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<150> 62/671,915

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<151> 2019-01-16

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<220>

<223> coFVIII-52-NT58

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<213> Artificial Sequence

<220>
<223> coFVIII-52-CT

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-25-CT

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aagcacaaga	tggtgtacga ggacaccctg accctcttcc ctttttccgg cgaaactgtg 300
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 <211> 1734
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-26-NT58

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 <211> 2583
 <212> DNA
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<211> 2332
<212> PRT
<213> Homo sapiens

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<400> 15

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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
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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
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```

```

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
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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

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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		
		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		
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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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Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val	Ile	Leu	Phe		
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Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp	Pro	Glu	Phe		
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Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val	Phe	Asp	Ser		
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625					630					635					640		
Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	Ser	Gly	Tyr		
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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	
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Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	Asn	Asn	Ala	725	730	735	
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Gln	Lys	Gln	Phe	Asn	Ala	Thr	Thr	Ile	Pro	Glu	Asn	Asp	Ile	Glu	Lys	755	760	765	
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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

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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

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	1175					1180					1185			
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Tyr 1925	Ile	Met	Asp	Thr	Leu	Pro 1930	Gly	Leu	Val	Met	Ala 1935	Gln	Asp	Gln
Arg 1940	Ile	Arg	Trp	Tyr	Leu	Leu 1945	Ser	Met	Gly	Ser	Asn 1950	Glu	Asn	Ile
His 1955	Ser	Ile	His	Phe	Ser	Gly 1960	His	Val	Phe	Thr	Val 1965	Arg	Lys	Lys
Glu 1970	Glu	Tyr	Lys	Met	Ala	Leu 1975	Tyr	Asn	Leu	Tyr	Pro 1980	Gly	Val	Phe
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Glu 2000	Cys	Leu	Ile	Gly	Glu	His 2005	Leu	His	Ala	Gly	Met 2010	Ser	Thr	Leu
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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
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<210> 16
 <211> 4371
 <212> DNA
 <213> Artificial Sequence

<220>

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

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<210> 17
<211> 1438
<212> PRT
<213> Artificial Sequence

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<220>
<223> BDD-FVIII (non-optimized; "parental"), Amino Acid Sequence

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<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

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

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

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Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
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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	225	230	235
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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	290	295	300
Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His	Asp	Gly	Met	305	310	315
Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro	Gln	Leu	Arg	325	330	335
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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

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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 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
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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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Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu
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Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met
