Leu Gln Asp
35 40 45

Gly Ile Gly Gln Arg Gln Thr Val Val Arg Thr Leu Asn Ala Thr Gly

50

55

60

Glu Glu Ile Ile Gln Gln Ser Ser Lys Thr Asp Ala Ser Ile Leu Gln
 65 70 75 80

Glu Lys Leu Gly Ser Leu Asn Leu Arg Trp Gln Glu Val Cys Lys Gln
 85 90 95

Leu Ser Asp Arg Lys Lys Arg Leu Glu Glu Gln
 100 105

<210> 78

<211> 41

<212> PRT

<213> Homo sapiens

<400> 78

Ala Pro Gly Leu Thr Thr Ile Gly Ala Ser Pro Thr Gln Thr Val Thr
 1 5 10 15

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

Glu Met Pro Ser Ser Leu Met Leu Glu
 35 40

<210> 79

<211> 129

<212> PRT

<213> Homo sapiens

<400> 79

Ser Asp Gln Trp Lys Arg Leu His Leu Ser Leu Gln Glu Leu Leu Val
 1 5 10 15

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

Gly Asp Phe Pro Ala Val Gln Lys Gln Asn Asp Val His Arg Ala Phe
 35 40 45

Lys Arg Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser Thr Leu Glu

50

55

60

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

Leu Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg Ala Gln Asn
85 90 95

Val Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn Thr Glu Trp
100 105 110

Glu Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys Ile Asp Glu
115 120 125

Thr

<210> 80

<211> 108

<212> PRT

<213> Homo sapiens

<400> 80

Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr Asp Glu Leu Asp Leu
1 5 10 15

Lys Leu Arg Gln Ala Glu Val Ile Lys Gly Ser Trp Gln Pro Val Gly
20 25 30

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

Leu Arg Gly Glu Ile Ala Pro Leu Lys Glu Asn Val Ser His Val Asn
50 55 60

Asp Leu Ala Arg Gln Leu Thr Thr Leu Gly Ile Gln Leu Ser Pro Tyr
65 70 75 80

Asn Leu Ser Thr Leu Glu Asp Leu Asn Thr Arg Trp Lys Leu Leu Gln
85 90 95

Val Ala Val Glu Asp Arg Val Arg Gln Leu His Glu
100 105

<210> 81
<211> 72
<212> PRT
<213> Homo sapiens

<400> 81

Ala His Arg Asp Phe Gly Pro Ala Ser Gln His Phe Leu Ser Thr Ser
1 5 10 15

Val Gln Gly Pro Trp Glu Arg Ala Ile Ser Pro Asn Lys Val Pro Tyr
20 25 30

Tyr Ile Asn His Glu Thr Gln Thr Thr Cys Trp Asp His Pro Lys Met
35 40 45

Thr Glu Leu Tyr Gln Ser Leu Ala Asp Leu Asn Asn Val Arg Phe Ser
50 55 60

Ala Tyr Arg Thr Ala Met Lys Leu
65 70

<210> 82
<211> 296
<212> PRT
<213> Homo sapiens

<400> 82

Arg Arg Leu Gln Lys Ala Leu Cys Leu Asp Leu Leu Ser Leu Ser Ala
1 5 10 15

Ala Cys Asp Ala Leu Asp Gln His Asn Leu Lys Gln Asn Asp Gln Pro
20 25 30

Met Asp Ile Leu Gln Ile Ile Asn Cys Leu Thr Thr Ile Tyr Asp Arg
35 40 45

Leu Glu Gln Glu His Asn Asn Leu Val Asn Val Pro Leu Cys Val Asp
50 55 60

Met Cys Leu Asn Trp Leu Leu Asn Val Tyr Asp Thr Gly Arg Thr Gly
65 70 75 80

Arg Ile Arg Val Leu Ser Phe Lys Thr Gly Ile Ile Ser Leu Cys Lys
85 90 95

Ala His Leu Glu Asp Lys Tyr Arg Tyr Leu Phe Lys Gln Val Ala Ser
100 105 110

Ser Thr Gly Phe Cys Asp Gln Arg Arg Leu Gly Leu Leu Leu His Asp
115 120 125

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

Ser Asn Ile Glu Pro Ser Val Arg Ser Cys Phe Gln Phe Ala Asn Asn
145 150 155 160

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

Pro Gln Ser Met Val Trp Leu Pro Val Leu His Arg Val Ala Ala Ala
180 185 190

Glu Thr Ala Lys His Gln Ala Lys Cys Asn Ile Cys Lys Glu Cys Pro
195 200 205

Ile Ile Gly Phe Arg Tyr Arg Ser Leu Lys His Phe Asn Tyr Asp Ile
210 215 220

Cys Gln Ser Cys Phe Phe Ser Gly Arg Val Ala Lys Gly His Lys Met
225 230 235 240

His Tyr Pro Met Val Glu Tyr Cys Thr Pro Thr Thr Ser Gly Glu Asp
245 250 255

Val Arg Asp Phe Ala Lys Val Leu Lys Asn Lys Phe Arg Thr Lys Arg
260 265 270

Tyr Phe Ala Lys His Pro Arg Met Gly Tyr Leu Pro Val Gln Thr Val
275 280 285

Leu Glu Gly Asp Asn Met Glu Thr
290 295

<210> 83
<211> 1311
<212> PRT
<213> Artificial Sequence

<220>
<223> BXA-212372-J4V13

<400> 83

Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
1 5 10 15

Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
20 25 30

Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
35 40 45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
50 55 60

Glu Lys Gly Ser Thr Arg Val His Ala Leu Asn Asn Val Asn Lys Ala
65 70 75 80

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
85 90 95

Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
100 105 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
115 120 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
130 135 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145 150 155 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
165 170 175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
180 185 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
195 200 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
210 215 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225 230 235 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu Met Leu Pro Arg
245 250 255

Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu His His Gln Met
260 265 270

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

Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala Tyr Thr Gln Ala
290 295 300

Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro Phe Pro Ser Gln
305 310 315 320

