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35 40 45

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
			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
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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
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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

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
370 375 380

Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
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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
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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
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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
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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
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Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
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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
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
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Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn Ser Leu Ser
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Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
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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
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Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met Pro Val His
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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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Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser Asp Thr Glu
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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
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Lys	Asp	Val	Gly	Leu	Lys	Glu	Met	Val	Phe	Pro	Ser	Ser	Arg	Asn
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Leu	Phe	Leu	Thr	Asn	Leu	Asp	Asn	Leu	His	Glu	Asn	Asn	Thr	His
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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
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1220						1225					1230			

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Gln	Asp	Phe	Arg	Ser	Leu	Asn	Asp	Ser	Thr	Asn	Arg	Thr	Lys	Lys
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His	Thr	Ala	His	Phe	Ser	Lys	Lys	Gly	Glu	Glu	Glu	Asn	Leu	Glu
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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
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Gln	Trp	Ser	Lys	Asn	Met	Lys	His	Leu	Thr	Pro	Ser	Thr	Leu	Thr
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Gln	Ile	Asp	Tyr	Asn	Glu	Lys	Glu	Lys	Gly	Ala	Ile	Thr	Gln	Ser
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Pro	Leu	Ser	Asp	Cys	Leu	Thr	Arg	Ser	His	Ser	Ile	Pro	Gln	Ala
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Asn	Arg	Ser	Pro	Leu	Pro	Ile	Ala	Lys	Val	Ser	Ser	Phe	Pro	Ser
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Ile	Arg	Pro	Ile	Tyr	Leu	Thr	Arg	Val	Leu	Phe	Gln	Asp	Asn	Ser
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Ser	His	Leu	Pro	Ala	Ala	Ser	Tyr	Arg	Lys	Lys	Asp	Ser	Gly	Val
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Gln	Glu	Ser	Ser	His	Phe	Leu	Gln	Gly	Ala	Lys	Lys	Asn	Asn	Leu
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Ser	Leu	Ala	Ile	Leu	Thr	Leu	Glu	Met	Thr	Gly	Asp	Gln	Arg	Glu
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Val	Gly	Ser	Leu	Gly	Thr	Ser	Ala	Thr	Asn	Ser	Val	Thr	Tyr	Lys
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Lys	Val	Glu	Asn	Thr	Val	Leu	Pro	Lys	Pro	Asp	Leu	Pro	Lys	Thr
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Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val Pro Phe Leu Arg				
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Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu Leu Asp				
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Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu				
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Glu Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys				
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Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys Glu Ser Asn His				
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Ser	Pro	His	Val	Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro
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Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Ser	Phe	Tyr	Ser	Ser
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Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly	Ala	Glu	Pro	Arg
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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
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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> 16

<211> 4371

<212> ADN

<213> Secuencia artificial

<220>

<223> BDD-FVIII (no optimizado; "parental"), Secuencia de nucleótidos

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aagtgatctc 120

ggtgagctgc ctgtggacgc aagatttcct cctagagtgc caaaatcttt
tccattcaac 180

acctcagtcg tgtacaaaaa gactctgttt gtagaattca cggatcacct
tttcaacatc 240

gctaagccaa ggccaccctg gatgggtctg ctaggtccta ccatccaggc
tgaggtttat 300

gatacagtgg tcattacact taagaacatg gcttcccatc ctgtcagtct
tcatgctggt 360

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cagtcaaagg 420

gagaaagaag atgataaagt cttccctggt ggaagccata catatgtctg
gcaggtcctg 480

aaagagaatg gtccaatggc ctctgaccca ctgtgcctta cctactcata
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atgtagagaa 600

