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<151> 2018-08-09

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caaaacggaa aggtcaaggt gttccagggg aaccaggact cgttcacacc cgtgggtgaac	4260
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<210> 7
<211> 1734
<212> DNA
<213> Artificial Sequence

<220>
<223> coFVIII-52-NT58

<400> 7
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<210> 8
 <211> 2583
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-52-CT

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<210> 9
 <211> 1734
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-62-NT58

<400> 9	
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tacgacaccg tggatgatcac cctgaagaac atggcgtccc acccgtgtc cctgcatgcg	300
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cgggaaaagg aggacgataa agtgttcccc ggcggtcgc atacttacgt gtggcaagtc	420
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catgtggacc tcgtgaagga cctgaacagc gggctgattg gtgcacttct cgtgtgccgc	540
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cgggacctgg catcgggact cattggaccg ctgctgatct gctacaaaga gtcggtggat	1680
caacgcggca accagatcat gtccgacaag cgcaacgtga tcctgttctc cgtg	1734

<210> 10
 <211> 2583
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-62-CT

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ggctacgtgt tcgacagcct gcagctgagc gtgtgcctgc acgaggtggc ctactggtac	180

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tga	2583

<210> 11
 <211> 1734
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-25-NT58

<400> 11	
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aacaccagcg tgggtgtacaa gaagaccctg ttcgtggagt tcttgacca cctgttcaac	180
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tacgacaccg tggatcatcac cctgaagaac atggccagcc acccgtctc cctgcacgcc	300
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<210> 12
<211> 2583
<212> DNA
<213> Artificial Sequence

<220>
<223> coFVIII-25-CT

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agggacctgg cctctggcct gattggcccc ctgctgatct gctacaagga gtctgtggac	1680
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aagcacaaga tgggtgtacga agataccctg accctgttcc ctttctccgg cgaaacgggtg	300
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Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
115 120 125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
130 135 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145 150 155 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
165 170 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
180 185 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
195 200 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
210 215 220

Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
225 230 235 240

Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
245 250 255

Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
260 265 270

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

Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
290 295 300

Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met

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

Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
515 520 525

Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
530 535 540

Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
545 550 555 560

Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
565 570 575

Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
580 585 590

Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
595 600 605

Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
610 615 620

Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
625 630 635 640

Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
645 650 655

Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
660 665 670

Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp
675 680 685

Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala
690 695 700

Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu

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Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	Asn	Asn	Ala
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Ile	Glu	Pro	Arg	Ser	Phe	Ser	Gln	Asn	Ser	Arg	His	Pro	Ser	Thr	Arg
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Gln	Lys	Gln	Phe	Asn	Ala	Thr	Thr	Ile	Pro	Glu	Asn	Asp	Ile	Glu	Lys
		755					760					765			
Thr	Asp	Pro	Trp	Phe	Ala	His	Arg	Thr	Pro	Met	Pro	Lys	Ile	Gln	Asn
	770					775					780				
Val	Ser	Ser	Ser	Asp	Leu	Leu	Met	Leu	Leu	Arg	Gln	Ser	Pro	Thr	Pro
785					790					795					800
His	Gly	Leu	Ser	Leu	Ser	Asp	Leu	Gln	Glu	Ala	Lys	Tyr	Glu	Thr	Phe
			805					810						815	
Ser	Asp	Asp	Pro	Ser	Pro	Gly	Ala	Ile	Asp	Ser	Asn	Asn	Ser	Leu	Ser
			820					825					830		
Glu	Met	Thr	His	Phe	Arg	Pro	Gln	Leu	His	His	Ser	Gly	Asp	Met	Val
		835					840					845			
Phe	Thr	Pro	Glu	Ser	Gly	Leu	Gln	Leu	Arg	Leu	Asn	Glu	Lys	Leu	Gly
	850					855					860				
Thr	Thr	Ala	Ala	Thr	Glu	Leu	Lys	Lys	Leu	Asp	Phe	Lys	Val	Ser	Ser
865					870					875					880
Thr	Ser	Asn	Asn	Leu	Ile	Ser	Thr	Ile	Pro	Ser	Asp	Asn	Leu	Ala	Ala
			885						890					895	
Gly	Thr	Asp	Asn	Thr	Ser	Ser	Leu	Gly	Pro	Pro	Ser	Met	Pro	Val	His
		900						905					910		

Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys Ser Ser Pro
915 920 925

Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn Asn Asp
930 935 940

Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp
945 950 955 960

Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys
965 970 975

Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys
980 985 990

Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala
995 1000 1005

Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser Leu Leu Ile Glu
1010 1015 1020

Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser Asp Thr Glu
1025 1030 1035

Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
1040 1045 1050

Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr
1055 1060 1065

Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly
1070 1075 1080

Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met Ser Phe Phe Lys
1085 1090 1095

Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile Gln Arg Thr His

1100

1105

1110

Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro Lys Gln
 1115 1120 1125

Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe
 1130 1135 1140

Leu Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr
 1145 1150 1155

Lys Asp Val Gly Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn
 1160 1165 1170

Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu Asn Asn Thr His
 1175 1180 1185

Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu Lys Lys Glu Thr
 1190 1195 1200

Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr Val Thr
 1205 1210 1215

Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg
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Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu
 1235 1240 1245

Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys
 1250 1255 1260

His Thr Ala His Phe Ser Lys Lys Gly Glu Glu Glu Asn Leu Glu
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Gly Leu Gly Asn Gln Thr Lys Gln Ile Val Glu Lys Tyr Ala Cys
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Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe Val Thr
1295 1300 1305

Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu
1310 1315 1320

Glu Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr
1325 1330 1335

Gln Trp Ser Lys Asn Met Lys His Leu Thr Pro Ser Thr Leu Thr
1340 1345 1350

Gln Ile Asp Tyr Asn Glu Lys Glu Lys Gly Ala Ile Thr Gln Ser
1355 1360 1365

Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile Pro Gln Ala
1370 1375 1380

Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser
1385 1390 1395

Ile Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser
1400 1405 1410

Ser His Leu Pro Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val
1415 1420 1425

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

Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly Asp Gln Arg Glu
1445 1450 1455

Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr Tyr Lys
1460 1465 1470

Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr

1475

1480

1485

Ser Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys
 1490 1495 1500

Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu
 1505 1510 1515

Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr Glu Gly Ala Ile
 1520 1525 1530

Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val Pro Phe Leu Arg
 1535 1540 1545

Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu Leu Asp
 1550 1555 1560

Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu
 1565 1570 1575

Glu Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys
 1580 1585 1590

Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys Glu Ser Asn His
 1595 1600 1605

Ala Ile Ala Ala Ile Asn Glu Gly Gln Asn Lys Pro Glu Ile Glu
 1610 1615 1620

Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg Leu Cys Ser Gln
 1625 1630 1635

Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg Thr
 1640 1645 1650

Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile
 1655 1660 1665

Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp
1670 1675 1680

Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr
1685 1690 1695

Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser
1700 1705 1710

Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro
1715 1720 1725

Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe
1730 1735 1740

Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu
1745 1750 1755

Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val
1760 1765 1770

Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser
1775 1780 1785

Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg
1790 1795 1800

Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys
1805 1810 1815

Val Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys
1820 1825 1830

Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His
1835 1840 1845

Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu

1850

1855

1860

Asn Pro Ala His Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu
 1865 1870 1875

Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu
 1880 1885 1890

Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu
 1895 1900 1905

Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly
 1910 1915 1920

Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln Asp Gln
 1925 1930 1935

Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile
 1940 1945 1950

His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys
 1955 1960 1965

Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe
 1970 1975 1980

Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val
 1985 1990 1995

Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu
 2000 2005 2010

Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala
 2015 2020 2025

Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr
 2030 2035 2040

Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser
2045 2050 2055

Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val
2060 2065 2070

Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly
2075 2080 2085

Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile
2090 2095 2100

Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn
2105 2110 2115

Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser
2120 2125 2130

Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr
2135 2140 2145

Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu Arg
2150 2155 2160

Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu
2165 2170 2175

Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser
2180 2185 2190

Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala
2195 2200 2205

Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val
2210 2215 2220

Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met

2225

2230

2235

Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr
 2240 2245 2250

Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly
 2255 2260 2265

His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
 2270 2275 2280

Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp
 2285 2290 2295

Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp
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Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala
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Gln Asp Leu Tyr
 2330

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<212> DNA

<213> Artificial Sequence

<220>

<223> BDD-FVIII (non-optimized; "parental"), Nucleotide Sequence

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acctcagtcg tgtacaaaaa gactctgttt gtagaattca cggatcacct tttcaacatc 240

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<211> 1438

<212> PRT

<213> Artificial Sequence

<220>

<223> BDD-FVIII (non-optimized; "parental"), Amino Acid Sequence

<400> 17

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Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
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Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
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Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
65 70 75 80

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
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Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
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Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
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Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
130 135 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
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His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
165 170 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
180 185 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
195 200 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser

210

215

220

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

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

Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
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Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
 305 310 315 320

Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
 325 330 335

Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp
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Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
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Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
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Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
 385 390 395 400

Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
 405 410 415

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

His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
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Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
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Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
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Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
545 550 555 560

Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
565 570 575

Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
580 585 590

Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
595 600 605

Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser

610

615

620

Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
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Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
 645 650 655

Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
 660 665 670

Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp
 675 680 685

Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala
 690 695 700

Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu
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Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala
 725 730 735

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

Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile
 755 760 765

Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp
 770 775 780

Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys
 785 790 795 800

Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly
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Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser
820 825 830

Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser
835 840 845

Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu
850 855 860

Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr
865 870 875 880

Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile
885 890 895

Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe
900 905 910

Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His
915 920 925

Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe
930 935 940

Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro
945 950 955 960

Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln
965 970 975

Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr
980 985 990

Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro
995 1000 1005

Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg

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Gly Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val				
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Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn				
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Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys				
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Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His				
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Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln				
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Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile				
1130		1135		1140
Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg				
1145		1150		1155
Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro				
1160		1165		1170
Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His				
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Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr				
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Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe
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Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro
1235 1240 1245

Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser
1250 1255 1260

Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn
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Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp
1280 1285 1290

Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr
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Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn
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Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val
1325 1330 1335

Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly
1340 1345 1350

Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile
1355 1360 1365

Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn
1370 1375 1380

Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro

1385

1390

1395

Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg
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<213> Artificial Sequence

<220>

<223> XTEN nucleotide sequence

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<212> DNA

<213> Artificial Sequence

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<220>
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<400> 23

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<400> 24

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Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu
20 25 30

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<213> Artificial Sequence

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Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg
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Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
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Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
1 5 10

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<400> 36

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
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Ser Ala Pro Ala
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<213> Artificial Sequence

<220>

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<400> 37

Ala Ala Pro Ala Ser Pro Ala Pro Ala Ala Pro Ser Ala Pro Ala Pro
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Ala Ala Pro Ser
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<213> Artificial Sequence

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<400> 38

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Ser Pro Ser Ser
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Ala Pro Ser Ser Pro Ser Pro Ser Ala Pro Ser Ser Pro Ser Pro Ala
1 5 10 15

Ser Pro Ser

<210> 40
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Ser Ser Pro Ser Ala Pro Ser Pro Ser Ser Pro Ala Ser Pro Ser Pro
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Ser Ser Pro Ala
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Ala Ala Pro Ser Ala Pro Pro Ala
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<400> 42

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Ser Ala Ala Ala
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23

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<400> 44

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

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
35 40 45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
50 55 60

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

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
85 90 95

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
100 105 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
115 120 125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
130 135 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145 150 155 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
165 170 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
180 185 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
195 200 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
210 215 220

Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
225 230 235 240

Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
245 250 255

Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
260 265 270

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

Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
290 295 300

Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
305 310 315 320

Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
325 330 335

Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp
340 345 350

Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
355 360 365

Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
370 375 380

Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
385 390 395 400

Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
405 410 415

Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
420 425 430

Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
435 440 445

Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
450 455 460

Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
465 470 475 480

Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys
485 490 495

His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
500 505 510

Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
515 520 525

Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
530 535 540

Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
545 550 555 560

Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
565 570 575

Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
580 585 590

Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
595 600 605

Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
610 615 620

Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
625 630 635 640

Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
645 650 655

Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
660 665 670

Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp
675 680 685

Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala
690 695 700

Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu
705 710 715 720

Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala
725 730 735

Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg
740 745 750

Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys
755 760 765

Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn
770 775 780

Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser Pro Thr Pro
785 790 795 800

His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr Glu Thr Phe
805 810 815

Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn Ser Leu Ser
820 825 830

Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
835 840 845

Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly
850 855 860

Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser
865 870 875 880

Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala
885 890 895

Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met Pro Val His
900 905 910

Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys Ser Ser Pro
915 920 925

Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn Asn Asp
930 935 940

Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp
945 950 955 960

Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys
965 970 975

Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys
980 985 990

Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala
995 1000 1005

Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser Leu Leu Ile Glu
1010 1015 1020

Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser Asp Thr Glu
1025 1030 1035

Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
1040 1045 1050

Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr
1055 1060 1065

Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly
1070 1075 1080

Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met Ser Phe Phe Lys
1085 1090 1095

Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile Gln Arg Thr His
1100 1105 1110

Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro Lys Gln
1115 1120 1125

Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe
1130 1135 1140

Leu Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr
1145 1150 1155

Lys Asp Val Gly Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn
1160 1165 1170

Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu Asn Asn Thr His
1175 1180 1185

Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu Lys Lys Glu Thr
1190 1195 1200

Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr Val Thr
1205 1210 1215

Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg
1220 1225 1230

Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu
1235 1240 1245

Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys
1250 1255 1260

His Thr Ala His Phe Ser Lys Lys Gly Glu Glu Glu Asn Leu Glu
1265 1270 1275

Gly Leu Gly Asn Gln Thr Lys Gln Ile Val Glu Lys Tyr Ala Cys
1280 1285 1290

Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe Val Thr
1295 1300 1305

Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu
1310 1315 1320

Glu Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr
1325 1330 1335

Gln Trp Ser Lys Asn Met Lys His Leu Thr Pro Ser Thr Leu Thr
1340 1345 1350

Gln Ile Asp Tyr Asn Glu Lys Glu Lys Gly Ala Ile Thr Gln Ser
1355 1360 1365

Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile Pro Gln Ala
1370 1375 1380

Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser
1385 1390 1395

Ile Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser
1400 1405 1410

Ser His Leu Pro Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val
1415 1420 1425

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

Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly Asp Gln Arg Glu
1445 1450 1455

Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr Tyr Lys
1460 1465 1470

Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr
1475 1480 1485

Ser Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys
1490 1495 1500

Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu
1505 1510 1515

Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr Glu Gly Ala Ile
1520 1525 1530

Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val Pro Phe Leu Arg
1535 1540 1545

Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu Leu Asp
1550 1555 1560

Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu
1565 1570 1575

Glu Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys
1580 1585 1590

Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys Glu Ser Asn His
1595 1600 1605

Ala Ile Ala Ala Ile Asn Glu Gly Gln Asn Lys Pro Glu Ile Glu
1610 1615 1620

Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg Leu Cys Ser Gln
1625 1630 1635

Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg Thr
1640 1645 1650

Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile
1655 1660 1665

Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp
1670 1675 1680

Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr
1685 1690 1695

Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser
1700 1705 1710

Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro
1715 1720 1725

Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe
1730 1735 1740

Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu
1745 1750 1755

Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val
1760 1765 1770

Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser
1775 1780 1785

Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg
1790 1795 1800

Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys
1805 1810 1815

Val Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys
1820 1825 1830

Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His
1835 1840 1845

Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu
1850 1855 1860

Asn Pro Ala His Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu
1865 1870 1875

Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu
1880 1885 1890

Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu
1895 1900 1905

Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly
1910 1915 1920

Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln Asp Gln
1925 1930 1935

Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile
1940 1945 1950

His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys
1955 1960 1965

Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe
1970 1975 1980

Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val
1985 1990 1995

Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu
2000 2005 2010

Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala
2015 2020 2025

Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr
2030 2035 2040

Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser
2045 2050 2055

Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val
2060 2065 2070

Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly
2075 2080 2085

Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile
2090 2095 2100

Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn
2105 2110 2115

Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser
2120 2125 2130

Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr
2135 2140 2145

Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu Arg
2150 2155 2160

Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu
2165 2170 2175

Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser
2180 2185 2190

Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala
2195 2200 2205

Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val
2210 2215 2220

Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met
2225 2230 2235

Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr
2240 2245 2250

Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly
2255 2260 2265

His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
2270 2275 2280

Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp
2285 2290 2295

Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp
2300 2305 2310

Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala
2315 2320 2325

Gln Asp Leu Tyr
2330

<210> 45
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acids 233-236 of human IgG1

<400> 45

Glu Leu Leu Gly
1

<210> 46
<211> 42
<212> PRT
<213> Artificial Sequence

<220>

<223> XTEN AE42-4, protein sequence

<400> 46

Gly Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
1 5 10 15

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
20 25 30

Thr Ser Gly Ser Glu Thr Pro Ala Ser Ser
35 40

<210> 47

<211> 126

<212> DNA

<213> Artificial Sequence

<220>

<223> XTEN AE42-4, DNA sequence

<400> 47

ggcgcgccag gttctcctgc tggctcccc acctcaacag aagaggggac aagcgaaagc 60

gctacgcctg agagtggccc tggctctgag ccagccacct ccggctctga aaccctgcc 120

tcgagc 126

<210> 48

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> XTEN AE144-2A, protein sequence

<400> 48

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly
1 5 10 15

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
65 70 75 80

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
85 90 95

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
100 105 110

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
115 120 125

Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
130 135 140

<210> 49
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AE144-2A, DNA sequence

<400> 49
ggcgcgccaa ccagtacgga gccgtccgag gggagcgcac caggaagccc ggctgggagc 60
ccgacttcta ccgaagaggg tacatctacc gaaccaagtg aaggttcagc accaggcacc 120
tcaacagaac cctctgaggg ctcggcgcct ggtacaagtg agtccgccac cccagaatcc 180
gggcctggga caagcacaga accttcggaa gggagtgtccc ctggaacatc cgaatcggca 240
accccagaat cagggccagg atctgagccc gcgacttcgg gctccgagac gcctgggaca 300
tccaccgagc cctccgaagg atcagcccca ggcaccagca cggagccctc tgagggaagc 360

gcacctggta ccagcgaaag cgcaactccc gaatcaggtc ccggtacgag cgagtcggcg 420
accccggaga gcgggccagg tgcctcgagc 450

<210> 50
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN AE144-3B, protein sequence

<400> 50

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
20 25 30

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
35 40 45

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
65 70 75 80

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
85 90 95

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
100 105 110

Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
115 120 125

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
130 135 140

<210> 51
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AE144-3B, DNA sequence

<400> 51
ggcgcgccaagtccccgctgg aagcccaact agcaccgaag aggggacctc agagtccgcc 60
acccccgagt ccggccctgg ctctgagcct gccactagcg gctccgagac tcctggcaca 120
tccgaaagcg ctacaccgga gagtggaccc ggcacctcta ccgagcccag tgagggtcc 180
gccccctggaa caagcaccga gccagcgaa ggcagcgccc cagggacctc cacagagccc 240
agtgaaggca gtgtccttgg caccagcacc gaaccaagcg agggctctgc acccgggacc 300
tccaccgagc caagcgaagg ctctgcccct ggcacttcca ccgagcccag cgaaggcagc 360
gccccctggga gccccgctgg ctctcccacc agcactgagg agggcacatc taccgaacca 420
agtgaaggct ctgcaccagg tgcctcgagc 450

<210> 52
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN AE144-4A, protein sequence

<400> 52

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1 5 10 15

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
20 25 30

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
65 70 75 80

Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
85 90 95

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
100 105 110

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu
115 120 125

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
130 135 140

<210> 53
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AE144-4A, DNA sequence

<400> 53
ggcgcgcca cgtccgaaag tgctaccct gagtcaggcc ctggtagtga gcctgccaca 60
agcgggaagcg aaactccggg gacctcagag tctgccactc ccgaatcggg gccaggctct 120
gaaccggcca cttcaggag cgaaacacca ggaacatcgg agagcgctac cccggagagc 180
gggccaggaa ctagtactga gcctagcgag ggaagtgcac ctggtacaag cgagtccgcc 240
acacccgagt ctggccctgg ctctccagcg ggctcaccca cgagcactga agagggctct 300
cccgctggca gccaacgtc gacagaagaa ggatcaccag caggctcccc cacatcaaca 360
gaggagggtta catcagaatc tgctactccc gagagtggac ccggtacctc cactgagccc 420
agcgagggga gtgcaccagg tgcctcgagc 450

<210> 54
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN AE144-5A, protein sequence

<400> 54

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1 5 10 15

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
20 25 30

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
65 70 75 80

Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
85 90 95

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser
100 105 110

Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
115 120 125

Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
130 135 140

<210> 55
<211> 450
<212> DNA
<213> Artificial Sequence

<220>

<223> XTEN AE144-5A, DNA sequence

<400> 55

```
ggcgcgcca catcagagag cgccacccct gaaagtggtc ccgggagcga gccagccaca      60
tctgggtcgg aaacgccagg cacaagtgag tctgcaactc ccgagtccgg acctggctcc      120
gagcctgcca ctagcggctc cgagactccg ggaacttccg agagcgctac accagaaagc      180
ggacccggaa ccagtaccga acctagcgag ggctctgctc cgggcagccc agccggctct      240
cctacatcca cggaggaggg cacttccgaa tccgccaccc cggagtcagg gccaggatct      300
gaacccgcta cctcaggcag tgagacgcca ggaacgagcg agtccgctac accggagagt      360
gggccaggga gccctgctgg atctcctacg tccactgagg aagggtcacc agcgggctcg      420
cccaccagca ctgaagaagg tgcctcgagc      450
```

<210> 56

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> XTEN AE144-6B, protein sequence

<400> 56

```
Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser
1           5           10          15

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
20        25        30

Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
35        40        45

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala
50        55        60

Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
65        70        75        80
```

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
85 90 95

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro Ala
100 105 110

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
115 120 125

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
130 135 140

<210> 57
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AE144-6B, DNA sequence

<400> 57
ggcgcgcca catctaccga gccttccgaa ggctctgccc ctgggacctc agaatctgca 60
accctgaaa gcggccctgg aacctccgaa agtgccactc ccgagagcgg cccagggaca 120
agcgagtcag caaccctga gtctggaccc ggcagcgagc ctgcaacctc tggctcagag 180
actcccggtc cagaaccgc tacctcaggc tccgagacac ccggctctcc tgctgggagt 240
cccacttcca ccgaggaagg aacatccact gagcctagtg agggctctgc ccctggaacc 300
agcacagagc caagtgaggg cagtgcacca ggatccgagc cagcaaccag cgggtccgag 360
actcccgga cctctgagtc tgccacccca gagagcggac ccggcacttc aaccgagccc 420
tccgaaggat cagcaccagg tgcctcgagc 450

<210> 58
<211> 144
<212> PRT
<213> Artificial Sequence

<220>

<223> XTEN AG144-1, protein sequence

<400> 58

Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser
1 5 10 15

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr
20 25 30

Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
35 40 45

Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser
50 55 60

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr
65 70 75 80

Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
85 90 95

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser
100 105 110

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser
115 120 125

Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser
130 135 140

<210> 59

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> XTEN AG144-1, DNA sequence

<400> 59

ggcgcgccac ccgggtcgtc cccgtcggcg tccaccggaa cagggccagg gtcatccccg

60

tcagcgtcga ctgggacggg acccgggaca cccggttcgg ggactgcatc ctcctcgcct	120
ggttcgtcca ccccgtcagg agccacgggt tcgccgggaa gcagcccaag cgcattccact	180
ggtacagggc ctggggcttc accgggtact tcatccacgg ggtcaccggg aacgcccgga	240
tcggggacgg cttcctcatc accaggatcg tcaacaccct cgggcgcaac gggcagcccc	300
ggaacccctg gttcgggtac ggcgtcgtcg agccccgggt cgagccccggg aacaagctcg	360
acaggatcgc ctggggcgtc acccggcacg tcgagcacag gcagccccgg aacccttgga	420
tcgggaaccg cgtcgtcaag cgcctcgagc	450

<210> 60
 <211> 144
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> XTEN AG144-A, protein sequence

<400> 60

Gly	Ala	Ser	Pro	Gly	Thr	Ser	Ser	Thr	Gly	Ser	Pro	Gly	Ser	Ser	Pro
1				5					10					15	

Ser	Ala	Ser	Thr	Gly	Thr	Gly	Pro	Gly	Ser	Ser	Pro	Ser	Ala	Ser	Thr
			20					25					30		