His Leu Glu Ala Pro Glu Asp Lys Ser Phe Gly Ser Ser Leu Met Glu
325 330 335

Ser Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu
340 345 350

Ser Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile
355 360 365

Ser Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly
370 375 380

Tyr Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu
385 390 395 400

Gln Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu
405 410 415

Glu Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu
420 425 430

Cys Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His Arg Val
435 440 445

Leu Met Asp Leu Gln Asn Gln Lys Leu Thr Glu Ile Thr His Val Ser
450 455 460

Gln Ala Leu Leu Glu Val Glu Gln Leu Leu Asn Ala Pro Asp Leu Cys
465 470 475 480

Ala Lys Asp Phe Glu Asp Leu Phe Lys Gln Glu Glu Ser Leu Lys Asn
485 490 495

Ile Lys Asp Ser Leu Gln Gln Ser Ser Gly Arg Ile Asp Ile Ile His
500 505 510

Ser Lys Lys Thr Ala Ala Leu Gln Ser Ala Thr Pro Val Glu Arg Val
515 520 525

Lys Leu Gln Glu Ala Leu Ser Gln Leu Asp Phe Gln Trp Glu Lys Val
530 535 540

Asn Lys Met Tyr Lys Asp Arg Gln Gly Arg Phe Asp Arg Ser Val Glu
545 550 555 560

Lys Trp Arg Arg Phe His Tyr Asp Ile Lys Ile Phe Asn Gln Trp Leu
565 570 575

Thr Glu Ala Glu Gln Phe Leu Arg Lys Thr Gln Ile Pro Glu Asn Trp
580 585 590

Glu His Ala Lys Tyr Lys Trp Tyr Leu Lys Glu Leu Gln Asp Gly Ile
595 600 605

Gly Gln Arg Gln Thr Val Val Arg Thr Leu Asn Ala Thr Gly Glu Glu
610 615 620

Ile Ile Gln Gln Ser Ser Lys Thr Asp Ala Ser Ile Leu Gln Glu Lys
625 630 635 640

Leu Gly Ser Leu Asn Leu Arg Trp Gln Glu Val Cys Lys Gln Leu Ser
645 650 655

Asp Arg Lys Lys Arg Leu Glu Glu Gln Ala Pro Gly Leu Thr Thr Ile
660 665 670

Gly Ala Ser Pro Thr Gln Thr Val Thr Leu Val Thr Gln Pro Val Val
675 680 685

Thr Lys Glu Thr Ala Ile Ser Lys Leu Glu Met Pro Ser Ser Leu Met
690 695 700

Leu Glu Ser Asp Gln Trp Lys Arg Leu His Leu Ser Leu Gln Glu Leu
705 710 715 720

Leu Val Trp Leu Gln Leu Lys Asp Asp Glu Leu Ser Arg Gln Ala Pro
725 730 735

Ile Gly Gly Asp Phe Pro Ala Val Gln Lys Gln Asn Asp Val His Arg
740 745 750

Ala Phe Lys Arg Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser Thr
755 760 765

Leu Glu Thr Val Arg Ile Phe Leu Thr Glu Gln Pro Leu Glu Gly Leu
770 775 780

Glu Lys Leu Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg Ala
785 790 795 800

Gln Asn Val Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn Thr
805 810 815

Glu Trp Glu Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys Ile
820 825 830

Asp Glu Thr Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr Asp Glu
835 840 845

Leu Asp Leu Lys Leu Arg Gln Ala Glu Val Ile Lys Gly Ser Trp Gln
850 855 860

Pro Val Gly Asp Leu Leu Ile Asp Ser Leu Gln Asp His Leu Glu Lys
865 870 875 880

Val Lys Ala Leu Arg Gly Glu Ile Ala Pro Leu Lys Glu Asn Val Ser
885 890 895

His Val Asn Asp Leu Ala Arg Gln Leu Thr Thr Leu Gly Ile Gln Leu
900 905 910

Ser Pro Tyr Asn Leu Ser Thr Leu Glu Asp Leu Asn Thr Arg Trp Lys
915 920 925

Leu Leu Gln Val Ala Val Glu Asp Arg Val Arg Gln Leu His Glu Ala
930 935 940

His Arg Asp Phe Gly Pro Ala Ser Gln His Phe Leu Ser Thr Ser Val
945 950 955 960

Gln Gly Pro Trp Glu Arg Ala Ile Ser Pro Asn Lys Val Pro Tyr Tyr
965 970 975

Ile Asn His Glu Thr Gln Thr Thr Cys Trp Asp His Pro Lys Met Thr
980 985 990

Glu Leu Tyr Gln Ser Leu Ala Asp Leu Asn Asn Val Arg Phe Ser Ala
995 1000 1005

Tyr Arg Thr Ala Met Lys Leu Arg Arg Leu Gln Lys Ala Leu Cys
1010 1015 1020

Leu Asp Leu Leu Ser Leu Ser Ala Ala Cys Asp Ala Leu Asp Gln
1025 1030 1035

His Asn Leu Lys Gln Asn Asp Gln Pro Met Asp Ile Leu Gln Ile
1040 1045 1050

Ile Asn Cys Leu Thr Thr Ile Tyr Asp Arg Leu Glu Gln Glu His
1055 1060 1065

Asn Asn Leu Val Asn Val Pro Leu Cys Val Asp Met Cys Leu Asn
1070 1075 1080

Trp Leu Leu Asn Val Tyr Asp Thr Gly Arg Thr Gly Arg Ile Arg
1085 1090 1095

Val Leu Ser Phe Lys Thr Gly Ile Ile Ser Leu Cys Lys Ala His
1100 1105 1110

Leu Glu Asp Lys Tyr Arg Tyr Leu Phe Lys Gln Val Ala Ser Ser
1115 1120 1125

Thr Gly Phe Cys Asp Gln Arg Arg Leu Gly Leu Leu Leu His Asp
1130 1135 1140

Ser Ile Gln Ile Pro Arg Gln Leu Gly Glu Val Ala Ser Phe Gly
1145 1150 1155

Gly Ser Asn Ile Glu Pro Ser Val Arg Ser Cys Phe Gln Phe Ala
1160 1165 1170

Asn Asn Lys Pro Glu Ile Glu Ala Ala Leu Phe Leu Asp Trp Met
1175 1180 1185

Arg Leu Glu Pro Gln Ser Met Val Trp Leu Pro Val Leu His Arg
1190 1195 1200

Val Ala Ala Ala Glu Thr Ala Lys His Gln Ala Lys Cys Asn Ile
1205 1210 1215

Cys Lys Glu Cys Pro Ile Ile Gly Phe Arg Tyr Arg Ser Leu Lys
1220 1225 1230

His Phe Asn Tyr Asp Ile Cys Gln Ser Cys Phe Phe Ser Gly Arg
1235 1240 1245

Val Ala Lys Gly His Lys Met His Tyr Pro Met Val Glu Tyr Cys
1250 1255 1260

Thr Pro Thr Thr Ser Gly Glu Asp Val Arg Asp Phe Ala Lys Val
1265 1270 1275

Leu Lys Asn Lys Phe Arg Thr Lys Arg Tyr Phe Ala Lys His Pro
1280 1285 1290

Arg Met Gly Tyr Leu Pro Val Gln Thr Val Leu Glu Gly Asp Asn
1295 1300 1305

Met Glu Thr
1310

<210> 84
<211> 1310
<212> PRT
<213> Artificial Sequence

<220>
<223> BXA-212372-J4V12

<400> 84

Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
1 5 10 15

Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
20 25 30

Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
35 40 45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
50 55 60

Glu Lys Gly Ser Thr Arg Val His Ala Leu Asn Asn Val Asn Lys Ala
65 70 75 80

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
85 90 95

Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
100 105 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
115 120 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
130 135 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145 150 155 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
165 170 175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
180 185 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
195 200 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
210 215 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225 230 235 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu Met Leu Pro Arg
245 250 255

Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu His His Gln Met
260 265 270

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

Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala Tyr Thr Gln Ala
290 295 300

Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro Phe Pro Ser Gln
305 310 315 320