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Gly Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val
 1055 1060 1065

Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn
 1070 1075 1080

Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys
 1085 1090 1095

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
 1115 1120 1125

Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile
 1130 1135 1140

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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
1175						1180					1185			
Gly	Ile	Lys	Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe	Ser	Ser	Leu	Tyr
1190						1195					1200			
Ile	Ser	Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu	Asp	Gly	Lys	Lys	Trp
1205						1210					1215			
Gln	Thr	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe
1220						1225					1230			
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
1265						1270					1275			
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
1295						1300					1305			
Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu	Gln	Gly	Arg	Ser	Asn
1310						1315					1320			
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
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Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg
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Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu
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Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
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cagggcgtga	aaagtctgct	gacctcaatg	tacgtcaagg	agttcctgat	ctctagttca	4620
caggacggac	atcagtggac	actgttcttt	cagaacggga	aggtgaaagt	cttccagggc	4680
aatcaggatt	cctttacacc	tgtgggtcaac	agtctagacc	ctccactgct	gaccagatac	4740
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attta 5

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taaata 5

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tttttt 6

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gccgccacca tgc

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<400> 33

Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser
1 5 10 15

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

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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
20 25

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Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
1 5 10

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

Ser Ala Ala Ala
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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
 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 1670	Glu Met Lys Lys	Glu Asp Phe Asp Ile 1675	Tyr Asp Glu Asp 1680	
Glu Asn 1685	Gln Ser Pro Arg	Ser Phe Gln Lys Lys 1690	Thr Arg His Tyr 1695	
Phe Ile 1700	Ala Ala Val Glu	Arg Leu Trp Asp Tyr 1705	Gly Met Ser Ser 1710	
Ser Pro 1715	His Val Leu Arg	Asn Arg Ala Gln Ser 1720	Gly Ser Val Pro 1725	
Gln Phe 1730	Lys Lys Val Val	Phe Gln Glu Phe Thr 1735	Asp Gly Ser Phe 1740	
Thr Gln 1745	Pro Leu Tyr Arg	Gly Glu Leu Asn Glu 1750	His Leu Gly Leu 1755	
Leu Gly 1760	Pro Tyr Ile Arg	Ala Glu Val Glu Asp 1765	Asn Ile Met Val 1770	
Thr Phe 1775	Arg Asn Gln Ala	Ser Arg Pro Tyr Ser 1780	Phe Tyr Ser Ser 1785	
Leu Ile 1790	Ser Tyr Glu Glu	Asp Gln Arg Gln Gly 1795	Ala Glu Pro Arg 1800	
Lys Asn 1805	Phe Val Lys Pro	Asn Glu Thr Lys Thr 1810	Tyr Phe Trp Lys 1815	
Val Gln 1820	His His Met Ala	Pro Thr Lys Asp Glu 1825	Phe Asp Cys Lys 1830	
Ala Trp 1835	Ala Tyr Phe Ser	Asp Val Asp Leu Glu 1840	Lys Asp Val His 1845	
Ser Gly 1850	Leu Ile Gly Pro	Leu Leu Val Cys His 1855	Thr Asn Thr Leu 1860	
Asn Pro 1865	Ala His Gly Arg	Gln Val Thr Val Gln 1870	Glu Phe Ala Leu 1875	
Phe Phe 1880	Thr Ile Phe Asp	Glu Thr Lys Ser Trp 1885	Tyr Phe Thr Glu 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 2150	His Tyr Ser Ile Arg 2155	Ser Thr Leu Arg 2160
Met Glu Leu Met Gly Cys 2165	Asp Leu Asn Ser Cys 2170	Ser Met Pro Leu 2175
Gly Met Glu Ser Lys Ala 2180	Ile Ser Asp Ala Gln 2185	Ile Thr Ala Ser 2190
Ser Tyr Phe Thr Asn Met 2195	Phe Ala Thr Trp Ser 2200	Pro Ser Lys Ala 2205
Arg Leu His Leu Gln Gly 2210	Arg Ser Asn Ala Trp 2215	Arg Pro Gln Val 2220
Asn Asn Pro Lys Glu Trp 2225	Leu Gln Val Asp Phe 2230	Gln Lys Thr Met 2235
Lys Val Thr Gly Val Thr 2240	Thr Gln Gly Val Lys 2245	Ser Leu Leu Thr 2250
Ser Met Tyr Val Lys Glu 2255	Phe Leu Ile Ser Ser 2260	Ser Gln Asp Gly 2265
His Gln Trp Thr Leu Phe 2270	Phe Gln Asn Gly Lys 2275	Val Lys Val Phe 2280
Gln Gly Asn Gln Asp Ser 2285	Phe Thr Pro Val Val 2290	Asn Ser Leu Asp 2295
Pro Pro Leu Leu Thr Arg 2300	Tyr Leu Arg Ile His 2305	Pro Gln Ser Trp 2310
Val His Gln Ile Ala Leu 2315	Arg Met Glu Val Leu 2320	Gly Cys Glu Ala 2325
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Glu Leu Leu Gly
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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 aagggtcagc 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 tgaggggaagc 360
gcacctggta ccagcgaaag cgcaactccc gaatcaggtc ccggtacgag cgagtcgggcg 420
accccgagga gcggggccagg 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