Gly	Thr	Gly	Pro	Gly	Thr	Pro	Gly	Ser	Gly	Thr	Ala	Ser	Ser	Ser	Pro
		35					40					45			

Gly	Ser	Ser	Thr	Pro	Ser	Gly	Ala	Thr	Gly	Ser	Pro	Gly	Ser	Ser	Pro
	50					55					60				

Ser	Ala	Ser	Thr	Gly	Thr	Gly	Pro	Gly	Ala	Ser	Pro	Gly	Thr	Ser	Ser
65					70				75					80	

Thr	Gly	Ser	Pro	Gly	Thr	Pro	Gly	Ser	Gly	Thr	Ala	Ser	Ser	Ser	Pro
				85					90					95	

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly
100 105 110

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
115 120 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
130 135 140

<210> 61
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AG144-A, DNA sequence

<400> 61
ggcgcgccag gtgcctcgcc gggaacatca tcaactgggtt caccgagggtc atccccctcg 60
gcctcaaccg ggacgggtcc cggctcatcc cccagcgcca gacttgaac aggtcctggc 120
actcctgggtt ccggtacggc atcgctcatcc ccgggaagct caacaccgtc cggagcgaca 180
ggatcacctg gctcgtcacc ttcggcggtca actggaacgg ggccagggggc ctcacccgga 240
acgtcctcga ctgggtcgcc tggtagcccg ggatcaggaa cggcctcatc ctcgcctggg 300
tcctcaacgc cctcgggtgc gactgggttcg ccgggaactc ctggctcggg gacggcctcg 360
tcgtcgcctg gggcatcacc ggggacgagc tccacgggggt cccctggagc gtcaccgggg 420
acctcctcga caggtagccc ggcctcgagc 450

<210> 62
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN AG144-B, protein sequence

<400> 62

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
1 5 10 15

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
20 25 30

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
35 40 45

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
50 55 60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
65 70 75 80

Gly Thr Gly Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
85 90 95

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro
100 105 110

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
115 120 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
130 135 140

<210> 63
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AG144-B, DNA sequence

<400> 63
ggcgcgccag gtacaccggg cagcggcacg gcttcgtcgt caccgggctc gtccacaccg 60
tcgggagcta cgggaagccc aggagcgtca ccgggaacgt cgtcaacggg gtcaccgggt 120
acgccaggta gcggcacggc cagcagctcg ccagggttcac cgaccccgctc gggagcgact 180
gggtcgcccc gatcaagccc gtcagcttcc actggaacag gacccgggtc gtcgccgtca 240

gcctcaacgg ggacaggacc tggttcatcg acgccgtcag gggcgacagg ctcgcccgga	300
tcgtcaacac cctcgggggc aacgggggagc cctggtgcgt cgcctggaac ctcatccacc	360
ggaagcccgg gggcctcgcc gggtagcagc tccacgggat cggccggagc gtcccccgga	420
acttcaagca caggagagccc tgcctcgagc	450

<210> 64
 <211> 144
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> XTEN AG144-C, protein sequence

<400> 64

Gly	Thr	Pro	Gly	Ser	Gly	Thr	Ala	Ser	Ser	Ser	Pro	Gly	Ala	Ser	Pro
1				5				10					15		

Gly	Thr	Ser	Ser	Thr	Gly	Ser	Pro	Gly	Ala	Ser	Pro	Gly	Thr	Ser	Ser
		20					25					30			

Thr	Gly	Ser	Pro	Gly	Ala	Ser	Pro	Gly	Thr	Ser	Ser	Thr	Gly	Ser	Pro
		35					40					45			

Gly	Ser	Ser	Pro	Ser	Ala	Ser	Thr	Gly	Thr	Gly	Pro	Gly	Thr	Pro	Gly
	50					55					60				

Ser	Gly	Thr	Ala	Ser	Ser	Ser	Pro	Gly	Ala	Ser	Pro	Gly	Thr	Ser	Ser
65					70					75				80	

Thr	Gly	Ser	Pro	Gly	Ala	Ser	Pro	Gly	Thr	Ser	Ser	Thr	Gly	Ser	Pro
				85				90					95		

Gly	Ala	Ser	Pro	Gly	Thr	Ser	Ser	Thr	Gly	Ser	Pro	Gly	Ser	Ser	Thr
			100					105				110			

Pro	Ser	Gly	Ala	Thr	Gly	Ser	Pro	Gly	Ser	Ser	Thr	Pro	Ser	Gly	Ala
		115					120					125			

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
130 135 140

<210> 65
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AG144-C, DNA sequence

<400> 65
ggcgcgccag gtacacccgg atcgggtaca gcgtcatcga gccccggtgc gtcacctggt 60
acgtcgagca cgggggtcgcc agggggtcgtcc cctgggacgt cctcaacagg ctgccccggt 120
gcgtcaccgg gcacgtcgtc cacgggttca cctggtagct ccccttccgc gtccactggc 180
accgggcctg gaactccggg gagcggcaca gcgagctcgt cgccgggagc atgcctggg 240
acatcgagca ccgggtcgcc aggagcatcg cccggaacat ccagcacagg aagccccggc 300
gcgtcgcccc ggacatcaag cacagggttcc ccgggatcga gcacgccgtc cggagccact 360
ggatcaccag ggagctcgac accttccggc gcaacgggat cgcccgagc cagccccgggt 420
acgtcaagca ctggctcccc tgcctcgagc 450

<210> 66
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN AG144-F, protein sequence

<400> 66

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro
1 5 10 15

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
20 25 30

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
35 40 45

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
50 55 60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
65 70 75 80

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
85 90 95

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
100 105 110

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
115 120 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
130 135 140

<210> 67
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AG144-F, DNA sequence

<400> 67
ggcgcgccag gctccagccc ctccgcgagc acgggaaccg gaccagggtc gtcaccctca 60
gcatcaacgg ggacgggacc gggggcgtca ccaggaacgt cctccaccgg ctgcgccgggt 120
gcatcaccgg gaacgtcatc gaccggatcg ccaggagct cgacgccatc aggcgcaaca 180
ggatcacctg gctcaagccc tagcgcgtca accggcacgg gtccgggtgc ctcccctggc 240
acgtccagca ccggatcacc cggatcgagc ccatccgcct caaccggaac cggacccggg 300
acaccagggg cgggaacagc ctccctgtca ccaggctcct caaccccctc gggagccacg 360
ggttcgcccc gttcgtcaac gccttccgga gcaactggta gccccggagc atcgccagga 420

acttcgagca cggggtcgcc cgcctcgagc

450

<210> 68

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> coFVIII-1 DNA Sequence

<400> 68

atgcagattg agctgtctac ttgctttttc ctgtgcctgc tgaggttttg cttttccgct 60

acacgaaggt attatctggg ggctgtggaa ctgtcttggg attacatgca gaggtagctg 120

ggagagctgc cagtggacgc aaggtttccc ctagaggtcc ctaagtcatt ccccttcaac 180

actagcgtgg tctacaagaa aacactgttc gtggagttaa ctgatcacct gttcaacatc 240

gcaaagccta ggccaccctg gatgggactg ctggggccaa caatccaggc cgagggtgtac 300

gacaccgtgg tcattacact taagaacatg gcctcacacc ccgtgagcct gcatgctgtg 360

ggcgtcagct actggaaggc ttccgaagga gcagagtatg acgatcagac ttcccagaga 420

gaaaaagagg acgataaggt gtttcctggc ggatctcata cctacgtgtg gcaggctcctg 480

aaagagaatg gccctatggc ctccgaccct ctgtgcctga cctactctta tctgagtcac 540

gtggacctgg tcaaggatct gaacagcggc ctgatcggag ccctgctggg gtgcagggaa 600

ggaagcctgg ctaaggagaa aaccagaca ctgcataagt tcattctgct gttcgccgtg 660

tttgacgaag ggaaatcatg gcacagcgag acaaagaata gtctgatgca ggacagggat 720

gccgcttcag ccagagcttg gcccataatg cactctgtga acggctacgt caatcgctca 780

ctgcctgggc tgatcggctg ccaccgaaag agcgtgtatt ggcatgtcat cgggatgggc 840

accacacctg aagtgcactc cattttcctg gagggacata cttttctggg ccgcaaccac 900

cgacaggctt ccctggagat ctctccaatt accttctga cagcacagac tctgctgatg 960

gacctggggc agttcctgct gttttgccac atcagctccc accagcatga tggcatggag 1020

gcttacgtga aagtggactc ttgtcccag gaacctcagc tgcggatgaa gaacaatgag 1080

gaagcagaag actatgacga tgacctgacc gactccgaga tggatgtggg ccgattcgat 1140

gacgataaca gcccctcctt tatccagatt agatctgtgg ccaagaaaca ccctaagaca	1200
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<220>
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<220>

<223> coFVIII-6

<400> 71

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<210> 73
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AD motif

<400> 73

Gly	Glu	Ser	Pro	Gly	Gly	Ser	Ser	Gly	Ser	Glu	Ser
1				5				10			

<210> 74
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AD motif

<400> 74

Gly	Ser	Glu	Gly	Ser	Ser	Gly	Pro	Gly	Glu	Ser	Ser
1				5				10			

<210> 75
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AD motif

<400> 75

Gly Ser Ser Glu Ser Gly Ser Ser Glu Gly Gly Pro
1 5 10

<210> 76
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AD motif

<400> 76

Gly Ser Gly Gly Glu Pro Ser Glu Ser Gly Ser Ser
1 5 10

<210> 77
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AE, AM motif

<400> 77

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
1 5 10

<210> 78
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> AE, AM, AQ motif

<400> 78

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
1 5 10

<210> 79

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> AE, AM, AQ motif

<400> 79

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
1 5 10

<210> 80

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> AE, AM, AQ motif

<400> 80

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
1 5 10

<210> 81

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> AF, AM motif

<400> 81

Gly Ser Thr Ser Glu Ser Pro Ser Gly Thr Ala Pro
1 5 10

<210> 82
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AF, AM motif

<400> 82

Gly Thr Ser Thr Pro Glu Ser Gly Ser Ala Ser Pro
1 5 10

<210> 83
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AF, AM motif

<400> 83

Gly Thr Ser Pro Ser Gly Glu Ser Ser Thr Ala Pro
1 5 10

<210> 84
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AF, AM motif

<400> 84

Gly Ser Thr Ser Ser Thr Ala Glu Ser Pro Gly Pro
1 5 10

<210> 85
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AG, AM motif

<400> 85

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
1 5 10

<210> 86

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> AG, AM motif

<400> 86

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
1 5 10

<210> 87

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> AG, AM motif

<400> 87

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
1 5 10

<210> 88

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> AG, AM motif

<400> 88

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
1 5 10

<210> 89

<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> AQ motif

<400> 89

Gly Glu Pro Ala Gly Ser Pro Thr Ser Thr Ser Glu
1 5 10

<210> 90
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AQ motif

<400> 90

Gly Thr Gly Glu Pro Ser Ser Thr Pro Ala Ser Glu
1 5 10

<210> 91
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AQ motif

<400> 91

Gly Ser Gly Pro Ser Thr Glu Ser Ala Pro Thr Glu
1 5 10

<210> 92
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AQ motif

<400> 92

Gly Ser Glu Thr Pro Ser Gly Pro Ser Glu Thr Ala
1 5 10

<210> 93
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 93

Gly Pro Ser Glu Thr Ser Thr Ser Glu Pro Gly Ala
1 5 10

<210> 94
<211> 12
<212> PRT
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<220>
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<400> 94

Gly Ser Pro Ser Glu Pro Thr Glu Gly Thr Ser Ala
1 5 10

<210> 95
<211> 12
<212> PRT
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<220>
<223> BC motif