His Leu Glu Ala Pro Glu Asp Lys Ser Phe Gly Ser Ser Leu Met Glu
325 330 335

Ser Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu
340 345 350

Ser Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile
355 360 365

Ser Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly
370 375 380

Tyr Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu
385 390 395 400

Gln Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu
405 410 415

Glu Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu
420 425 430

Cys Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His Arg Val
435 440 445

Leu Met Asp Leu Gln Asn Gln Lys Thr Glu Ile Thr His Val Ser Gln
450 455 460

Ala Leu Leu Glu Val Glu Gln Leu Leu Asn Ala Pro Asp Leu Cys Ala
465 470 475 480

Lys Asp Phe Glu Asp Leu Phe Lys Gln Glu Glu Ser Leu Lys Asn Ile
485 490 495

Lys Asp Ser Leu Gln Gln Ser Ser Gly Arg Ile Asp Ile Ile His Ser
500 505 510

Lys Lys Thr Ala Ala Leu Gln Ser Ala Thr Pro Val Glu Arg Val Lys
515 520 525

Leu Gln Glu Ala Leu Ser Gln Leu Asp Phe Gln Trp Glu Lys Val Asn
530 535 540

Lys Met Tyr Lys Asp Arg Gln Gly Arg Phe Asp Arg Ser Val Glu Lys
545 550 555 560

Trp Arg Arg Phe His Tyr Asp Ile Lys Ile Phe Asn Gln Trp Leu Thr
565 570 575

Glu Ala Glu Gln Phe Leu Arg Lys Thr Gln Ile Pro Glu Asn Trp Glu
580 585 590

His Ala Lys Tyr Lys Trp Tyr Leu Lys Glu Leu Gln Asp Gly Ile Gly
595 600 605

Gln Arg Gln Thr Val Val Arg Thr Leu Asn Ala Thr Gly Glu Glu Ile
610 615 620

Ile Gln Gln Ser Ser Lys Thr Asp Ala Ser Ile Leu Gln Glu Lys Leu
625 630 635 640

Gly Ser Leu Asn Leu Arg Trp Gln Glu Val Cys Lys Gln Leu Ser Asp
645 650 655

Arg Lys Lys Arg Leu Glu Glu Gln Ala Pro Gly Leu Thr Thr Ile Gly
660 665 670

Ala Ser Pro Thr Gln Thr Val Thr Leu Val Thr Gln Pro Val Val Thr
675 680 685

Lys Glu Thr Ala Ile Ser Lys Leu Glu Met Pro Ser Ser Leu Met Leu
690 695 700

Glu Ser Asp Gln Trp Lys Arg Leu His Leu Ser Leu Gln Glu Leu Leu
705 710 715 720

Val Trp Leu Gln Leu Lys Asp Asp Glu Leu Ser Arg Gln Ala Pro Ile
725 730 735

Gly Gly Asp Phe Pro Ala Val Gln Lys Gln Asn Asp Val His Arg Ala
740 745 750

Phe Lys Arg Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser Thr Leu
755 760 765

Glu Thr Val Arg Ile Phe Leu Thr Glu Gln Pro Leu Glu Gly Leu Glu
770 775 780

Lys Leu Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg Ala Gln
785 790 795 800

Asn Val Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn Thr Glu
805 810 815

Trp Glu Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys Ile Asp
820 825 830

Glu Thr Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr Asp Glu Leu
835 840 845

Asp Leu Lys Leu Arg Gln Ala Glu Val Ile Lys Gly Ser Trp Gln Pro
850 855 860

Val Gly Asp Leu Leu Ile Asp Ser Leu Gln Asp His Leu Glu Lys Val
865 870 875 880

Lys Ala Leu Arg Gly Glu Ile Ala Pro Leu Lys Glu Asn Val Ser His
885 890 895

Val Asn Asp Leu Ala Arg Gln Leu Thr Thr Leu Gly Ile Gln Leu Ser
900 905 910

Pro Tyr Asn Leu Ser Thr Leu Glu Asp Leu Asn Thr Arg Trp Lys Leu
915 920 925

Leu Gln Val Ala Val Glu Asp Arg Val Arg Gln Leu His Glu Ala His
930 935 940

Arg Asp Phe Gly Pro Ala Ser Gln His Phe Leu Ser Thr Ser Val Gln
945 950 955 960

Gly Pro Trp Glu Arg Ala Ile Ser Pro Asn Lys Val Pro Tyr Tyr Ile
965 970 975

Asn His Glu Thr Gln Thr Thr Cys Trp Asp His Pro Lys Met Thr Glu
980 985 990

Leu Tyr Gln Ser Leu Ala Asp Leu Asn Asn Val Arg Phe Ser Ala Tyr
995 1000 1005

Arg Thr Ala Met Lys Leu Arg Arg Leu Gln Lys Ala Leu Cys Leu
1010 1015 1020

Asp Leu Leu Ser Leu Ser Ala Ala Cys Asp Ala Leu Asp Gln His
1025 1030 1035

Asn Leu Lys Gln Asn Asp Gln Pro Met Asp Ile Leu Gln Ile Ile
1040 1045 1050

Asn Cys Leu Thr Thr Ile Tyr Asp Arg Leu Glu Gln Glu His Asn
1055 1060 1065

Asn Leu Val Asn Val Pro Leu Cys Val Asp Met Cys Leu Asn Trp
1070 1075 1080

Leu Leu Asn Val Tyr Asp Thr Gly Arg Thr Gly Arg Ile Arg Val
1085 1090 1095

Leu Ser Phe Lys Thr Gly Ile Ile Ser Leu Cys Lys Ala His Leu
1100 1105 1110

Glu Asp Lys Tyr Arg Tyr Leu Phe Lys Gln Val Ala Ser Ser Thr
1115 1120 1125

Gly Phe Cys Asp Gln Arg Arg Leu Gly Leu Leu Leu His Asp Ser
1130 1135 1140

Ile Gln Ile Pro Arg Gln Leu Gly Glu Val Ala Ser Phe Gly Gly
1145 1150 1155

Ser Asn Ile Glu Pro Ser Val Arg Ser Cys Phe Gln Phe Ala Asn
1160 1165 1170

Asn Lys Pro Glu Ile Glu Ala Ala Leu Phe Leu Asp Trp Met Arg
1175 1180 1185

Leu Glu Pro Gln Ser Met Val Trp Leu Pro Val Leu His Arg Val
1190 1195 1200

Ala Ala Ala Glu Thr Ala Lys His Gln Ala Lys Cys Asn Ile Cys
1205 1210 1215

Lys Glu Cys Pro Ile Ile Gly Phe Arg Tyr Arg Ser Leu Lys His
1220 1225 1230

Phe Asn Tyr Asp Ile Cys Gln Ser Cys Phe Phe Ser Gly Arg Val
1235 1240 1245

Ala Lys Gly His Lys Met His Tyr Pro Met Val Glu Tyr Cys Thr
1250 1255 1260

Pro Thr Thr Ser Gly Glu Asp Val Arg Asp Phe Ala Lys Val Leu
1265 1270 1275

Lys Asn Lys Phe Arg Thr Lys Arg Tyr Phe Ala Lys His Pro Arg
1280 1285 1290

Met Gly Tyr Leu Pro Val Gln Thr Val Leu Glu Gly Asp Asn Met
1295 1300 1305

Glu Thr
1310

<210> 85
<211> 1309
<212> PRT
<213> Artificial Sequence

<220>

<223> BXA-212372-J4V11

<400> 85

Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
1 5 10 15

Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
20 25 30

Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
35 40 45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
50 55 60