ggcgcgcgcaa gtcccgcctgg aagcccaact agcaccgaag aggggacctc agagtccgcc 60
acccccgagt ccggccctgg ctctgagcct gccactagcg gctccgagac tcctggcaca 120
tccgaaagcg ctacaccgga gagtggaccc ggcacctcta ccgagcccag tgagggctcc 180
gcccttgga caagcaccga gccagcgaa ggcagcgccc cagggacctc cacagagccc 240
agtgaaggca gtgctcctgg caccagcacc gaaccaagcg agggctctgc acccgggacc 300
tccaccgagc caagcgaagg ctctgccctt ggcacttcca ccgagcccag cgaaggcagc 360
gcccttgga gcccgctgg 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

ggcgcgccaa cgtccgaaag tgctaccctt 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 ggctcaccga cgagcactga agagggctct 300

cccgtggca gcccaacgtc gacagaagaa ggatcaccag caggctcccc cacatcaaca 360

gaggagggta catcagaatc tgctactccc gagagtggac ccggtacctc cactgagccc 420

<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

ggcgcgccaa catcagagag cgccaccct gaaagtggtc ccgggagcga gccagccaca 60

tctgggtcgg aaacgccagg cacaagtgag tctgcaactc ccgagtccgg acctggctcc 120

gagcctgcc a tagcggctc cgagactccg ggaacttccg agagcgctac accagaaagc 180

ggacccggaa ccagtaccga acctagcgag ggctctgctc cgggcagccc agccggctct 240
 cctacatcca cggaggaggg cacttccgaa tccgccaccc cggagtcagg gccaggatct 300
 gaaccgccta 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
ggcgcgccaa catctaccga gccttccgaa ggctctgccc ctgggacctc agaatctgca 60
acccttgaaa 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 tgccaccca gagagcggac ccggcacttc aaccgagccc 420
tccgaaggat cagcaccagg tgctcagc 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 gtcacccccg 60
tcagcgtcga ctgggacggg acccgggaca cccggttcgg ggactgcatc ctcctcgcct 120
ggttcgtcca ccccgtcagg agccacgggt tcgccgggaa gcagcccaag cgcacccact 180
ggtacagggc ctggggcttc accgggtact tcacccacgg ggtcaccggg aacgcccgga 240
tcggggacgg cttcctcatc accaggatcg tcaacaccct cgggcgcaac gggcagcccc 300
ggaacccttg gttcgggtac ggcgtcgtcg agccccggtg cgagcccggg 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 tcaactgggt caccggggtc atccccctcg 60
gcctcaaccg ggacgggtcc cggctcatcc ccagcgcca gcaactggaac aggtcctggc 120
actcctgggt ccggtacggc atcgatcatcc ccgggaagct caacaccgtc cggagcgaca 180
ggatcacctg gctcgtcacc ttcggcgatca actggaacgg ggccaggggc ctcaccgga 240
acgtcctcga ctgggtcgcc tggtagccg ggatcaggaa cggcctcatc ctcgcctggg 300
tcctcaacgc cctcgggtgc gactgggttc cgggaactc ctgggtcggg gacggcctcg 360
tcgtcgctg gggcatcacc ggggacgagc tccacggggg cccctggagc gtcaccgggg 420
acctcctcga caggtagccc ggctcgcgagc 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 ccaggttcat cgaccccgctc gggagcgact 180
gggtcgcccc gatcaagccc gtcagcttcc actggaacag gacccgggctc gtcgccgtca 240
gcctcaacgg ggacaggacc tggttcatcg acgccgtcag gggcgacagg ctgcgccgga 300
tcgtcaacac cctcgggggc aacggggagc cctgggtcgt cgcctggaac ctcatccacc 360
ggaagccccg gggcctcgcc ggggtacgagc tccacgggat cgcccggagc 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 cggggtcgcc aggggcgtcc cctgggacgt cctcaacagg ctgccccggt 120
gcgtcaccgc gcacgtcgtc cacgggttca cctggtagct ccccttccgc gtccactggc 180
accgggcctg gaactccggg gagcggcaca gcgagctcgt cgccgggagc atcgccctggg 240
acatcgagca ccgggtcgcc aggagcatcg cccggaacat ccagcacagg aagccccggc 300
gcgtcgcccc ggacatcaag cacagggtcc ccgggatcga gcacgccgtc cggagccact 360
ggatcaccag ggagctcgac accttccggc gcaacgggat cgcccggagc cagcccgggt 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 gaccaggttc gtcaccctca 60
gcatcaacgg ggacgggacc gggggcggtca ccaggaacgt cctccaccgg ctcgccgggt 120
gcatcacccg gaacgtcatc gaccggatcg ccaggagct cgacgccatc aggcgcaaca 180
ggatcacctg gctcaagccc tagcgcgtca accggcacgg gtccgggtgc ctcccctggc 240
acgtccagca ccggatcacc cggatcgagc ccatccgcct caaccggaac cggaccgggt 300
acaccagggt cggaacagc 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

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acacgaaggt attatctggg ggctgtggaa ctgtcttggg attacatgca gagtgacctg	120
ggagagctgc cagtggacgc aaggtttccc cctagagtcc ctaagtcatt ccccttcaac	180
actagcgtgg tctacaagaa aacactgttc gtggagttta ctgatcacct gttcaacatc	240
gcaaagccta ggccaccctg gatgggactg ctggggccaa caatccaggc cgagggtgtac	300
gacaccgtgg tcattacact taagaacatg gcctcacacc ccgtgagcct gcatgctgtg	360
ggcgctcagct actggaaggc ttccgaagga gcagagtatg acgatcagac ttcccagaga	420
gaaaaagagg acgataaggt gtttcctggc ggatctcata cctacgtgtg gcaggctctg	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 gcccaaatg cacactgtga acggctacgt caatcgctca	780
ctgcctgggc tgatcggctg ccaccgaaag agcgtgtatt ggcatgtcat cgggatgggc	840
accacacctg aagtgcactc cattttcctg gagggacata cttttctggg ccgcaaccac	900
cgacaggctt ccctggagat ctctccaatt accttcctga 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 gccctcctt tatccagatt agatctgtgg ccaagaaaca ccctaagaca	1200
tgggtccatt acatcgcagc cgaggaagag gactgggatt atgcaccact ggtgctggca	1260
ccagacgatc gtcctacaa atctcagtat ctgaacaatg ggccacagag gattggcaga	1320
aagtacaaga aagtgcgggt catggcatat accgatgaga ctttcaagac tcgcgaagcc	1380
atccagcacg agagcggcat cctgggacca ctgctgtacg gagaagtggg agacaccctg	1440
ctgatcattt tcaagaacca ggccagccgg cttacaata tctatccaca tgggattaca	1500
gatgtgcgcc ctctgtacag caggagactg ccaaagggcg tcaaacacct gaaggacttc	1560
ccaatcctgc ccggagaaat cttcaagtac aagtggactg tcaccgtcga ggatggcccc	1620