<400> 95

Gly Ser Gly Ala Ser Glu Pro Thr Ser Thr Glu Pro
1 5 10

<210> 96
<211> 12
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<220>

<223> BC motif

<400> 96

Gly Ser Glu Pro Ala Thr Ser Gly Thr Glu Pro Ser
1 5 10

<210> 97

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> BC motif

<400> 97

Gly Thr Ser Glu Pro Ser Thr Ser Glu Pro Gly Ala
1 5 10

<210> 98

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> BC motif

<400> 98

Gly Thr Ser Thr Glu Pro Ser Glu Pro Gly Ser Ala
1 5 10

<210> 99

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> BD motif

<400> 99

Gly Ser Thr Ala Gly Ser Glu Thr Ser Thr Glu Ala
1 5 10

<210> 100
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> BD motif

<400> 100

Gly Ser Glu Thr Ala Thr Ser Gly Ser Glu Thr Ala
1 5 10

<210> 101
<211> 12
<212> PRT
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<220>
<223> BD motif

<400> 101

Gly Thr Ser Glu Ser Ala Thr Ser Glu Ser Gly Ala
1 5 10

<210> 102
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> BD motif

<400> 102

Gly Thr Ser Thr Glu Ala Ser Glu Gly Ser Ala Ser
1 5 10

<210> 103
<211> 1607
<212> PRT
<213> Artificial Sequence

<220>

<223> coFVIII-6-XTEN Protein Sequence

<400> 103

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
85 90 95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190

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

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

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
275 280 285

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

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
450 455 460

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

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545 550 555 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
565 570 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
580 585 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
645 650 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
660 665 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
740 745 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Gly Ala Pro Thr
755 760 765

Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr
770 775 780

Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser
785 790 795 800

Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr
805 810 815

Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro
820 825 830

Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr
835 840 845

Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser
850 855 860

Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala
865 870 875 880

Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr
885 890 895

Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ala
900 905 910

Ser Ser Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg Thr
915 920 925

Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser
930 935 940

Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn
945 950 955 960

Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala
965 970 975

Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser Ser Pro His Val
980 985 990

Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro Gln Phe Lys Lys Val
995 1000 1005

Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro Leu Tyr
1010 1015 1020

Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile
1025 1030 1035

Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln
1040 1045 1050

Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu
1055 1060 1065

Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys
1070 1075 1080

Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met
1085 1090 1095

Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe
1100 1105 1110

Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly
1115 1120 1125

Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly
1130 1135 1140

Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe
1145 1150 1155

Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn
1160 1165 1170

Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys
1175 1180 1185

Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr
1190 1195 1200

Leu Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr
1205 1210 1215

Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His Phe
1220 1225 1230

Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met
1235 1240 1245

Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met
1250 1255 1260

Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly
1265 1270 1275

Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser
1280 1285 1290

Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg
1295 1300 1305

Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro
1310 1315 1320

Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser
1325 1330 1335

Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro
1340 1345 1350

Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe
1355 1360 1365

Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp
1370 1375 1380

Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu
1385 1390 1395

Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn
1400 1405 1410

Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro
1415 1420 1425

Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly
1430 1435 1440

Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys
1445 1450 1455

Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn
1460 1465 1470

Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln
1475 1480 1485

Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
1490 1495 1500

Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val
1505 1510 1515

Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys
1520 1525 1530

Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu
1535 1540 1545

Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp
1550 1555 1560

Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr
1565 1570 1575

Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala
1580 1585 1590

Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
1595 1600 1605

<210> 104
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Rep-binding site (RBS) for AAV2

<400> 104
gcgcgctcgc tcgctc

16

<210> 105
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> terminal resolution site (TRS) for AAV2

<400> 105
agttgg

6

<210> 106
<211> 2328
<212> PRT
<213> Artificial Sequence

<220>
<223> mature full length FVIII

<400> 106

Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr
1 5 10 15

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

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
35 40 45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
50 55 60

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

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
85 90 95

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
100 105 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
115 120 125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
130 135 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145 150 155 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
165 170 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
180 185 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
195 200 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
210 215 220

Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
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ctgactcgct accttcgaat tcacccccag agttgggtgc accagattgc cctgaggatg	7020
gaggttctgg gctgcgaggc acaggacctc tac	7053

<210> 108

<400> 108
000

<210> 109

<211> 1718

<212> PRT

<213> Artificial Sequence

<220>

<223> BIVV001 BDD-FVIII(XTEN) Sequence (no Fc)

<400> 109

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

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
35 40 45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
50 55 60

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

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
85 90 95

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
100 105 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
115 120 125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
130 135 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145 150 155 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
165 170 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
180 185 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
195 200 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
210 215 220

Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
225 230 235 240

Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
245 250 255

Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
260 265 270

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

Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
290 295 300

Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
305 310 315 320

Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
325 330 335

Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp

340

345

350

Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
 355 360 365

Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
 370 375 380

Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
 385 390 395 400

Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
 405 410 415

Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
 420 425 430

Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
 435 440 445

Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
 450 455 460

Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
 465 470 475 480

Thr Asp Val Arg Pro Lys Arg Arg Leu Pro Lys Gly Val Lys His Leu
 485 490 495

Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr
 500 505 510

Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr
 515 520 525

Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser Gly
 530 535 540

Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg
545 550 555 560

Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val
565 570 575

Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe
580 585 590

Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe Gln Ala
595 600 605

Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln
610 615 620

Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile
625 630 635 640

Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe
645 650 655

Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser
660 665 670

Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu
675 680 685

Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala Leu Leu
690 695 700

Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser
705 710 715 720

Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu
725 730 735

Pro Arg Ser Phe Ser Gln Asn Gly Thr Ser Glu Ser Ala Thr Pro Glu

740

745

750

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
 755 760 765

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
 770 775 780

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
 785 790 795 800

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
 805 810 815

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
 820 825 830

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
 835 840 845

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
 850 855 860

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
 865 870 875 880

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly
 885 890 895

Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
 900 905 910

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser
 915 920 925

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
 930 935 940

Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
945 950 955 960

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu
965 970 975

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
980 985 990

Ser Ala Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
995 1000 1005

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
1010 1015 1020

Glu Pro Ser Glu Gly Ser Ala Pro Ala Ser Ser Glu Ile Thr Arg
1025 1030 1035

Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr
1040 1045 1050

Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu
1055 1060 1065

Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His
1070 1075 1080

Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser
1085 1090 1095

Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val
1100 1105 1110

Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser
1115 1120 1125

Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly

1130

1135

1140

Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met
 1145 1150 1155

Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser
 1160 1165 1170

Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro
 1175 1180 1185

Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp
 1190 1195 1200

Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys
 1205 1210 1215

Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val
 1220 1225 1230

His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr
 1235 1240 1245

Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln Glu Phe Ala
 1250 1255 1260

Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr
 1265 1270 1275

Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met
 1280 1285 1290

Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn
 1295 1300 1305

Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln Asp
 1310 1315 1320

Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn
1325 1330 1335

Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys
1340 1345 1350

Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val
1355 1360 1365

Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg
1370 1375 1380

Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr
1385 1390 1395

Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met
1400 1405 1410

Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln
1415 1420 1425

Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly
1430 1435 1440

Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys
1445 1450 1455

Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile Lys Thr Gln
1460 1465 1470

Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile
1475 1480 1485

Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly
1490 1495 1500

Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser

1505

1510

1515

Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg
 1520 1525 1530

Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu
 1535 1540 1545

Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro
 1550 1555 1560

Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala
 1565 1570 1575

Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys
 1580 1585 1590

Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln
 1595 1600 1605

Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr
 1610 1615 1620

Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu
 1625 1630 1635

Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp
 1640 1645 1650

Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val
 1655 1660 1665

Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu
 1670 1675 1680

Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser
 1685 1690 1695

Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu
1700 1705 1710

Ala Gln Asp Leu Tyr
1715

<210> 110
<211> 6526
<212> DNA
<213> Artificial Sequence

<220>
<223> NB15.1v32 construct (AAV-FVIIIco6XTEN-ssDNA)

<400> 110
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aggggttcct gcggcaattc agtcgataac tataacggtc ctaaggttagc gatttaaata 180
cgcgctctct taaggttagc ccgggacgcg tcaattgaga tctggatccg gtaccgaatt 240
cgcggccgcc tcgacgacta gcgtttaatt aaacgcgtgt ctgtctgcac atttcgtaga 300
gcgagtgttc cgatactcta atctccctag gcaagggttc tatttggtga gggttacttat 360
tctccttttg ttgactaagt caataatcag aatcagcagg ttggagtc gcttggcagg 420
gatcagcagc ctgggttgaaggagggggt ataaaagccc cttcaccagg agaagccgtc 480
acacagatcc acaagctcct gaggtaagt ccgtgtgtgg ttcccgcggg cctggcctct 540
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actacatgca gagcgacctg ggcgaactcc ccgtggatgc cagattcccc ccccgctgc 780
caaagtcctt cccctttaac acctccgtgg tgtacaagaa aaccctcttt gtcgagttca 840
ctgaccacct gttcaacatc gccaaagcgc gccaccttg gatgggcctc ctgggaccga 900
ccattcaagc tgaagtgtac gacaccgtgg tgatcacct gaagaacatg gcgtcccacc 960

ccgtgtccct gcatgcggtc ggagtgtcct actggaaggc ctccgaagga gctgagtacg	1020
acgaccagac tagccagcgg gaaaaggagg acgataaagt gttcccgggc ggctcgcata	1080
cttacgtgtg gcaagtcctg aaggaaaacg gacctatggc atccgacacct ctgtgcctga	1140
cttactccta cctttcccat gtggacctcg tgaaggacct gaacagcggg ctgattgggtg	1200
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cgcatgtgt gagtaggtgt cattctattc tgggggggtg ggtggggcag gacagcaagg	6240
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ttaaattagg gataacagg taatggcgcg ggccgcagga acccctagt atggagttgg	6420
ccactccctc tctgcgcgct cgctcgctca ctgaggccgg gcgaccaaag gtcgcccgc	6480
gcccgggctt tgcccgggcg gcctcagtga gcgagcgagc gcgcag	6526

<210> 111
 <211> 130
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' ITR (5'-end AAV2 inverted terminal repeat)

<400> 111	
ctgcgcgctc gctcgtcac tgaggccgcc cgggcaaagc ccgggcgtcg ggcgaccttt	60
ggtcgcccgg cctcagttag cgagcgagcg cgcagagagg gaggggccaa ctccatcact	120

aggggttcct 130

<210> 112
<211> 142
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid Backbone Sequence (PBS)-1

<400> 112
gcggcaattc agtcgataac tataacgggc ctaaggtagc gatttaaata cgcgctctct 60
taaggtagcc ccgggacgcg tcaattgaga tctggatccg gtaccgaatt cgcggccgcc 120
tcgacgacta gcgtttaatt aa 142

<210> 113
<211> 229
<212> DNA
<213> Artificial Sequence

<220>
<223> TTPp (liver-specific promoter)

<400> 113
acgcgtgtct gtctgcacat ttcgtagagc gagtggtccg atactctaata ctccctaggc 60
aaggttcata tttgtgtagg ttacttattc tccttttggt gactaagtca ataatacagaa 120
tcagcagggtt tggagtcagc ttggcaggga tcagcagcct gggttggaag gaggggggtat 180
aaaagcccct tcaccaggag aagccgtcac acagatccac aagctcctg 229

<210> 114
<211> 2
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid Backbone Sequence (PBS)-2

<400> 114
ag 2

<210> 115

<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Intron

<400> 115
gtaagtgccg tgtgtgggtc ccgcgggcct ggctcttta cgggttatgg cccttgctg 60
ccttgaatta ctgacactga catccacttt ttctttttct ccacag 106

<210> 116
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid Backbone Sequence (PBS)-3

<400> 116
ctagcgccac c 11

<210> 117
<211> 4824
<212> DNA
<213> Artificial Sequence

<220>
<223> FVIIIco6XTEN (open reading frame for codon-optimized FVIII version 6 containing XTEN144)