Glu Lys Gly Ser Thr Arg Val His Ala Leu Asn Asn Val Asn Lys Ala
65 70 75 80

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
85 90 95

Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
100 105 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
115 120 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
130 135 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145 150 155 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
165 170 175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
180 185 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
195 200 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
210 215 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225 230 235 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu Met Leu Pro Arg
245 250 255

Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu His His Gln Met
260 265 270

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

Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala Tyr Thr Gln Ala
290 295 300

Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro Phe Pro Ser Gln
305 310 315 320

His Leu Glu Ala Pro Glu Asp Lys Ser Phe Gly Ser Ser Leu Met Glu
325 330 335

Ser Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu
340 345 350

Ser Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile
355 360 365

Ser Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly
370 375 380

Tyr Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu
385 390 395 400

Gln Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu
405 410 415

Glu Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu
420 425 430

Cys Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His Arg Val
435 440 445

Leu Met Asp Leu Gln Asn Gln Lys Glu Ile Thr His Val Ser Gln Ala
450 455 460

Leu Leu Glu Val Glu Gln Leu Leu Asn Ala Pro Asp Leu Cys Ala Lys
465 470 475 480

Asp Phe Glu Asp Leu Phe Lys Gln Glu Glu Ser Leu Lys Asn Ile Lys
485 490 495

Asp Ser Leu Gln Gln Ser Ser Gly Arg Ile Asp Ile Ile His Ser Lys
500 505 510

Lys Thr Ala Ala Leu Gln Ser Ala Thr Pro Val Glu Arg Val Lys Leu
515 520 525

Gln Glu Ala Leu Ser Gln Leu Asp Phe Gln Trp Glu Lys Val Asn Lys
530 535 540

Met Tyr Lys Asp Arg Gln Gly Arg Phe Asp Arg Ser Val Glu Lys Trp
545 550 555 560

Arg Arg Phe His Tyr Asp Ile Lys Ile Phe Asn Gln Trp Leu Thr Glu
565 570 575

Ala Glu Gln Phe Leu Arg Lys Thr Gln Ile Pro Glu Asn Trp Glu His
580 585 590

Ala Lys Tyr Lys Trp Tyr Leu Lys Glu Leu Gln Asp Gly Ile Gly Gln
595 600 605

Arg Gln Thr Val Val Arg Thr Leu Asn Ala Thr Gly Glu Glu Ile Ile
610 615 620

Gln Gln Ser Ser Lys Thr Asp Ala Ser Ile Leu Gln Glu Lys Leu Gly
625 630 635 640

Ser Leu Asn Leu Arg Trp Gln Glu Val Cys Lys Gln Leu Ser Asp Arg
645 650 655

Lys Lys Arg Leu Glu Glu Gln Ala Pro Gly Leu Thr Thr Ile Gly Ala
660 665 670

Ser Pro Thr Gln Thr Val Thr Leu Val Thr Gln Pro Val Val Thr Lys
675 680 685

Glu Thr Ala Ile Ser Lys Leu Glu Met Pro Ser Ser Leu Met Leu Glu
690 695 700

Ser Asp Gln Trp Lys Arg Leu His Leu Ser Leu Gln Glu Leu Leu Val
705 710 715 720

Trp Leu Gln Leu Lys Asp Asp Glu Leu Ser Arg Gln Ala Pro Ile Gly
725 730 735

Gly Asp Phe Pro Ala Val Gln Lys Gln Asn Asp Val His Arg Ala Phe
740 745 750

Lys Arg Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser Thr Leu Glu
755 760 765

Thr Val Arg Ile Phe Leu Thr Glu Gln Pro Leu Glu Gly Leu Glu Lys
770 775 780

Leu Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg Ala Gln Asn
785 790 795 800

Val Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn Thr Glu Trp
805 810 815

Glu Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys Ile Asp Glu
820 825 830

Thr Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr Asp Glu Leu Asp
835 840 845