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ttttgctgta 660

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ggatagggat 720

gctgcatctg ctcgggcctg gcctaaaatg cacacagtca atggttatgt
aaacaggtct 780

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tggaatgggc 840

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gaggaaccat 900

cgccaggcgt ccttggaat ctgcgaata actttcctta ctgctcaaac
actcttgatg 960

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aaataatgaa 1080

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tcctaaaact 1200

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agtcctcgcc 1260

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gattggtagg 1320

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tcgtgaagct 1380

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agacacactg 1440

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cggaatcact 1500

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gaaggatttt 1560

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agatgggcca 1620

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tatggagaga 1680

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tgtagatcaa 1740

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atttgatgag 1800

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agctggagtg 1860

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tggctatggt 1920

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cattctaagc 1980

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caaacacaaa 2040

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cttcatgtcg 2100

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gaacagaggc 2160

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accaagaagc 2280

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tactactctt 2340

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gaagaaggaa 2400

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aaagaaaaca 2460

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agtacaggaa 3000

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tgaaaatatg 3060

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taaagagaat 3120

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catccattct 3240

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aatggcactg 3300

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agctggaatt 3360

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actttttctg 3420

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tagagatttt 3480

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acttcattat 3540

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ggtggatctg 3600

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cccaactcat 3840

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ggacttccag 4080

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4371

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<211> 1438

<212> PRT

<213> Secuencia artificial

<220>

<223> BDD-FVIII (no optimizado; "parental"), Secuencia de aminoácidos

<400> 17

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 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
805 810 815

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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Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu				
1025		1030		1035
Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met				
1040		1045		1050
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				
1100		1105		1110
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

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
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
1385						1390					1395			

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

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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<220>
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 acctggctcc 120

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		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
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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
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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> Secuencia artificial