<400> 117
atgcagattg agctgtccac ttgtttcttc ctgtgcctcc tgcgcttctg tttctccgcc 60
actcgccggt actaccttgg agccgtggag ctttcatggg actacatgca gagcgacctg 120
ggcgaactcc ccgtggatgc cagattcccc cccgcgtgc caaagtcctt cccctttaac 180
acctccgtgg tgtacaagaa aaccctcttt gtcgagttca ctgaccacct gttcaacatc 240
gccaagccgc gcccaccttg gatgggcctc ctgggaccga ccattcaagc tgaagtgtac 300
gacaccgtgg tgatcaccct gaagaacatg gcggtcccacc ccgtgtccct gcatgcggtc 360
ggagtgtcct actggaaggc ctccgaagga gctgagtacg acgaccagac tagccagcgg 420
gaaaaggagg acgataaagt gttcccgggc ggctcgcata cttacgtgtg gcaagtcctg 480

aaggaaaacg gacctatggc atccgatcct ctgtgcctga cttactccta cttttcccat	540
gtggacctcg tgaaggacct gaacagcggg ctgattgggtg cacttctcgt gtgccgcgaa	600
ggttcgctcg ctaaggaaaa gacccagacc ctccataagt tcatcctttt gttcgtctgtg	660
ttcgatgaag gaaagtcattg gcattccgaa actaagaact cgctgatgca ggaccgggat	720
gccgcctcag cccgcgcctg gcctaaaatg catacagtca acggatacgt gaatcgggtca	780
ctgcccgggc tcatcggttg tcacagaaaag tccgtgtact ggcacgtcat cggcatgggc	840
actacgcctg aagtgcactc catcttcctg gaagggcaca ctttcctcgt gcgcaaccac	900
cgccaggcct ctctggaaat ctccccgatt acctttctga ccgcccagac tctgctcatg	960
gacctggggc agttccttct cttctgccac atctccagcc atcagcacga cggaatggag	1020
gcctacgtga aggtggactc atgcccggaa gaacctcagt tgcggatgaa gaacaacgag	1080
gaggccgagg actatgacga cgatttgact gactccgaga tggacgtcgt gcggttcgat	1140
gacgacaaca gccccagctt catccagatt cgcagcgtgg ccaagaagca ccccaaaacc	1200
tgggtgcact acatcgcggc cgaggaagaa gattgggact acgccccgtt ggtgctggca	1260
cccgatgacc ggtcgtacaa gtcccagtat ctgaacaatg gtccgcagcg gattggcaga	1320
aagtacaaga aagtgcggtt catggcgtac actgacgaaa cgtttaagac ccgggaggcc	1380
attcaacatg agagcggcat tctgggacca ctgctgtacg gagaggtcgg cgataccctg	1440
ctcatcatct taaaaacca ggccctcccg cttacaaca tctaccctca cggaatcacc	1500
gacgtgcggc cactctactc gcggcgcctg ccgaagggcg tcaagcacct gaaagacttc	1560
cctatcctgc cgggcgaaat cttcaagtat aagtggaccg tcaccgtgga ggacgggccc	1620
accaagagcg atcctagggtg tctgactcgg tactactcca gcttcgtgaa catggaacgg	1680
gacctggcat cgggactcat tggaccgctg ctgatctgct acaaagagtc ggtggatcaa	1740
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aacagatcct ggtacctcac tgaaaacatc cagagggtcc tcccaaacc cgcaggagtg	1860
caactggagg accctgagtt tcaggcctcg aatatcatgc actcgattaa cggttacgtg	1920
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atcggcgccc agactgactt cctgagcgtg ttcttttccg gttacacctt taagcacaag	2040
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atggagaacc cgggtctgtg gatttctggga tgccacaaca gcgactttcg gaaccgcgga	2160
atgactgccc tgctgaaggt gtcctcatgc gacaagaaca ccggagacta ctacgaggac	2220
tcctacgagg atatctcagc ctacctcctg tccaagaaca acgcgatcga gccgcgcagc	2280
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caccagcgag aaattaccgc gaccaccctc caatcggatc aggaggaaat cgactacgac	2820
gacaccatct cgggtggaaat gaagaaggaa gatttcgata tctacgacga ggacgaaaat	2880
cagtccccctc gctcattcca aaagaaaact agacactact ttatcgccgc ggtggaaaga	2940
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tcggtgcctc agttcaagaa agtgggtgtc caggagtcca ccgacggcag cttcaccag	3060
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actaagtcct ggtacttcac cgagaatatg gagcgaaact gtagagcgcc ctgcaatatc	3540
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atggatactc tgccggggct ggtcatggcc caggatcaga ggattcgggtg gtacttgctg	3660
tcaatgggat cgaacgaaaa cattcactcc attcacttct ccggtcacgt gttcactgtg	3720
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gccagatata ttaggctcca cccactcac tactcaatcc gctcaactct tcggatggaa	4320
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aaccaggact cgttcacacc cgtgggtgaac tccctggacc cccactgct gacgcggtac	4740
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tgcgaggccc aggacctgta ctga	4824

<210> 118

<211> 450

<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN144

<400> 118
ggcgcgcaaa catcagagag cgccacccct gaaagtggtc ccgggagcga gccagccaca 60
tctgggtcgg aaacgccagg cacaagtgag tctgcaactc ccgagtccgg acctggctcc 120
gagcctgcca ctagcggctc cgagactccg ggaacttccg agagcgctac accagaaagc 180
ggacccggaa ccagtaccga acctagcgag ggctctgctc cgggcagccc agccggctct 240
cctacatcca cggaggaggg cacttccgaa tccgccaccc cggagtcagg gccaggatct 300
gaacccgcta cctcaggcag tgagacgcca ggaacgagcg agtccgctac accggagagt 360
gggccaggga gccctgctgg atctcctacg tccactgagg aagggtcacc agcgggctcg 420
cccaccagca ctgaagaagg tgcctcgagc 450

<210> 119
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid Backbone Sequence (PBS)-4

<400> 119
atcagcctga gctcgctga 19

<210> 120
<211> 595
<212> DNA
<213> Artificial Sequence

<220>
<223> WPRE (mutated woodchuck hepatitis virus post-transcriptional
regulatory element)

<400> 120
tcataatcaa cctctggatt acaaaatttg tgaaagattg actggtattc ttaactatgt 60
tgctcctttt acgctatgtg gatacgctgc tttaatgcct ttgtatcatg ctattgcttc 120

ccgtatggct ttcattttct cctccttgta taaatcctgg ttgctgtctc tttatgagga	180
gttgtggccc gttgtcaggc aacgtggcgt ggtgtgact gtgtttgctg acgcaacccc	240
cactggttgg ggcattgcc aacacctgtca gctcctttcc gggactttcg ctttccccct	300
ccctattgcc acggcggaac tcatcgccgc ctgccttgcc cgctgctgga caggggctcg	360
gctgttgggc actgacaatt ccgtgggtgtt gtcggggaaa tcatcgtcct ttccttggct	420
gctcgcctgt gttgccacct ggattctgcg cgggacgtcc ttctgctacg tcccttcggc	480
cctcaatcca gcggaccttc cttcccgcg cctgctgccg gctctgcggc ctcttccgcg	540
tcttcgcctt cgccctcaga cgagtcggat ctccctttgg gccgcctccc cgctg	595

<210> 121
 <211> 8
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Plasmid Backbone Sequence (PBS)-5

<400> 121	
atcagcct	8

<210> 122
 <211> 211
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> bGHpA (bovine growth hormone polyadenylation signal)

<400> 122	
cgactgtgcc ttctagttgc cagccatctg ttgtttgccc ctccccctg ctttccttga	60
ccctggaagg tgccactccc actgtccttt cctaataaaa tgaggaaatt gcatcgcat	120
gtctgagtag gtgtcattct attctggggg gtgggggtggg gcaggacagc aagggggagg	180
attgggaaga caatagcagg catgctgggg a	211

<210> 123
 <211> 119
 <212> DNA

<213> Artificial Sequence

<220>

<223> Plasmid Backbone Sequence (PBS)-6

<400> 123

tgcggtgggc tctatggctt ctgaggcggg aagaacgggc tcgagaagct tctagatatc 60

ctctcttaag gtagcatcga gatttaaatt agggataaca gggtaatggc gcgggccgc 119

<210> 124

<211> 130

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'ITR (3'-end AAV2 inverted terminal repeat)

<400> 124

aggaaccctt agtgatggag ttggccactc cctctctgcg cgctcgctcg ctcactgagg 60

ccgggcgacc aaaggctgcc cgacgcccg gctttgccc ggcggcctca gtgagcgagc 120

gagcgcgagc 130

<210> 125

<211> 415

<212> PRT

<213> Artificial Sequence

<220>

<223> Mature FIX polypeptide

<400> 125

Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg
1 5 10 15

Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe
20 25 30

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

Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp

50

55

60

Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys
 65 70 75 80

Asn Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu
 85 90 95

Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr
 100 105 110

Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val
 115 120 125

Pro Phe Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr
 130 135 140

Arg Ala Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu
 145 150 155 160

Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn
 165 170 175

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

Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly
 195 200 205

Ser Ile Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu
 210 215 220

Thr Gly Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu
 225 230 235 240

Thr Glu His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His
 245 250 255

His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu
260 265 270

Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile
275 280 285

Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser
290 295 300

Gly Tyr Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala
305 310 315 320

Leu Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys
325 330 335

Leu Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly
340 345 350

Phe His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
355 360 365

His Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser
370 375 380

Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys
385 390 395 400

Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
405 410 415

<210> 126

<211> 415

<212> PRT

<213> Artificial Sequence

<220>

<223> Mature Padua(R338L)FIX Polypeptide

<400> 126

Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg
1 5 10 15

Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe
20 25 30

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

Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp
50 55 60

Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys
65 70 75 80

Asn Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu
85 90 95

Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr
100 105 110

Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val
115 120 125

Pro Phe Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr
130 135 140

Arg Ala Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu
145 150 155 160

Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn
165 170 175

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

Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly

195

200

205

Ser Ile Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu
 210 215 220

Thr Gly Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu
 225 230 235 240

Thr Glu His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His
 245 250 255

His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu
 260 265 270

Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile
 275 280 285

Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser
 290 295 300

Gly Tyr Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala
 305 310 315 320

Leu Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys
 325 330 335

Leu Leu Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly
 340 345 350

Phe His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 355 360 365

His Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser
 370 375 380

Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys
 385 390 395 400

Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
405 410 415

<210> 127
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> FIX Signal Polypeptide and Propeptide

<400> 127

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
20 25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg
35 40 45

<210> 128
<211> 8442
<212> DNA
<213> Artificial Sequence

<220>
<223> human VWF

<400> 128

atgattcctg ccagatttgc cggggtgctg cttgctctgg ccctcatttt gccagggacc 60
ctttgtgcag aaggaactcg cggcaggtca tccacggccc gatgcagcct tttcggaagt 120
gacttcgtca acacctttga tgggagcatg tacagctttg cgggatactg cagttacctc 180
ctggcagggg gctgccagaa acgctccttc tcgattattg gggacttcca gaatggcaag 240
agagtgagcc tctccgtgta tcttggggaa ttttttgaca tccatttggt tgtcaatggt 300
accgtgacac agggggacca aagagtctcc atgccctatg cctccaaagg gctgtatcta 360
gaaactgagg ctgggtacta caagctgtcc ggtgaggcct atggctttgt ggccaggatc 420

gatggcagcg gcaactttca agtcctgctg tcagacagat acttcaacaa gacctgcggg	480
ctgtgtggca actttaacat ctttgctgaa gatgacttta tgaccaaga agggaccttg	540
acctcggacc cttatgactt tgccaactca tgggctctga gcagtggaga acagtgggtgt	600
gaacgggcat ctctcccag cagctcatgc aacatctcct ctggggaaat gcagaagggc	660
ctgtgggagc agtgccagct tctgaagagc acctcgggtgt ttgcccgctg ccaccctctg	720
gtggaccccg agccttttgt ggccctgtgt gagaagactt tgtgtgagtgt tgctgggggg	780
ctggagtgcg cctgccctgc cctcctggag tacgcccga cctgtgcca ggagggaatg	840
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tataggcagt gtgtgtcccc ttgcgccagg acctgccaga gcctgcacat caatgaaatg	960
tgtcaggagc gatgcgtgga tggctgcagc tgccctgagg gacagctcct ggatgaaggc	1020
ctctgcgtgg agagcaccga gtgtccctgc gtgcattccg gaaagcgcta ccctcccggc	1080
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aacagatact tcaccttcag tgggatctgc cagtacctgc tggcccggga ttgccaggac	1260
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gcgtggcgcg agccaggccg ctgtgagctg aactgcccga aaggccaggt gtacctgcag	1980
tgcgggaccc cctgcaacct gacctgccgc tctctctctt acccggatga ggaatgcaat	2040
gaggcctgcc tggagggtctg cttctgcccc ccagggtctt acatggatga gaggggggac	2100
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catgtgtgtg atgccacgtg ctccacgac ggcatggccc actacctcac cttcgacggg	2640
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aaccctggga cctttcggat cctagtgggg aataagggat gcagccaccc ctcatgaaa	2760
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20