Leu Lys Leu Arg Gln Ala Glu Val Ile Lys Gly Ser Trp Gln Pro Val
850 855 860

Gly Asp Leu Leu Ile Asp Ser Leu Gln Asp His Leu Glu Lys Val Lys
865 870 875 880

Ala Leu Arg Gly Glu Ile Ala Pro Leu Lys Glu Asn Val Ser His Val
885 890 895

Asn Asp Leu Ala Arg Gln Leu Thr Thr Leu Gly Ile Gln Leu Ser Pro
900 905 910

Tyr Asn Leu Ser Thr Leu Glu Asp Leu Asn Thr Arg Trp Lys Leu Leu
915 920 925

Gln Val Ala Val Glu Asp Arg Val Arg Gln Leu His Glu Ala His Arg
930 935 940

Asp Phe Gly Pro Ala Ser Gln His Phe Leu Ser Thr Ser Val Gln Gly
945 950 955 960

Pro Trp Glu Arg Ala Ile Ser Pro Asn Lys Val Pro Tyr Tyr Ile Asn
965 970 975

His Glu Thr Gln Thr Thr Cys Trp Asp His Pro Lys Met Thr Glu Leu
980 985 990

Tyr Gln Ser Leu Ala Asp Leu Asn Asn Val Arg Phe Ser Ala Tyr Arg
995 1000 1005

Thr Ala Met Lys Leu Arg Arg Leu Gln Lys Ala Leu Cys Leu Asp
1010 1015 1020

Leu Leu Ser Leu Ser Ala Ala Cys Asp Ala Leu Asp Gln His Asn
1025 1030 1035

Leu Lys Gln Asn Asp Gln Pro Met Asp Ile Leu Gln Ile Ile Asn
1040 1045 1050

Cys	Leu	Thr	Thr	Ile	Tyr	Asp	Arg	Leu	Glu	Gln	Glu	His	Asn	Asn
1055						1060					1065			
Leu	Val	Asn	Val	Pro	Leu	Cys	Val	Asp	Met	Cys	Leu	Asn	Trp	Leu
1070						1075					1080			
Leu	Asn	Val	Tyr	Asp	Thr	Gly	Arg	Thr	Gly	Arg	Ile	Arg	Val	Leu
1085						1090					1095			
Ser	Phe	Lys	Thr	Gly	Ile	Ile	Ser	Leu	Cys	Lys	Ala	His	Leu	Glu
1100						1105					1110			
Asp	Lys	Tyr	Arg	Tyr	Leu	Phe	Lys	Gln	Val	Ala	Ser	Ser	Thr	Gly
1115						1120					1125			
Phe	Cys	Asp	Gln	Arg	Arg	Leu	Gly	Leu	Leu	Leu	His	Asp	Ser	Ile
1130						1135					1140			
Gln	Ile	Pro	Arg	Gln	Leu	Gly	Glu	Val	Ala	Ser	Phe	Gly	Gly	Ser
1145						1150					1155			
Asn	Ile	Glu	Pro	Ser	Val	Arg	Ser	Cys	Phe	Gln	Phe	Ala	Asn	Asn
1160						1165					1170			
Lys	Pro	Glu	Ile	Glu	Ala	Ala	Leu	Phe	Leu	Asp	Trp	Met	Arg	Leu
1175						1180					1185			
Glu	Pro	Gln	Ser	Met	Val	Trp	Leu	Pro	Val	Leu	His	Arg	Val	Ala
1190						1195					1200			
Ala	Ala	Glu	Thr	Ala	Lys	His	Gln	Ala	Lys	Cys	Asn	Ile	Cys	Lys
1205						1210					1215			
Glu	Cys	Pro	Ile	Ile	Gly	Phe	Arg	Tyr	Arg	Ser	Leu	Lys	His	Phe
1220						1225					1230			
Asn	Tyr	Asp	Ile	Cys	Gln	Ser	Cys	Phe	Phe	Ser	Gly	Arg	Val	Ala
1235						1240					1245			
Lys	Gly	His	Lys	Met	His	Tyr	Pro	Met	Val	Glu	Tyr	Cys	Thr	Pro
1250						1255					1260			

Thr Thr Ser Gly Glu Asp Val Arg Asp Phe Ala Lys Val Leu Lys
1265 1270 1275

Asn Lys Phe Arg Thr Lys Arg Tyr Phe Ala Lys His Pro Arg Met
1280 1285 1290

Gly Tyr Leu Pro Val Gln Thr Val Leu Glu Gly Asp Asn Met Glu
1295 1300 1305

Thr

<210> 86
<211> 1309
<212> PRT
<213> Artificial Sequence

<220>
<223> BXA-212372-J4V4

<400> 86

Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
1 5 10 15

Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
20 25 30

Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
35 40 45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
50 55 60

Glu Lys Gly Ser Thr Arg Val His Ala Leu Asn Asn Val Asn Lys Ala
65 70 75 80

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
85 90 95

Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
100 105 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
115 120 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
130 135 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145 150 155 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
165 170 175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
180 185 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
195 200 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
210 215 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225 230 235 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu Met Leu Pro Arg
245 250 255

Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu His His Gln Met
260 265 270

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

Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala Tyr Thr Gln Ala
290 295 300

Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro Phe Pro Ser Gln
305 310 315 320

His Leu Glu Ala Pro Glu Asp Lys Ser Phe Gly Ser Ser Leu Met Glu
325 330 335

Ser Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu
340 345 350

Ser Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile
355 360 365

Ser Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly
370 375 380

Tyr Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu
385 390 395 400

Gln Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu
405 410 415

Glu Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu
420 425 430

Cys Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His Arg Val
435 440 445

Leu Met Asp Leu Thr Tyr Leu Thr Glu Ile Thr His Val Ser Gln Ala
450 455 460

Leu Leu Glu Val Glu Gln Leu Leu Asn Ala Pro Asp Leu Cys Ala Lys
465 470 475 480

Asp Phe Glu Asp Leu Phe Lys Gln Glu Glu Ser Leu Lys Asn Ile Lys
485 490 495

Asp Ser Leu Gln Gln Ser Ser Gly Arg Ile Asp Ile Ile His Ser Lys
500 505 510

Lys Thr Ala Ala Leu Gln Ser Ala Thr Pro Val Glu Arg Val Lys Leu
515 520 525

Gln Glu Ala Leu Ser Gln Leu Asp Phe Gln Trp Glu Lys Val Asn Lys
530 535 540

Met Tyr Lys Asp Arg Gln Gly Arg Phe Asp Arg Ser Val Glu Lys Trp
545 550 555 560

Arg Arg Phe His Tyr Asp Ile Lys Ile Phe Asn Gln Trp Leu Thr Glu
565 570 575

Ala Glu Gln Phe Leu Arg Lys Thr Gln Ile Pro Glu Asn Trp Glu His
580 585 590

Ala Lys Tyr Lys Trp Tyr Leu Lys Glu Leu Gln Asp Gly Ile Gly Gln
595 600 605

Arg Gln Thr Val Val Arg Thr Leu Asn Ala Thr Gly Glu Glu Ile Ile
610 615 620

Gln Gln Ser Ser Lys Thr Asp Ala Ser Ile Leu Gln Glu Lys Leu Gly
625 630 635 640

Ser Leu Asn Leu Arg Trp Gln Glu Val Cys Lys Gln Leu Ser Asp Arg
645 650 655

Lys Lys Arg Leu Glu Glu Gln Ala Pro Gly Leu Thr Thr Ile Gly Ala
660 665 670

Ser Pro Thr Gln Thr Val Thr Leu Val Thr Gln Pro Val Val Thr Lys
675 680 685

Glu Thr Ala Ile Ser Lys Leu Glu Met Pro Ser Ser Leu Met Leu Glu
690 695 700

Ser Asp Gln Trp Lys Arg Leu His Leu Ser Leu Gln Glu Leu Leu Val
705 710 715 720

Trp Leu Gln Leu Lys Asp Asp Glu Leu Ser Arg Gln Ala Pro Ile Gly
725 730 735

Gly Asp Phe Pro Ala Val Gln Lys Gln Asn Asp Val His Arg Ala Phe
740 745 750

Lys Arg Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser Thr Leu Glu
755 760 765

Thr Val Arg Ile Phe Leu Thr Glu Gln Pro Leu Glu Gly Leu Glu Lys
770 775 780

Leu Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg Ala Gln Asn
785 790 795 800

Val Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn Thr Glu Trp
805 810 815

Glu Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys Ile Asp Glu
820 825 830

Thr Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr Asp Glu Leu Asp
835 840 845