<220>

<223> aminoácidos 233-236 de la IgG1 humana

<400> 45

Glu Leu Leu Gly

1

<210> 46

<211> 42

<212> PRT

<213> Secuencia artificial

<220>

<223> XTEN AE42-4, secuencia de proteínas

<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> ADN

<213> Secuencia artificial

<220>

<223> XTEN AE42-4, secuencia de ADN

<400> 47

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aagcgaaagc 60

gctacgcctg agagtggccc tggctctgag ccagccacct ccggctctga
aaccctgcc 120

tcgagc

126

<210> 48

<211> 144

<212> PRT

<213> Secuencia artificial

<220>

<223> XTEN AE144-2A, secuencia de proteínas

<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> ADN

<213> Secuencia artificial

<220>

<223> XTEN AE144-2A, secuencia de ADN

<400> 49

ggcgcgccaa ccagtacgga gccgtccgag gggagcgcac caggaagccc
ggctgggagc 60

ccgacttcta ccgaagaggg tacatctacc gaaccaagtg aaggttcagc
accaggcacc 120

tcaacagaac cctctgaggg ctcgggcgcct ggtacaagtg agtccgccac
cccagaatcc 180

gggcctggga caagcacaga accttcggaa gggagtgtcc ctggaacatc
cgaatcggca 240

accccagaat cagggccagg atctgagccc gcgacttcgg gctccgagac
gcctgggaca 300

tccaccgagc cctccgaagg atcagcccca ggcaccagca cggagccctc
tgaggggaagc 360

gcacctggta ccagcgaaag cgcaactccc gaatcaggtc ccggtacgag
cgagtcggcg 420

accccgagaga gcgggccagg tgcctcgagc

450

<210> 50

<211> 144

<212> PRT

<213> Secuencia artificial

<220>

<223> XTEN AE144-3B, secuencia de proteínas

<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> ADN

<213> Secuencia artificial

<220>

<223> XTEN AE144-3B, secuencia de ADN

<400> 51

ggcgcgccaa gtcccgctgg aagcccaact agcaccgaag aggggacctc
agagtccgcc 60

acccccgagt ccggccctgg ctctgagcct gccactagcg gctccgagac
tcctggcaca 120

tccgaaagcg ctacacccga gagtggaccc ggcacctcta ccgagcccag
tgagggctcc 180

gcccctggaa caagcaccga gccagcgaa ggcagcgccc cagggacctc
cacagagccc 240

agtgaaggca gtgctcctgg caccagcacc gaaccaagcg agggctctgc
accgaggacc 300

tccaccgagc caagcgaagg ctctgcccct ggcacttcca ccgagcccag
cgaaggcagc 360

gcccctggga gcccgcctgg ctctcccacc agcactgagg agggcacatc
taccgaacca 420

agtgaaggct ctgcaccagg tgcctcgagc
450

<210> 52

<211> 144

<212> PRT

<213> Secuencia artificial

<220>

<223> XTEN AE144-4A, secuencia de proteínas

<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> ADN

<213> Secuencia artificial

<220>

<223> XTEN AE144-4A, secuencia de ADN

<400> 53

ggcgcgccaa cgtccgaaag tgctaccct gagtcaggcc ctggtagtga
gcctgccaca 60

agcggaaagc 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 gcccaacgtc gacagaagaa ggatcaccag caggctcccc
cacatcaaca 360