25

30

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Ser Met Tyr Ser Phe Ala Gly Tyr Cys Ser Tyr Leu Leu Ala Gly Gly
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Cys Gln Lys Arg Ser Phe Ser Ile Ile Gly Asp Phe Gln Asn Gly Lys
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Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
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Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro
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Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
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Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
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425

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Gln His Thr Val Thr Ala Ser Val Arg Leu Ser Tyr Gly Glu Asp Leu
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Gln Met Asp Trp Asp Gly Arg Gly Arg Leu Leu Val Lys Leu Ser Pro
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Gln Lys Gln His Ser Asp Pro Cys Ala Leu Asn Pro Arg Met Thr Arg
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1835 1840 1845

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1960

1965

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2555 2560 2565

Ser Cys Arg Cys Glu Arg Met Glu Ala Cys Met Leu Asn Gly Thr
2570 2575 2580

Val Ile Gly Pro Gly Lys Thr Val Met Ile Asp Val Cys Thr Thr
2585 2590 2595

Cys Arg Cys Met Val Gln Val Gly Val Ile Ser Gly Phe Lys Leu
2600 2605 2610

Glu Cys Arg Lys Thr Thr Cys Asn Pro Cys Pro Leu Gly Tyr Lys
2615 2620 2625

Glu Glu Asn Asn Thr Gly Glu Cys Cys Gly Arg Cys Leu Pro Thr
2630 2635 2640

Ala Cys Thr Ile Gln Leu Arg Gly Gly Gln Ile Met Thr Leu Lys
2645 2650 2655

Arg Asp Glu Thr Leu Gln Asp Gly Cys Asp Thr His Phe Cys Lys
2660 2665 2670

Val Asn Glu Arg Gly Glu Tyr Phe Trp Glu Lys Arg Val Thr Gly
2675 2680 2685

Cys Pro Pro Phe Asp Glu His Lys Cys Leu Ala Glu Gly Gly Lys
2690 2695 2700

Ile Met Lys Ile Pro Gly Thr Cys Cys Asp Thr Cys Glu Glu Pro

2705

2710

2715

Glu Cys Asn Asp Ile Thr Ala Arg Leu Gln Tyr Val Lys Val Gly
2720 2725 2730

Ser Cys Lys Ser Glu Val Glu Val Asp Ile His Tyr Cys Gln Gly
2735 2740 2745

Lys Cys Ala Ser Lys Ala Met Tyr Ser Ile Asp Ile Asn Asp Val
2750 2755 2760

Gln Asp Gln Cys Ser Cys Cys Ser Pro Thr Arg Thr Glu Pro Met
2765 2770 2775

Gln Val Ala Leu His Cys Thr Asn Gly Ser Val Val Tyr His Glu
2780 2785 2790

Val Leu Asn Ala Met Glu Cys Lys Cys Ser Pro Arg Lys Cys Ser
2795 2800 2805

Lys

<210> 130

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> AE36

<400> 130

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
1 5 10 15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
20 25 30

Ser Glu Thr Pro

35

<210> 131
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> AE42

<400> 131

Gly Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
1 5 10 15

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
20 25 30

Thr Ser Gly Ser Glu Thr Pro Ala Ser Ser
35 40

<210> 132
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> AE72

<400> 132

Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser
1 5 10 15

Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala
20 25 30

Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu
35 40 45

Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr
50 55 60

Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ala Ser Ser
65 70 75

<210> 133
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> AE78

<400> 133

Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser
1 5 10 15

Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala
20 25 30

Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu
35 40 45

Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr
50 55 60

Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ala Ser Ser
65 70 75

<210> 134
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> AE144

<400> 134

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
1 5 10 15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly

20

25

30

Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
 35 40 45

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro
 50 55 60

Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly
 65 70 75 80

Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
 85 90 95

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu
 100 105 110

Ser Ala Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
 115 120 125

Glu Thr Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 130 135 140

<210> 135
 <211> 144
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AE144_6B

<400> 135

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser
 1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
 20 25 30

Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly

35

40

45

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala
 50 55 60

Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
 65 70 75 80

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
 85 90 95

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro Ala
 100 105 110

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
 115 120 125

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
 130 135 140

<210> 136

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AG144

<400> 136

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
 1 5 10 15

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr
 20 25 30

Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
 35 40 45

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro

50

55

60

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
65 70 75 80

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
85 90 95

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro
100 105 110

Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr Ala
115 120 125

Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
130 135 140

<210> 137
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> AG144_A

<400> 137

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro
1 5 10 15

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
20 25 30

Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
35 40 45

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
50 55 60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser

65		70		75		80									
Thr	Gly	Ser	Pro	Gly	Thr	Pro	Gly	Ser	Gly	Thr	Ala	Ser	Ser	Ser	Pro
				85					90					95	

Gly	Ser	Ser	Thr	Pro	Ser	Gly	Ala	Thr	Gly	Ser	Pro	Gly	Thr	Pro	Gly
			100					105					110		

Ser	Gly	Thr	Ala	Ser	Ser	Ser	Pro	Gly	Ala	Ser	Pro	Gly	Thr	Ser	Ser
		115					120					125			

Thr	Gly	Ser	Pro	Gly	Ala	Ser	Pro	Gly	Thr	Ser	Ser	Thr	Gly	Ser	Pro
	130					135					140				

<210> 138
 <211> 288
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AE288

<400> 138

Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Ser	Glu	Pro
1				5					10					15	

Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro
			20					25					30		

Glu	Ser	Gly	Pro	Gly	Ser	Glu	Pro	Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro
		35					40					45			

Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Thr	Ser	Thr
	50					55					60				

Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr
65					70				75						80

Ser	Thr	Glu	Glu	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
 100 105 110

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr
 115 120 125

Ser Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
 130 135 140

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu
 145 150 155 160

Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro
 165 170 175

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
 180 185 190

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro
 195 200 205

Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr
 210 215 220

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 225 230 235 240

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro
 245 250 255

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
 260 265 270

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 275 280 285

<210> 139
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> AE288_2

<400> 139

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
1 5 10 15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
20 25 30

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
35 40 45

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
50 55 60

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu
65 70 75 80

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
85 90 95

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
100 105 110

Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
115 120 125

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
130 135 140

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
145 150 155 160

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
165 170 175

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
180 185 190

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
195 200 205

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
210 215 220

Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
225 230 235 240

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala
245 250 255

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
260 265 270

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
275 280 285

<210> 140
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> AG288

<400> 140

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser
1 5 10 15

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr
20 25 30

Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
35 40 45

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser
50 55 60

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr
65 70 75 80

Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
85 90 95

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser
100 105 110

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser
115 120 125

Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
130 135 140

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser
145 150 155 160

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser
165 170 175

Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly
180 185 190

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser
195 200 205

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly
210 215 220

Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly

100

105

110

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
 115 120 125

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 130 135 140

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala
 145 150 155 160

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu
 165 170 175

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 180 185 190

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
 195 200 205

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
 210 215 220

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
 225 230 235 240

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
 245 250 255

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
 260 265 270

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
 275 280 285

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
 290 295 300

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
305 310 315 320

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
325 330 335

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
340 345 350

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu
355 360 365

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
370 375 380

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
385 390 395 400

Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
405 410 415

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
420 425 430

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
435 440 445

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
450 455 460

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
465 470 475 480

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
485 490 495

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro

500

505

510

Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
515 520 525

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala
530 535 540

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
545 550 555 560

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
565 570 575

<210> 142
<211> 576
<212> PRT
<213> Artificial Sequence

<220>
<223> AG576

<400> 142

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser
1 5 10 15

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser
20 25 30

Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly
35 40 45

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser
50 55 60

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser
65 70 75 80

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser

85

90

95

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro
 100 105 110

Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser
 115 120 125

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
 130 135 140

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser
 145 150 155 160

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr
 165 170 175

Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
 180 185 190

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser
 195 200 205

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly
 210 215 220

Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
 225 230 235 240

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro
 245 250 255

Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly
 260 265 270

Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
 275 280 285

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser
290 295 300

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser
305 310 315 320

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
325 330 335

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser
340 345 350

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser
355 360 365

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
370 375 380

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro
385 390 395 400

Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly
405 410 415

Ala Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser
420 425 430

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro
435 440 445

Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly
450 455 460

Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
465 470 475 480

Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser

485

490

495

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser
 500 505 510

Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser
 515 520 525

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser
 530 535 540

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser
 545 550 555 560

Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
 565 570 575

<210> 143
 <211> 864
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AE864

<400> 143

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
 1 5 10 15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu
 20 25 30

Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
 35 40 45

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
 50 55 60

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro

65		70		75		80
Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro						
	85		90		95	
Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala						
	100		105		110	
Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro						
	115		120		125	
Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro						
	130		135		140	
Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala						
145		150		155		160
Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu						
	165		170		175	
Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro						
	180		185		190	
Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr						
	195		200		205	
Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro						
	210		215		220	
Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro						
225		230		235		240
Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr						
	245		250		255	
Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro						
	260		265		270	

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
275 280 285

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
290 295 300

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
305 310 315 320

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
325 330 335

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
340 345 350

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu
355 360 365

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
370 375 380

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
385 390 395 400

Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
405 410 415

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
420 425 430

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
435 440 445

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
450 455 460

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro

465				470				475				480				
Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Thr	Ser	Thr	
				485					490					495		
Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	
				500					505					510		
Glu	Ser	Gly	Pro	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	Ser	Thr	Glu	Glu	
				515					520					525		
Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	Ser	Thr	Glu	Glu	Gly	Ser	Pro	Ala	
				530					535					540		
Gly	Ser	Pro	Thr	Ser	Thr	Glu	Glu	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	
				545					550					555		
Glu	Ser	Gly	Pro	Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	
				565					570					575		
Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Ser	Glu	Pro	
				580					585					590		
Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	
				595					600					605		
Glu	Ser	Gly	Pro	Gly	Ser	Glu	Pro	Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	
				610					615					620		
Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Thr	Ser	Thr	
				625					630					635		
Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	
				645					650					655		
Ser	Thr	Glu	Glu	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	
				660					665					670		

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
675 680 685

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr
690 695 700

Ser Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
705 710 715 720

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu
725 730 735

Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro
740 745 750

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
755 760 765

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro
770 775 780

Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr
785 790 795 800

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
805 810 815

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro
820 825 830

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
835 840 845

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
850 855 860

<210> 144

<211> 864
<212> PRT
<213> Artificial Sequence

<220>
<223> AG864

<400> 144

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro
1 5 10 15

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
20 25 30

Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
35 40 45

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
50 55 60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
65 70 75 80

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
85 90 95

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly
100 105 110

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
115 120 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
130 135 140

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
145 150 155 160

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser

165

170

175

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
180 185 190

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
195 200 205

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
210 215 220

Gly Thr Gly Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
225 230 235 240

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro
245 250 255

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
260 265 270

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
275 280 285

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro
290 295 300

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
305 310 315 320

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
325 330 335

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly
340 345 350

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
355 360 365

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
370 375 380

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr
385 390 395 400

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
405 410 415

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
420 425 430

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
435 440 445

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
450 455 460

Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
465 470 475 480

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro
485 490 495

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
500 505 510

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
515 520 525

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro
530 535 540

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
545 550 555 560

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro

565

570

575

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
 580 585 590

Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala
 595 600 605

Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
 610 615 620

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
 625 630 635 640

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
 645 650 655

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
 660 665 670

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro
 675 680 685

Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala
 690 695 700

Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
 705 710 715 720

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro
 725 730 735

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
 740 745 750

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
 755 760 765

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
770 775 780

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
785 790 795 800

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
805 810 815

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
820 825 830

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
835 840 845

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
850 855 860

<210> 145
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_2A_1

<400> 145

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly
1 5 10 15

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 146
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_2A_2