Leu Lys Leu Arg Gln Ala Glu Val Ile Lys Gly Ser Trp Gln Pro Val
850 855 860

Gly Asp Leu Leu Ile Asp Ser Leu Gln Asp His Leu Glu Lys Val Lys
865 870 875 880

Ala Leu Arg Gly Glu Ile Ala Pro Leu Lys Glu Asn Val Ser His Val
885 890 895

Asn Asp Leu Ala Arg Gln Leu Thr Thr Leu Gly Ile Gln Leu Ser Pro
900 905 910

Tyr Asn Leu Ser Thr Leu Glu Asp Leu Asn Thr Arg Trp Lys Leu Leu
915 920 925

Gln Val Ala Val Glu Asp Arg Val Arg Gln Leu His Glu Ala His Arg
930 935 940

Asp Phe Gly Pro Ala Ser Gln His Phe Leu Ser Thr Ser Val Gln Gly
945 950 955 960

Pro Trp Glu Arg Ala Ile Ser Pro Asn Lys Val Pro Tyr Tyr Ile Asn
965 970 975

His Glu Thr Gln Thr Thr Cys Trp Asp His Pro Lys Met Thr Glu Leu
980 985 990

Tyr Gln Ser Leu Ala Asp Leu Asn Asn Val Arg Phe Ser Ala Tyr Arg
995 1000 1005

Thr Ala Met Lys Leu Arg Arg Leu Gln Lys Ala Leu Cys Leu Asp
1010 1015 1020

Leu Leu Ser Leu Ser Ala Ala Cys Asp Ala Leu Asp Gln His Asn
1025 1030 1035

Leu Lys Gln Asn Asp Gln Pro Met Asp Ile Leu Gln Ile Ile Asn
1040 1045 1050

Cys Leu Thr Thr Ile Tyr Asp Arg Leu Glu Gln Glu His Asn Asn
1055 1060 1065

Leu Val Asn Val Pro Leu Cys Val Asp Met Cys Leu Asn Trp Leu
1070 1075 1080

Leu Asn Val Tyr Asp Thr Gly Arg Thr Gly Arg Ile Arg Val Leu
1085 1090 1095

Ser Phe Lys Thr Gly Ile Ile Ser Leu Cys Lys Ala His Leu Glu
1100 1105 1110

Asp Lys Tyr Arg Tyr Leu Phe Lys Gln Val Ala Ser Ser Thr Gly
1115 1120 1125

Phe Cys Asp Gln Arg Arg Leu Gly Leu Leu Leu His Asp Ser Ile
1130 1135 1140

Gln Ile Pro Arg Gln Leu Gly Glu Val Ala Ser Phe Gly Gly Ser
1145 1150 1155

Asn Ile Glu Pro Ser Val Arg Ser Cys Phe Gln Phe Ala Asn Asn
1160 1165 1170

Lys Pro Glu Ile Glu Ala Ala Leu Phe Leu Asp Trp Met Arg Leu
1175 1180 1185

Glu Pro Gln Ser Met Val Trp Leu Pro Val Leu His Arg Val Ala
1190 1195 1200

Ala Ala Glu Thr Ala Lys His Gln Ala Lys Cys Asn Ile Cys Lys
1205 1210 1215

Glu Cys Pro Ile Ile Gly Phe Arg Tyr Arg Ser Leu Lys His Phe
1220 1225 1230

Asn Tyr Asp Ile Cys Gln Ser Cys Phe Phe Ser Gly Arg Val Ala
1235 1240 1245

Lys Gly His Lys Met His Tyr Pro Met Val Glu Tyr Cys Thr Pro
1250 1255 1260

Thr Thr Ser Gly Glu Asp Val Arg Asp Phe Ala Lys Val Leu Lys
1265 1270 1275

Asn Lys Phe Arg Thr Lys Arg Tyr Phe Ala Lys His Pro Arg Met
1280 1285 1290

Gly Tyr Leu Pro Val Gln Thr Val Leu Glu Gly Asp Asn Met Glu
1295 1300 1305

Thr

<210> 87

<211> 1308

<212> PRT

<213> Artificial Sequence

<220>

<223> BXA-212372-J4

<400> 87

Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
1 5 10 15

Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
20 25 30

Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
35 40 45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
50 55 60

Glu Lys Gly Ser Thr Arg Val His Ala Leu Asn Asn Val Asn Lys Ala
65 70 75 80

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
85 90 95

Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
100 105 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
115 120 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
130 135 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145 150 155 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
165 170 175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
180 185 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
195 200 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
210 215 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225 230 235 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu Met Leu Pro Arg
245 250 255

Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu His His Gln Met
260 265 270

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

Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala Tyr Thr Gln Ala
290 295 300

Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro Phe Pro Ser Gln
305 310 315 320

His Leu Glu Ala Pro Glu Asp Lys Ser Phe Gly Ser Ser Leu Met Glu
325 330 335

Ser Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu
340 345 350

Ser Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile
355 360 365

Ser Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly
370 375 380

Tyr Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu
385 390 395 400

Gln Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu
405 410 415

Glu Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu
420 425 430

Cys Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His Ser Tyr
435 440 445

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

Leu Glu Val Glu Gln Leu Leu Asn Ala Pro Asp Leu Cys Ala Lys Asp
465 470 475 480

Phe Glu Asp Leu Phe Lys Gln Glu Glu Ser Leu Lys Asn Ile Lys Asp
485 490 495

Ser Leu Gln Gln Ser Ser Gly Arg Ile Asp Ile Ile His Ser Lys Lys
500 505 510

Thr Ala Ala Leu Gln Ser Ala Thr Pro Val Glu Arg Val Lys Leu Gln
515 520 525

Glu Ala Leu Ser Gln Leu Asp Phe Gln Trp Glu Lys Val Asn Lys Met
530 535 540

Tyr Lys Asp Arg Gln Gly Arg Phe Asp Arg Ser Val Glu Lys Trp Arg
545 550 555 560

Arg Phe His Tyr Asp Ile Lys Ile Phe Asn Gln Trp Leu Thr Glu Ala
565 570 575

Glu Gln Phe Leu Arg Lys Thr Gln Ile Pro Glu Asn Trp Glu His Ala
580 585 590

Lys Tyr Lys Trp Tyr Leu Lys Glu Leu Gln Asp Gly Ile Gly Gln Arg
595 600 605

Gln Thr Val Val Arg Thr Leu Asn Ala Thr Gly Glu Glu Ile Ile Gln
610 615 620

Gln Ser Ser Lys Thr Asp Ala Ser Ile Leu Gln Glu Lys Leu Gly Ser
625 630 635 640

Leu Asn Leu Arg Trp Gln Glu Val Cys Lys Gln Leu Ser Asp Arg Lys
645 650 655

Lys Arg Leu Glu Glu Gln Ala Pro Gly Leu Thr Thr Ile Gly Ala Ser
660 665 670

Pro Thr Gln Thr Val Thr Leu Val Thr Gln Pro Val Val Thr Lys Glu
675 680 685

Thr Ala Ile Ser Lys Leu Glu Met Pro Ser Ser Leu Met Leu Glu Ser
690 695 700

Asp Gln Trp Lys Arg Leu His Leu Ser Leu Gln Glu Leu Leu Val Trp
705 710 715 720

Leu Gln Leu Lys Asp Asp Glu Leu Ser Arg Gln Ala Pro Ile Gly Gly
725 730 735

Asp Phe Pro Ala Val Gln Lys Gln Asn Asp Val His Arg Ala Phe Lys
740 745 750

Arg Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser Thr Leu Glu Thr
755 760 765

Val Arg Ile Phe Leu Thr Glu Gln Pro Leu Glu Gly Leu Glu Lys Leu
770 775 780

Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg Ala Gln Asn Val
785 790 795 800

Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn Thr Glu Trp Glu
805 810 815

Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys Ile Asp Glu Thr
820 825 830

Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr Asp Glu Leu Asp Leu
835 840 845