actaagagcg accctcgggt cctgaccgc tactattcta gtttcgtgaa tatggaaaga	1680
gatctggcaa gcggactgat cggaccactg ctgatttggt acaaagagag cgtggatcag	1740
agaggcaacc agatcatgtc cgacaagcgg aatgtgattc tgttcagtgt ctttgacgaa	1800

aacaggtcat	ggtacctgac	cgagaacatc	cagagattcc	tgcctaatacc	agctggggtg	1860
cagctggaag	atcctgagtt	tcaggcatct	aacatcatgc	atagtattaa	tggttacgtg	1920
ttcgacagtt	tgcagctgag	cgtgtgcctg	cacgaggtcg	cttactggta	tatcctgagc	1980
attggggcac	agacagatth	cctgagcgtg	ttcttttccg	gctacactth	taagcataaa	2040
atggtctatg	aggacacact	gactctgttc	cccttcagcg	gcgaaaccgt	gtttatgagc	2100
atggagaatc	ccggactgtg	gattctgggg	tgccacaaca	gcgatttcag	aaatcgcgga	2160
atgactgcc	tgctgaaagt	gtcaagctgt	gacaagaaca	ccggggacta	ctatgaagat	2220
tcatacgagg	acatcagcgc	atatctgctg	tccaaaaaca	atgccattga	accccggtct	2280
tttagtcaga	atcctccagt	gctgaagagg	caccagaggg	agatcacccg	cactaccctg	2340
cagagtgatc	aggaagagat	cgactacgac	gatacaatth	ctgtggaaat	gaagaaagag	2400
gacttcgata	tctatgacga	agatgagaac	cagagtcctc	gatcattcca	gaagaaaacc	2460
aggcattact	ttattgccgc	agtggagcgg	ctgtgggatt	atggcatgtc	ctctagtctt	2520
cacgtgctgc	gaaatagggc	ccagtcagga	agcgtcccac	agttcaagaa	agtggctctt	2580
caggagttta	cagacgggtc	ctttactcag	ccactgtaca	ggggcgaact	gaacgagcac	2640
ctgggactgc	tggggcccta	tatcagagca	gaagtggagg	ataacattat	ggtcaccttc	2700
agaaatcagg	cctctcggcc	ttacagttth	tattcaagcc	tgatctctta	cgaagaggac	2760
cagcgacagg	gagctgaacc	acgaaaaaac	ttcgtgaagc	ctaatgagac	caaaacatac	2820
ttttggaagg	tgcagcacca	tatggcccca	acaaaagacg	agttcgattg	caaggcatgg	2880
gcctatthth	ctgacgtgga	tctggagaag	gacgtgcaca	gtggcctgat	tggtccactg	2940
ctggtgtgcc	atactaacac	cctgaatcca	gccacggcc	ggcaggtcac	tgtccaggag	3000
ttcgctctgt	tctttaccat	ctttgatgag	acaaagagct	ggtacttcac	cgaaaacatg	3060
gagcgaaatt	gcagggtctc	atgtaacatt	cagatggaag	acccacatt	caaggagaac	3120
taccgctth	atgctatcaa	tggatacatc	atggatactc	tgcccgggct	ggcatggca	3180
caggaccaga	gaatccggtg	gtatctgctg	agcatgggca	gcaacgagaa	tatccactca	3240
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<220>
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<220>
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<400> 73

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

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 <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
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<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
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<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
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<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
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<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
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<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
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<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
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<220>
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<400> 86

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

<210> 87
<211> 12
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<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>
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<400> 88

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

<210> 89
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<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>

<223> AQ motif

<400> 93

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

<210> 94

<211> 12
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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
<212> PRT
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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
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<220>
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<400> 97

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

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<220>
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<400> 98

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

<210> 99
<211> 12
<212> PRT
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<220>
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<400> 99

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

<210> 100
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<400> 100

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

<210> 101
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<220>
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<400> 101

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

<210> 102
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<220>
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<400> 102

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

<210> 103
<211> 1607
<212> PRT

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<220>

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<400> 103

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1 5 10 15

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				