<400> 146

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1 5 10 15

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser
50 55 60

Ala Thr Pro Glu Ser Gly Pro Gly
65 70

<210> 147
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_3B_1

<400> 147

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser

20

25

30

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
35 40 45

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 148

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> XTEN_AE72_3B_2

<400> 148

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
1 5 10 15

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
35 40 45

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 149

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> XTEN_AE72_4A_2

<400> 149

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly
1 5 10 15

Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser
20 25 30

Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 150

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> XTEN_AE72_5A_2

<400> 150

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
20 25 30

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
35 40 45

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
50 55 60

Ser Pro Thr Ser Thr Glu Glu Gly
65 70

<210> 151
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_6B_1

<400> 151

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
20 25 30

Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
35 40 45

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala
50 55 60

Thr Ser Gly Ser Glu Thr Pro Gly
65 70

<210> 152
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_6B_2

<400> 152

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu
1 5 10 15

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly

20

25

30

Ser Ala Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 153
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_1A_1

<400> 153

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
35 40 45

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 154
<211> 72
<212> PRT
<213> Artificial Sequence

<220>

<223> XTEN_AE72_1A_2

<400> 154

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1 5 10 15

Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
20 25 30

Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 155

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> XTEN_AE144_1A

<400> 155

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
35 40 45

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
65 70 75 80

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
85 90 95

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly
100 105 110

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu
115 120 125

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
130 135 140

<210> 156
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> AE150

<400> 156

Gly Ala Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
1 5 10 15

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
20 25 30

Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
35 40 45

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
50 55 60

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala
65 70 75 80

Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
85 90 95

Glu Thr Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
100 105 110

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
115 120 125

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
130 135 140

Ser Ala Pro Ala Ser Ser
145 150

<210> 157
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> G150

<400> 157

Gly Ala Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly
1 5 10 15

Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser
20 25 30

Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly
35 40 45

Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly
50 55 60

Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr Pro
65 70 75 80

Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly
85 90 95

Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly
100 105 110

Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser
115 120 125

Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr
130 135 140

Gly Ser Pro Ala Ser Ser
145 150

<210> 158
<211> 294
<212> PRT
<213> Artificial Sequence

<220>
<223> AE294

<400> 158

Gly Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
1 5 10 15

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser
20 25 30

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
35 40 45

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
50 55 60

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly
65 70 75 80

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu
85 90 95

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
100 105 110

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly
115 120 125

Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser
130 135 140

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
145 150 155 160

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser
165 170 175

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
180 185 190

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
195 200 205

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly
210 215 220

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly
225 230 235 240

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
245 250 255

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser
260 265 270

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly

275

280

285

Ser Ala Pro Ala Ser Ser
290

<210> 159

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> AG294

<400> 159

Gly Ala Pro Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
1 5 10 15

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro Gly
20 25 30

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
35 40 45

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
50 55 60

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly
65 70 75 80

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
85 90 95

Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
100 105 110

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro
115 120 125

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser

130

135

140

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
 145 150 155 160

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
 165 170 175

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
 180 185 190

Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
 195 200 205

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr
 210 215 220

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr
 225 230 235 240

Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
 245 250 255

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly
 260 265 270

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
 275 280 285

Thr Gly Ser Ala Ser Ser
 290

<210> 160

<211> 1016

<212> PRT

<213> Artificial Sequence

<220>

<223> FIX-Linker-Albumin

<400> 160

Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg
1 5 10 15

Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe
20 25 30

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

Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp
50 55 60

Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys
65 70 75 80

Asn Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu
85 90 95

Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr
100 105 110

Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val
115 120 125

Pro Phe Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr
130 135 140

Arg Ala Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu
145 150 155 160

Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn
165 170 175

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

Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly
195 200 205

Ser Ile Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu
210 215 220

Thr Gly Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu
225 230 235 240

Thr Glu His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His
245 250 255

His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu
260 265 270

Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile
275 280 285

Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser
290 295 300

Gly Tyr Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala
305 310 315 320

Leu Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys
325 330 335

Leu Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly
340 345 350

Phe His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
355 360 365

His Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser
370 375 380

Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys

385 390 395 400

Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Pro
405 410 415

Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Thr Val Phe Pro Asp
420 425 430

Val Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly
435 440 445

Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu
450 455 460

Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr
465 470 475 480

Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp
485 490 495

Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr
500 505 510

Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu
515 520 525

Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn
530 535 540

Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe
545 550 555 560

His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala
565 570 575

Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys
580 585 590

Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala
595 600 605

Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala
610 615 620

Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly
625 630 635 640

Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe
645 650 655

Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr
660 665 670

Lys Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp
675 680 685

Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile
690 695 700

Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser
705 710 715 720

His Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro
725 730 735

Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr
740 745 750

Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala
755 760 765

Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys
770 775 780

Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Phe Cys

785		790		795		800									
Tyr	Ala	Lys	Val	Phe	Asp	Glu	Phe	Lys	Pro	Leu	Val	Glu	Glu	Pro	Gln
				805					810					815	
Asn	Leu	Ile	Lys	Gln	Asn	Cys	Glu	Leu	Phe	Glu	Gln	Leu	Gly	Glu	Tyr
			820					825					830		
Lys	Phe	Gln	Asn	Ala	Leu	Leu	Val	Arg	Tyr	Thr	Lys	Lys	Val	Pro	Gln
		835					840					845			
Val	Ser	Thr	Pro	Thr	Leu	Val	Glu	Val	Ser	Arg	Asn	Leu	Gly	Lys	Val
	850					855					860				
Gly	Ser	Lys	Cys	Cys	Lys	His	Pro	Glu	Ala	Lys	Arg	Met	Pro	Cys	Ala
865					870					875					880
Glu	Asp	Tyr	Leu	Ser	Val	Val	Leu	Asn	Gln	Leu	Cys	Val	Leu	His	Glu
				885					890					895	
Lys	Thr	Pro	Val	Ser	Asp	Arg	Val	Thr	Lys	Cys	Cys	Thr	Glu	Ser	Leu
			900					905					910		
Val	Asn	Arg	Arg	Pro	Cys	Phe	Ser	Ala	Leu	Glu	Val	Asp	Glu	Thr	Tyr
	915						920					925			
Val	Pro	Lys	Glu	Phe	Asn	Ala	Glu	Thr	Phe	Thr	Phe	His	Ala	Asp	Ile
	930					935					940				
Cys	Thr	Leu	Ser	Glu	Lys	Glu	Arg	Gln	Ile	Lys	Lys	Gln	Thr	Ala	Leu
945					950					955					960
Val	Glu	Leu	Val	Lys	His	Lys	Pro	Lys	Ala	Thr	Lys	Glu	Gln	Leu	Lys
				965					970					975	
Ala	Val	Met	Asp	Asp	Phe	Ala	Ala	Phe	Val	Glu	Lys	Cys	Cys	Lys	Ala
			980					985					990		

Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala
995 1000 1005

Ala Ser Gln Ala Ala Leu Gly Leu
1010 1015

<210> 161
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> FIX

<400> 161

Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg
1 5 10 15

Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe
20 25 30

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

Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp
50 55 60

Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys
65 70 75 80

Asn Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu
85 90 95

Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr
100 105 110

Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val
115 120 125

Pro Phe Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr
130 135 140

Arg Ala Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu
145 150 155 160

Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn
165 170 175

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

Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly
195 200 205

Ser Ile Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu
210 215 220

Thr Gly Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu
225 230 235 240

Thr Glu His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His
245 250 255

His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu
260 265 270

Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile
275 280 285

Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser
290 295 300

Gly Tyr Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala
305 310 315 320

Leu Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys

325

330

335

Leu Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly
340 345 350

Phe His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
355 360 365

His Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser
370 375 380

Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys
385 390 395 400

Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Pro
405 410 415

Val Ser Gln Thr Ser Lys Leu Thr
420

<210> 162
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 162

Arg Ala Glu Thr Val Phe Pro Asp Val
1 5

<210> 163
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Albumin

<400> 163

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

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

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

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

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

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

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195

200

205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 164

<211> 763
<212> PRT
<213> Artificial Sequence

<220>
<223> FIX(XTEN)-Fc

<400> 164

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
20 25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
65 70 75 80

Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
130 135 140

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

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe

165

170

175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
 180 185 190

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

Thr Ile Leu Asp Gly Pro Ser Pro Gly Ser Pro Thr Ser Thr Glu Glu
 210 215 220

Gly Thr Ser Glu Ser Ala Thr Pro Gly Ser Gly Pro Gly Ser Glu Pro
 225 230 235 240

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
 245 250 255

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 260 265 270

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ala Ser Ser
 275 280 285

Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe Thr Arg Val Val
 290 295 300

Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp Gln Val Val Leu
 305 310 315 320

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

Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr
 340 345 350

Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln
 355 360 365

Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn Tyr Asn Ala Ala
370 375 380

Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro
385 390 395 400

Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile Ala Asp Lys Glu
405 410 415

Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr Val Ser Gly Trp
420 425 430

Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln Tyr Leu
435 440 445

Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Leu Ser Thr Lys Phe
450 455 460

Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg
465 470 475 480

Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu
485 490 495

Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala
500 505 510

Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser Arg Tyr Val Asn
515 520 525

Trp Ile Lys Glu Lys Thr Lys Leu Thr Asp Lys Thr His Thr Cys Pro
530 535 540

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
545 550 555 560

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

565

570

575

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 580 585 590

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 595 600 605

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 610 615 620

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 625 630 635 640

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 645 650 655

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 660 665 670

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 675 680 685

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 690 695 700

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 705 710 715 720

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 725 730 735

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 740 745 750

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 755 760

<210> 165
<211> 712
<212> PRT
<213> Artificial Sequence

<220>
<223> FIX-FXIa-AE288

<400> 165

Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg
1 5 10 15

Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe
20 25 30

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

Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp
50 55 60

Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys
65 70 75 80

Asn Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu
85 90 95

Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr
100 105 110

Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val
115 120 125

Pro Phe Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr
130 135 140

Arg Ala Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu
145 150 155 160

Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn
165 170 175

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

Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly
195 200 205

Ser Ile Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu
210 215 220

Thr Gly Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu
225 230 235 240

Thr Glu His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His
245 250 255

His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu
260 265 270

Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile
275 280 285

Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser
290 295 300

Gly Tyr Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala
305 310 315 320

Leu Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys
325 330 335

Leu Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly
340 345 350

Phe His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro

355

360

365

His Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser
 370 375 380

Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys
 385 390 395 400

Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Gly
 405 410 415

Lys Leu Thr Arg Ala Glu Thr Gly Gly Thr Ser Glu Ser Ala Thr Pro
 420 425 430

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
 435 440 445

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
 450 455 460

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
 465 470 475 480

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 485 490 495

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
 500 505 510

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
 515 520 525

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
 530 535 540

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala
 545 550 555 560

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu
565 570 575

Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
580 585 590

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu
595 600 605

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
610 615 620

Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
625 630 635 640

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr
645 650 655

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu
660 665 670

Gly Ser Ala Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
675 680 685

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
690 695 700

Glu Pro Ser Glu Gly Ser Ala Pro
705 710

<210> 166
<211> 944
<212> PRT
<213> Artificial Sequence

<220>
<223> FIX-Fc-Fc

<400> 166

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
20 25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
65 70 75 80

Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
130 135 140

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

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
165 170 175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
180 185 190

Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu

195

200

205

Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe
 210 215 220

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

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

Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
 260 265 270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
 275 280 285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn
 290 295 300

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

Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile
 325 330 335

Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr
 340 345 350

Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val
 355 360 365

Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg
 370 375 380

Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His
 385 390 395 400

Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val
405 410 415

Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly
420 425 430

Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser
435 440 445

Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Asp Lys Thr
450 455 460

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
465 470 475 480

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
485 490 495

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
500 505 510

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
515 520 525

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
530 535 540

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
545 550 555 560

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
565 570 575

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
580 585 590

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys

595

600

605

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 625 630 635 640

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 645 650 655

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 660 665 670

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 675 680 685

Arg Arg Arg Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 690 695 700

Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Arg Arg Arg Asp Lys Thr
 705 710 715 720