Lys Leu Arg Gln Ala Glu Val Ile Lys Gly Ser Trp Gln Pro Val Gly
850 855 860

Asp Leu Leu Ile Asp Ser Leu Gln Asp His Leu Glu Lys Val Lys Ala
865 870 875 880

Leu Arg Gly Glu Ile Ala Pro Leu Lys Glu Asn Val Ser His Val Asn
885 890 895

Asp Leu Ala Arg Gln Leu Thr Thr Leu Gly Ile Gln Leu Ser Pro Tyr
900 905 910

Asn Leu Ser Thr Leu Glu Asp Leu Asn Thr Arg Trp Lys Leu Leu Gln
915 920 925

Val Ala Val Glu Asp Arg Val Arg Gln Leu His Glu Ala His Arg Asp
930 935 940

Phe Gly Pro Ala Ser Gln His Phe Leu Ser Thr Ser Val Gln Gly Pro
945 950 955 960

Trp Glu Arg Ala Ile Ser Pro Asn Lys Val Pro Tyr Tyr Ile Asn His
965 970 975

Glu Thr Gln Thr Thr Cys Trp Asp His Pro Lys Met Thr Glu Leu Tyr
980 985 990

Gln Ser Leu Ala Asp Leu Asn Asn Val Arg Phe Ser Ala Tyr Arg Thr
995 1000 1005

Ala Met Lys Leu Arg Arg Leu Gln Lys Ala Leu Cys Leu Asp Leu
1010 1015 1020

Leu Ser Leu Ser Ala Ala Cys Asp Ala Leu Asp Gln His Asn Leu
1025 1030 1035

Lys Gln Asn Asp Gln Pro Met Asp Ile Leu Gln Ile Ile Asn Cys
1040 1045 1050

Leu Thr Thr Ile Tyr Asp Arg Leu Glu Gln Glu His Asn Asn Leu
1055 1060 1065

Val Asn Val Pro Leu Cys Val Asp Met Cys Leu Asn Trp Leu Leu
1070 1075 1080

Asn Val Tyr Asp Thr Gly Arg Thr Gly Arg Ile Arg Val Leu Ser
1085 1090 1095

Phe Lys Thr Gly Ile Ile Ser Leu Cys Lys Ala His Leu Glu Asp
1100 1105 1110

Lys Tyr Arg Tyr Leu Phe Lys Gln Val Ala Ser Ser Thr Gly Phe
1115 1120 1125

Cys Asp Gln Arg Arg Leu Gly Leu Leu Leu His Asp Ser Ile Gln
1130 1135 1140

Ile Pro Arg Gln Leu Gly Glu Val Ala Ser Phe Gly Gly Ser Asn
1145 1150 1155

Ile Glu Pro Ser Val Arg Ser Cys Phe Gln Phe Ala Asn Asn Lys
1160 1165 1170

Pro Glu Ile Glu Ala Ala Leu Phe Leu Asp Trp Met Arg Leu Glu
1175 1180 1185

Pro Gln Ser Met Val Trp Leu Pro Val Leu His Arg Val Ala Ala
1190 1195 1200

Ala Glu Thr Ala Lys His Gln Ala Lys Cys Asn Ile Cys Lys Glu
1205 1210 1215

Cys Pro Ile Ile Gly Phe Arg Tyr Arg Ser Leu Lys His Phe Asn
1220 1225 1230

Tyr Asp Ile Cys Gln Ser Cys Phe Phe Ser Gly Arg Val Ala Lys
1235 1240 1245

Gly His Lys Met His Tyr Pro Met Val Glu Tyr Cys Thr Pro Thr
1250 1255 1260

Thr Ser Gly Glu Asp Val Arg Asp Phe Ala Lys Val Leu Lys Asn
1265 1270 1275

Lys Phe Arg Thr Lys Arg Tyr Phe Ala Lys His Pro Arg Met Gly
1280 1285 1290

Tyr Leu Pro Val Gln Thr Val Leu Glu Gly Asp Asn Met Glu Thr
1295 1300 1305

<210> 88
<211> 1328
<212> PRT
<213> Artificial Sequence

<220>
<223> BXA-212372

<400> 88

Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
1 5 10 15

Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
20 25 30

Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
35 40 45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
50 55 60

Glu Lys Gly Ser Thr Arg Val His Ala Leu Asn Asn Val Asn Lys Ala
65 70 75 80

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
85 90 95

Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
100 105 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
115 120 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
130 135 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145 150 155 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
165 170 175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
180 185 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
195 200 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
210 215 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225 230 235 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu Met Leu Pro Arg
245 250 255

Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu His His Gln Met
260 265 270

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

Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala Tyr Thr Gln Ala
290 295 300

Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro Phe Pro Ser Gln
305 310 315 320

His Leu Glu Ala Pro Glu Asp Lys Ser Phe Gly Ser Ser Leu Met Glu
325 330 335

Ser Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu
340 345 350

Ser Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile
355 360 365

Ser Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly
370 375 380

Tyr Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu
385 390 395 400

Gln Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu
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Glu Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu
420 425 430

Cys Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His Ile His
435 440 445

Thr Val Arg Glu Glu Thr Met Met Val Met Thr Glu Asp Met Pro Leu
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Glu Ile Ser Tyr Val Pro Ser Thr Tyr Leu Thr Glu Ile Thr His Val
465 470 475 480

Ser Gln Ala Leu Leu Glu Val Glu Gln Leu Leu Asn Ala Pro Asp Leu
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Cys Ala Lys Asp Phe Glu Asp Leu Phe Lys Gln Glu Glu Ser Leu Lys
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Asn Ile Lys Asp Ser Leu Gln Gln Ser Ser Gly Arg Ile Asp Ile Ile
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His Ser Lys Lys Thr Ala Ala Leu Gln Ser Ala Thr Pro Val Glu Arg
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Val Lys Leu Gln Glu Ala Leu Ser Gln Leu Asp Phe Gln Trp Glu Lys
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Val Asn Lys Met Tyr Lys Asp Arg Gln Gly Arg Phe Asp Arg Ser Val
565 570 575

Glu Lys Trp Arg Arg Phe His Tyr Asp Ile Lys Ile Phe Asn Gln Trp
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Leu Thr Glu Ala Glu Gln Phe Leu Arg Lys Thr Gln Ile Pro Glu Asn
595 600 605

Trp Glu His Ala Lys Tyr Lys Trp Tyr Leu Lys Glu Leu Gln Asp Gly
610 615 620

Ile Gly Gln Arg Gln Thr Val Val Arg Thr Leu Asn Ala Thr Gly Glu
625 630 635 640

Glu Ile Ile Gln Gln Ser Ser Lys Thr Asp Ala Ser Ile Leu Gln Glu
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Lys Leu Gly Ser Leu Asn Leu Arg Trp Gln Glu Val Cys Lys Gln Leu
660 665 670

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

Ile Gly Ala Ser Pro Thr Gln Thr Val Thr Leu Val Thr Gln Pro Val
690 695 700

Val Thr Lys Glu Thr Ala Ile Ser Lys Leu Glu Met Pro Ser Ser Leu
705 710 715 720

Met Leu Glu Ser Asp Gln Trp Lys Arg Leu His Leu Ser Leu Gln Glu
725 730 735

Leu Leu Val Trp Leu Gln Leu Lys Asp Asp Glu Leu Ser Arg Gln Ala
740 745 750

Pro Ile Gly Gly Asp Phe Pro Ala Val Gln Lys Gln Asn Asp Val His
755 760 765

Arg Ala Phe Lys Arg Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser
770 775 780