gaggagggta catcagaatc tgctactccc gagagtggac ccggtacctc
cactgagccc 420

agcgagggga gtgcaccagg tgctctgagc
450

<210> 54
<211> 144
<212> PRT
<213> Secuencia artificial

<220>

<223> XTEN AE144-5A, secuencia de proteínas

<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> ADN

<213> Secuencia artificial

<220>

<223> XTEN AE144-5A, secuencia de ADN

<400> 55

ggcgcgccaa catcagagag cgccaccct gaaagtggtc ccgggagcga
gccagccaca 60

tctgggtcgg aaacgccagg cacaagtgag tctgcaactc ccgagtccgg
acctggctcc 120

gagcctgcc aatagcggctc 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

gggccagggga gccctgctgg atctcctacg tccactgagg aagggtcacc
agcgggctcg 420

cccaccagca ctgaagaagg tgcctcgagc
450

<210> 56

<211> 144

<212> PRT

<213> Secuencia artificial

<220>

<223> XTEN AE144-6B, secuencia de proteínas

<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> ADN

<213> Secuencia artificial

<220>

<223> XTEN AE144-6B, secuencia de ADN

<400> 57

ggcgcgccaa catctaccga gccttccgaa ggctctgccc ctgggacctc
agaatctgca 60

accctgaaa gcggccctgg aacctccgaa agtgccactc ccgagagcgg
cccagggaca 120

agcgagtcag caaccctga gtctggaccc ggcagcgagc ctgcaacctc
tggtcagag 180

actcccgggt cagaaccgc tacctcaggc tccgagacac ccggctctcc
tgctgggagt 240

cccacttcca ccgaggaagg aacatccact gagcctagtg agggctctgc
ccctggaacc 300

agcacagagc caagtgaggg cagtgcacca ggatccgagc cagcaaccag
cgggtccgag 360

actcccggga cctctgagtc tgccacccca gagagcggac ccggcacttc
aaccgagccc 420

tccgaaggat cagcaccagg tgcttcgagc
450

<210> 58

<211> 144

<212> PRT

<213> Secuencia artificial

<220>

<223> XTEN AG144-1, secuencia de proteínas

<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> ADN

<213> Secuencia artificial

<220>

<223> XTEN AG144-1, secuencia de ADN

<400> 59

ggcgcgccac ccgggtcgtc cccgtcggcg tccaccggaa cagggccagg
 gtcattccccg 60

tcagcgtcga ctgggacggg acccgggaca cccgggttcgg ggactgcatt
 ctctcgcct 120

ggttcgtcca ccccgtcagg agccacgggt tcgccgggaa gcagcccaag
 cgcattccact 180

ggtacagggc ctggggcttc accgggtact tcatccacgg ggtcaccggg
 aacgcccga 240

tcggggacgg cttcctcatt accaggatcg tcaacaccct cgggcgcaac
 gggcagcccc 300

ggaacccctg gttcgggtac ggcgtcgtcg agccccggtg cgagccccggg
aacaagctcg 360

acaggatcgc ctggggcgtc acccggcacg tcgagcacag gcagccccgg
aaccctgga 420

tcgggaaccg cgtcgtcaag cgcctcgagc
450

<210> 60

<211> 144

<212> PRT

<213> Secuencia artificial

<220>

<223> XTEN AG144-A, secuencia de proteínas

<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> ADN

<213> Secuencia artificial

<220>

<223> XTEN AG144-A, secuencia de ADN

<400> 61

ggcgcgccag gtgcctcgcc gggaacatca tcaactgggt caccgggtc
atccccctcg 60

gcctcaaccg ggacgggtcc cggctcatcc cccagcgcca gcactggaac
aggtcctggc 120

actcctgggt ccggtacggc atcgtcatcc ccgggaagct caacaccgtc
cggagcgaca 180

ggatcacctg gctcgtcacc ttcggcgtca actggaacgg ggccaggggc
ctcacccgga 240

acgtcctcga ctgggtcgcc tggtagccg ggatcaggaa cggcctcatc
ctcgctggg 300

tcctcaacgc cctcgggtgc gactgggttc cggggaactc ctggctcggg
gacggcctcg 360

tcgtcgcttg gggcatcacc ggggacgagc tccacggggg cccctggagc
gtcaccgggg 420

acctcctcga caggtagccc ggcctcgagc
450

<210> 62

<211> 144

<212> PRT

<213> Secuencia artificial

<220>

<223> XTEN AG144-B, secuencia de proteínas

<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> ADN

<213> Secuencia artificial

<220>

<223> XTEN AG144-B, secuencia de ADN

<400> 63

ggcgcgccag gtacaccggg cagcggcacg gcttcgtcgt caccgggctc
gtccacaccg 60

tcgggagcta cggaagccc aggagcgtca ccgggaacgt cgtcaacggg
gtcaccgggt 120

acgccaggta gcggcacggc cagcagctcg ccagggtcat cgaccccgtc
gggagcgact 180

gggtcgcccg gatcaagccc gtcagcttcc actggaacag gaccggggtc
gtcgccgtca 240

gcctcaacgg ggacaggacc tggttcatcg acgccgtcag gggcgacagg
ctcgcccgga 300

tcgtcaacac cctcgggggc aacggggagc cctggtgcgt cgcctggaac
ctcatccacc 360