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 725 730 735

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 740 745 750

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 755 760 765

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 770 775 780

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 785 790 795 800

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
805 810 815

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
820 825 830

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
835 840 845

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
850 855 860

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
865 870 875 880

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
885 890 895

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
900 905 910

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
915 920 925

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
930 935 940

<210> 167

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Parvovirus B19 KY940273.1

<400> 167

ccaaatcaga tgccgccggt cgccgccggt aggcgggact tccggtacaa gatggcggac 60

aattacgtca tttcctgtga cgtcatttcc tgtgacgtca cttccggtgg gcgggacttc 120

cggaattagg gttggctctg ggccagcttg cttgggggttg ccttgacact aagacaagcg	180
gcgcgccgct tgatcttagt ggcacgtcaa cccaagcgc tggcccagag ccaaccctaa	240
ttccggaagt cccgcccacc ggaagtgacg tcacaggaaa tgacgtcaca ggaaatgacg	300
taattgtccg ccatcttgta ccggaagtcc cgcctaccgg cggcgaccgg cggcatctga	360
tttgggtgtct tcttttaaatt ttt	383

<210> 168
 <211> 248
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Parvovirus B19 d135

<400> 168	
ctctgggccca gcttgcttgg ggttgcccttg acactaagac aagcggcgcg ccgcttgatc	60
ttagtggcac gtcaacccca agcgttgcc cagagccaac cctaattccg gaagtccgcg	120
ccaccggaag tgacgtcaca ggaaatgacg tcacaggaaa tgacgtaatt gtccgccatc	180
ttgtaccgga agtccccgct accggcggcg accggcggca tctgatttgg tgtcttcttt	240
taaatttt	248

<210> 169
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Parvovirus v1 AAV2

<400> 169	
cggcgcgccg cttgatctta gtggcacgtc aaccagcgtt ggcccagagc caaccctaatt	60
tccggaagtc ctcagtccgc catcttgccc gcctaccggc ggcgaccggc ggcatcattt	120
ggtgttctt	129

<210> 170
 <211> 113
 <212> DNA

<213> Artificial Sequence

<220>

<223> Parvovirus V2

<400> 170

ctctgggcca gcttgcttgg ggttgccctg acactaagac aagcggcgcg ccgcttgatc 60

ttagtggcac gtcaacccca agcgtggcc cagagtgtct tcttttaaatt ttt 113

<210> 171

<211> 340

<212> DNA

<213> Artificial Sequence

<220>

<223> Parvovirus V3

<400> 171

caaatacagat gccgccggtc gccgccggta ggccgggactt ccggtacaag atggcggaca 60

attacgtcat ttcctgtgac gtatttcctg tgacgtactt ccggtggcgg gacttccgga 120

atatttggtc tgggccagct tgcttggggg tgccttgacc aagcgcgcgc cgcttgatca 180

ccccaagcgc tggcccagag ccacctaacc ggaagtcccc ccaccggaag tgacgtcaca 240

ggaaagacgt cacaggaagt aattgtccgc catcttgtag cggaagtccc gcaccggcgg 300

cgaccggcgg catctgattt ggtgtcttct tttaaatttt 340

<210> 172

<211> 444

<212> DNA

<213> Artificial Sequence

<220>

<223> Parvovirus U25749.1

<400> 172

ctcattggag gggttcgttcg ttcgaaccag ccaatcaggg gagggggaag tgacgcaagt 60

tccggtcaca tgcttccggg gacgcacatc cggtagcgtg gttccgggtca cgtgcttcct 120

gtcacgtgtt tccgggtcacg tgacttccgg tcatgtgact tccggtgacg tgtttccggc 180

tgtaggttg accacgcgca tgccgcgcgg tcagcccaat agttaagccg gaaacacgtc 240

accggaagtc acatgaccgg aagtcacgtg accggaaaca cgtgacagga agcacgtgac	300
cggaactacg tcaccggatg tgcgtcaccg gaagcatgtg accggaactt gcgtcacttc	360
cccctcccct gattggctgg ttcgaacgaa cgaaccctcc aatgagactc aaggacaaga	420
ggatattttg cgcgccagga agtg	444

<210> 173
 <211> 282
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Parvovirus GPV AAV2 V1

<400> 173	
cggtgacgtg tttccggctg ttaggttgac cacgcgcatg ccgcgcggtc agcccaatag	60
ttaagccgga aacacgtcac cggaagtcac atgaccggaa gtcacgtgac cggaaacacg	120
tgacaggaag cacgtgaccg gaactacgtc accggatgtg cgtcaccgga agcatgtgac	180
cggaaacttg ctcacttccc cctcccctga ttggctgggt cgaacgaacg aaccctccaa	240
tgagactcaa ggacaagagg atattttgcg cgccaggaag tg	282

<210> 174
 <211> 145
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Parvovirus GPV AAV2 V1

<400> 174	
ttgaccacgc gcatgccgcg cggtcagccc aatagttaag ccgggtgacc acacgtgaca	60
ggaagcacgg gatgtgcgtc accggaagca gtgaccgggc tggttcgaac gaacgaaccc	120
tccaactcaa ggacaagagg atatt	145

<210> 175
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Parvovirus GPV V2

<400> 175

cgggtgacgtg tttccggctg ttaggttgac cacgcgcatg ccgcgcggtc agcccaatag 60

ttaagccgga aacacgtcac cgactcaagg acaagaggat attttgcgcg ccaggaagtg 120

<210> 176

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> Parvovirus GPV V3

<400> 176

gggaacaatc aggggaagtg accggtgacg tcatgtaact tgcgtcactt cccgttcgaa 60

cgaacgaacg agactcaagg acaagaggcg cgccaggaag tg 102

<210> 177

<211> 145

<212> DNA

<213> Artificial Sequence

<220>

<223> Parvovirus AAV2 NC_001401.2

<400> 177

ttggccactc cctctctgcg cgctcgctcg ctactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggccggcctca gtgagcgagc gagcgcgag agagggagtg 120

gccaactcca tcactagggg ttcct 145

<210> 178

<211> 130

<212> DNA

<213> Artificial Sequence

<220>

<223> Parvovirus Gtx

<400> 178

ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgctc ggcgaccttt 60

ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gaggggccaa ctccatcact	120
aggggttcct	130

<210> 179
 <211> 6762
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> B19-FVIII construct

<400> 179	
ctctgggcca gcttgcttgg ggttgccttg acactaagac aagcggcgcg ccgcttgatc	60
ttagtggcac gtcaacccca agcgctggcc cagagccaac cctaattccg gaagtcccgc	120
ccaccggaag tgacgtcaca ggaaatgacg tcacaggaaa tgacgtaatt gtccgccatc	180
ttgtaccgga agtcccgctt accggcgggcg accggcggca tctgatttgg tgtcttcttt	240
taaattttgc ggcaattcag tcgataacta taacggtcct aaggtagcga tttaaatacg	300
cgctctctta aggtagcccc gggacgcgtc aattgagatc tggatccggt accgaattcg	360
cggccgcctc gacgactagc gtttaattaa acgcgtgtct gtctgcacat ttcgtagagc	420
gagtgttccg atactcta atctccctaggc aaggttcata tttgtgtagg ttacttattc	480
tcctttttgtt gactaagtca ataatacaga tcagcagggt tggagtcagc ttggcaggga	540
tcagcagcct gggttgggaag gaggggggtat aaaagcccct tcaccaggag aagccgtcac	600
acagatccac aagctcctga ggtaagtgcc gtgtgtgggt cccgcgggcc tggcctcttt	660
acgggttatg gcccttgcgt gccttgaatt actgacactg acatccactt tttctttttc	720
tccacagcta gcgccaccat gcagattgag ctgtccactt gtttcttcct gtgcctcctg	780
cgcttctgtt tctccgccac tcgccgttac taccttggag ccgtggagct ttcattgggac	840
tacatgcaga gcgacctggg cgaactcccc gtggatgcca gattcccccc ccgcgtgcca	900
aagtccttcc cctttaacac ctccgtgggt tacaagaaaa ccctctttgt cgagttcact	960
gaccacctgt tcaacatcgc caagccgcgc ccaccttggg tgggcctcct gggaccgacc	1020
attcaagctg aagtgtacga caccgtgggt atcacctga agaacaatggc gtcccccccc	1080

gtgtccctgc atgcggtcgg agtgtcctac tggaaggcct ccgaaggagc tgagtacgac	1140
gaccagacta gccagcggga aaaggaggac gataaagtgt tcccgggcgg ctgcatact	1200
tacgtgtggc aagtcctgaa ggaaaacgga cctatggcat ccgatcctct gtgcctgact	1260
tactcctacc tttcccatgt ggacctcgtg aaggacctga acagcgggct gattggtgca	1320
cttctcgtgt gccgcgaagg ttcgctcgtc aaggaaaaga cccagaccct ccataagttc	1380
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ctgatgcagg accgggatgc cgcctcagcc cgcgcctggc ctaaaatgca tacagtcaac	1500
ggatacgtga atcggtcact gcccgggctc atcggttgtc acagaaagtc cgtgtactgg	1560
cacgtcatcg gcatgggcac tacgcctgaa gtgcactcca tcttcctgga agggcacacc	1620
ttcctcgtgc gcaaccaccg ccaggcctct ctggaaatct ccccgattac ctttctgacc	1680
gcccagactc tgctcatgga cctggggcag ttccttctct tctgccacat ctccagccat	1740
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cggatgaaga acaacgagga ggccgaggac tatgacgacg atttgactga ctccgagatg	1860
gacgtcgtgc ggttcgatga cgacaacagc cccagcttca tccagattcg cagcgtggcc	1920
aagaagcacc ccaaaacctg ggtgcactac atcgcggccg aggaagaaga ttgggactac	1980
gccccgttgg tgctggcacc cgatgaccgg tcgtacaagt cccagtatct gaacaatggt	2040
ccgcagcggga ttggcagaaa gtacaagaaa gtgcggttca tggcgtacac tgacgaaacg	2100
tttaagaccc gggaggccat tcaacatgag agcggcattc tgggaccact gctgtacgga	2160
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taccctcacg gaatcaccga cgtgcggcca ctctactcgc ggcgctgcc gaaggcgctc	2280
aagcacctga aagacttccc tatcctgccg ggcgaaatct tcaagtataa gtggaccgtc	2340
accgtggagg acggggccac caagagcgat cctaggtgtc tgactcggta ctactccagc	2400
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ccaaacccccg caggagtgca actggaggac cctgagtttc aggcctcgaa tatcatgcac	2640
tcgattaacg gttacgtgtt cgactcgctg caactgagcg tgtgcctcca tgaagtcgct	2700
tactggtaca ttctgtccat cggcgcccag actgacttcc tgagcgtgtt cttttccggt	2760
tacaccttta agcacaagat ggtgtacgaa gataccctga ccctgttccc tttctccggc	2820
gaaacgggtg tcatgtcgat ggagaacccg ggtctgtgga ttctgggatg ccacaacagc	2880
gactttcggga accgcggaat gactgccctg ctgaagggtg cctcatgcga caagaacacc	2940
ggagactact acgaggactc ctacgaggat atctcagcct acctcctgtc caagaacaac	3000
gcgatcgagc cgcgcagctt cagccagaac ggcgcgccaa catcagagag cgccaccctt	3060
gaaagtggtc ccgggagcga gccagccaca tctgggtcgg aaacgccagg cacaagtgag	3120
tctgcaactc ccgagtccgg acctggctcc gagcctgcc a tagcggctc cgagactccg	3180
ggaacttccg agagcgctac accagaaagc ggacccggaa ccagtaccga acctagcgag	3240
ggctctgctc cgggcagccc agccggctct cctacatcca cggaggaggg cacttccgaa	3300
tccgccaccc cggagtcagg gccaggatct gaacccgcta cctcaggcag tgagacgcca	3360
ggaacgagcg agtccgctac accggagagt gggccaggga gccctgctgg atctcctacg	3420
tccactgagg aagggtcacc agcgggctcg cccaccagca ctgaagaagg tgcctcgagc	3480
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 <213> Artificial Sequence

 <220>
 <223> 5' ITR

 <400> 180

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<220>
 <223> 3' ITR

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 <211> 282
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' ITR

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tgacaggaag cacgtgaccg gaactacgtc accggatgtg cgtcaccgga agcatgtgac	180
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tgagactcaa ggacaagagg atattttgcg cgccaggaag tg	282

<210> 184
 <211> 282
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3' ITR

<400> 184	
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<220>
 <223> 5' ITR

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<210> 186
 <211> 383
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3' ITR

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<210> 187
 <211> 444
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' ITR

<400> 187	
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 <211> 444
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3' ITR

<400> 188	
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide sequence

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