Thr Leu Glu Thr Val Arg Ile Phe Leu Thr Glu Gln Pro Leu Glu Gly
785 790 795 800

Leu Glu Lys Leu Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg
805 810 815

Ala Gln Asn Val Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn
820 825 830

Thr Glu Trp Glu Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys
835 840 845

Ile Asp Glu Thr Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr Asp
850 855 860

Glu Leu Asp Leu Lys Leu Arg Gln Ala Glu Val Ile Lys Gly Ser Trp
865 870 875 880

Gln Pro Val Gly Asp Leu Leu Ile Asp Ser Leu Gln Asp His Leu Glu
885 890 895

Lys Val Lys Ala Leu Arg Gly Glu Ile Ala Pro Leu Lys Glu Asn Val
900 905 910

Ser His Val Asn Asp Leu Ala Arg Gln Leu Thr Thr Leu Gly Ile Gln
915 920 925

Leu Ser Pro Tyr Asn Leu Ser Thr Leu Glu Asp Leu Asn Thr Arg Trp
930 935 940

Lys Leu Leu Gln Val Ala Val Glu Asp Arg Val Arg Gln Leu His Glu
945 950 955 960

Ala His Arg Asp Phe Gly Pro Ala Ser Gln His Phe Leu Ser Thr Ser
965 970 975

Val Gln Gly Pro Trp Glu Arg Ala Ile Ser Pro Asn Lys Val Pro Tyr
980 985 990

Tyr Ile Asn His Glu Thr Gln Thr Thr Cys Trp Asp His Pro Lys Met
995 1000 1005

Thr Glu Leu Tyr Gln Ser Leu Ala Asp Leu Asn Asn Val Arg Phe
1010 1015 1020

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Leu	Cys	Leu	Asp	Leu	Leu	Ser	Leu	Ser	Ala	Ala	Cys	Asp	Ala	Leu
1040						1045					1050			
Asp	Gln	His	Asn	Leu	Lys	Gln	Asn	Asp	Gln	Pro	Met	Asp	Ile	Leu
1055						1060					1065			
Gln	Ile	Ile	Asn	Cys	Leu	Thr	Thr	Ile	Tyr	Asp	Arg	Leu	Glu	Gln
1070						1075					1080			
Glu	His	Asn	Asn	Leu	Val	Asn	Val	Pro	Leu	Cys	Val	Asp	Met	Cys
1085						1090					1095			
Leu	Asn	Trp	Leu	Leu	Asn	Val	Tyr	Asp	Thr	Gly	Arg	Thr	Gly	Arg
1100						1105					1110			
Ile	Arg	Val	Leu	Ser	Phe	Lys	Thr	Gly	Ile	Ile	Ser	Leu	Cys	Lys
1115						1120					1125			
Ala	His	Leu	Glu	Asp	Lys	Tyr	Arg	Tyr	Leu	Phe	Lys	Gln	Val	Ala
1130						1135					1140			
Ser	Ser	Thr	Gly	Phe	Cys	Asp	Gln	Arg	Arg	Leu	Gly	Leu	Leu	Leu
1145						1150					1155			
His	Asp	Ser	Ile	Gln	Ile	Pro	Arg	Gln	Leu	Gly	Glu	Val	Ala	Ser
1160						1165					1170			
Phe	Gly	Gly	Ser	Asn	Ile	Glu	Pro	Ser	Val	Arg	Ser	Cys	Phe	Gln
1175						1180					1185			
Phe	Ala	Asn	Asn	Lys	Pro	Glu	Ile	Glu	Ala	Ala	Leu	Phe	Leu	Asp
1190						1195					1200			
Trp	Met	Arg	Leu	Glu	Pro	Gln	Ser	Met	Val	Trp	Leu	Pro	Val	Leu
1205						1210					1215			
His	Arg	Val	Ala	Ala	Ala	Glu	Thr	Ala	Lys	His	Gln	Ala	Lys	Cys
1220						1225					1230			

Asn	Ile	Cys	Lys	Glu	Cys	Pro	Ile	Ile	Gly	Phe	Arg	Tyr	Arg	Ser
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Leu	Lys	His	Phe	Asn	Tyr	Asp	Ile	Cys	Gln	Ser	Cys	Phe	Phe	Ser
1250						1255					1260			
Gly	Arg	Val	Ala	Lys	Gly	His	Lys	Met	His	Tyr	Pro	Met	Val	Glu
1265						1270					1275			
Tyr	Cys	Thr	Pro	Thr	Thr	Ser	Gly	Glu	Asp	Val	Arg	Asp	Phe	Ala
1280						1285					1290			
Lys	Val	Leu	Lys	Asn	Lys	Phe	Arg	Thr	Lys	Arg	Tyr	Phe	Ala	Lys
1295						1300					1305			
His	Pro	Arg	Met	Gly	Tyr	Leu	Pro	Val	Gln	Thr	Val	Leu	Glu	Gly
1310						1315					1320			
Asp	Asn	Met	Glu	Thr										
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gcggtgctcc cgccgcctc gataaaaggc tccggggccg gcggcggccc acgagctacc	300
cggaggagcg ggaggcacgc gtctctaagg taaatataaa atTTTtaagt gtataatgtg	360
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accacc	426

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aagcctcggg tcaagagcta cgcctataca caggccgcct acgtgaccac cagcgatccc 180
acaagaagcc catttccaag ccagcatctg gaagcccctg aggacaagag ctttggcagc 240

agcctgatgg aaagc 255

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<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Spectrin-1

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cagtttcaca cccacgaggg ctacatgatg gacctgacag cccatcaggg cagagtgggc 180
aatatcctgc agctgggctc taagctgatc ggcacaggca agctgagcga ggacgaagag 240
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agcatggaaa agcagagcaa cctgcac 327

<210> 93
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Modified Spectrin-16

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<211> 321
<212> DNA
<213> Artificial Sequence

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<223> Spectrin-17

<400> 94

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tggtatctga aagaactgca ggacggcatc ggccagaggc agacagtcgt tagaactg	180
aatgccaccg gcgaggaaat catccagcag agcagcaaga ccgacgccag catcctgcaa	240
gagaagctgg gcagcctgaa cctgagatgg caagaagtgt gcaagcagct gtccgaccgg	300
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<210> 95

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Hinge 3

<400> 95

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gag	123

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<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> Spectrin-23

<400> 96

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cagaacgacg tgcacagagc cttcaagcgg gaactgaaaa caaaagaacc cgtgatcatg	180
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<211> 324
<212> DNA
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<220>
<223> Spectrin-24

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tcccacgtga acgacctggc cagacagctg acaaccctgg gaatccagct gtccccttac 240
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gatagagtgc gacagctgca cgag 324

<210> 98
<211> 216
<212> DNA
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<220>
<223> Hinge 4

<400> 98
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gtgcgcttta gcgctaccg gaccgcatg aagctg 216

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<212> DNA
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<223> CR

<400> 99
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tgctgacca ccatctacga ccggctggaa caagagcaca acaacctcgt gaatgtgccc	180
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