ggaagcccgg gggcctcgcc gggtacgagc tccacgggat cgcccggagc
gtcccccgga 420

acttcaagca caggagccc tgcctcgagc
450

<210> 64

<211> 144

<212> PRT

<213> Secuencia artificial

<220>

<223> XTEN AG144-C, secuencia de proteínas

<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> ADN

<213> Secuencia artificial

<220>

<223> XTEN AG144-C, secuencia de ADN

<400> 65

ggcgcgccag gtacacccgg atcgggtaca gcgtcatcga gccccggtgc

gtcacctggt 60

acgtcgagca cggggtcgcc aggggcgtcc cctgggacgt cctcaacagg
ctcgcccggg 120

gcgtcaccgg gcacgtcgtc cacgggttca cctggtagct ccccttcggc
gtccactggc 180

accgggcctg gaactccggg gagcggcaca gcgagctcgt cgccgggagc
atcgccctggg 240

acatcgagca ccgggtcgcc aggagcatcg cccggaacat ccagcacagg
aagccccggc 300

gcgtcgcccg ggacatcaag cacagggtcc ccgggatcga gcacgcccgtc
cgagaccact 360

ggatcaccag ggagctcgac accttcgggc gcaacgggat cgcccggagc
cagcccgggt 420

acgtcaagca ctggctcccc tgcctcgagc
450

<210> 66

<211> 144

<212> PRT

<213> Secuencia artificial

<220>

<223> XTEN AG144-F, secuencia de proteínas

<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> ADN

<213> Secuencia artificial

<220>

<223> XTEN AG144-F, secuencia de ADN

<400> 67

ggcgcgccag gctccagccc ctccgcgagc acgggaaccg gaccagggttc
gtcacacctca 60

gcatcaacgg ggacgggacc gggggcgctca ccaggaacgt cctccaccgg
ctcgccgggt 120

gcatcacccg gaacgtcatc gaccggatcg ccaggagct cgacgccatc
aggcgcaaca 180

ggatcacctg gctcaagccc tagcgcgtca accggcacgg gtccgggtgc
ctcccctggc 240

acgtccagca ccggatcacc cggatcgagc ccatccgcct caaccggaac
cggacccggt 300

acaccagggt cggaacagc ctctcgtca ccaggctcct caaccccctc
gggagccacg 360

ggttcgcccg gttcgtcaac gccttccgga gcaactggta gccccggagc
atcgccagga 420

acttcgagca cggggctgcc cgcctcgagc

450

<210> 68

<211> 4374

<212> ADN

<213> Secuencia artificial

<220>

<223> coFVIII-1 secuencia de ADN

<400> 68

atgcagattg agctgtctac ttgctttttc ctgtgcctgc tgaggttttg
cttttccgct 60

acacgaaggt attatctggg ggctgtggaa ctgtcttggg attacatgca
gagtgacctg 120

ggagagctgc cagtggacgc aaggttttccc cctagagtcc ctaagtcatt
ccccttcaac 180

actagcgtgg tctacaagaa aacactgttc gtggagttta ctgatcacct
gttcaacatc 240

gcaaagccta ggccaccctg gatgggactg ctggggccaa caatccaggc
cgaggtgtac 300

gacaccgtgg tcattacact taagaacatg gcctcacacc ccgtgagcct
gcatgctgtg 360

ggcgtcagct actggaaggc ttccgaagga gcagagtatg acgatcagac
ttcccagaga 420

gaaaaagagg acgataaggt gtttcctggc ggatctcata cctacgtgtg
gcaggtcctg 480

aaagagaatg gccctatggc ctccgaccct ctgtgcctga cctactctta
tctgagtcac 540

gtggacctgg tcaaggatct gaacagcggc ctgatcggag ccctgctggt
gtgcagggaa 600

ggaagcctgg ctaaggagaa aaccagaca ctgcataagt tcattctgct
gttcgccgtg 660

tttgacgaag ggaaatcatg gcacagcggc acaaagaata gtctgatgca
ggacagggat 720

gccgcttcag ccagagcttg gcccaaatg cacactgtga acggctacgt
caatcgctca 780

ctgcctgggc tgatcggctg ccaccgaaag agcgtgtatt ggcattgcat
cgggatgggc 840

accacacctg aagtgcactc cattttcctg gagggacata cctttctggt
ccgcaaccac 900

cgacaggctt ccctggagat ctctccaatt accttcctga cagcacagac
tctgctgatg 960

gacctggggc agttcctgct gttttgccac atcagctccc accagcatga
tggcatggag 1020

gcttacgtga aagtggactc ttgtcccggag gaacctcagc tgcggatgaa
gaacaatgag 1080

gaagcagaag actatgacga tgacctgacc gactccgaga tggatgtggt
ccgattcgat 1140

gacgataaca gcccctcctt tatccagatt agatctgtgg ccaagaaaca
ccctaagaca 1200

tgggtccatt acatcgacgc cgaggaagag gactgggatt atgcaccact
ggtgctggca 1260

ccagacgatc gctcctacaa atctcagtat ctgaacaatg ggccacagag
gattggcaga 1320

aagtacaaga aagtgcggtt catggcatat accgatgaga ccttcaagac
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 accctcgggtg cctgaccgcg tactattcta gtttcgtgaa
tatggaaaga 1680

gatctggcaa gcggactgat cggaccactg ctgatttggtt acaaagagag
cgtggatcag 1740

agaggcaacc agatcatgtc cgacaagcgg aatgtgattc tgttcagtgt
ctttgacgaa 1800

aacaggtcat ggtacctgac cgagaacatc cagagattcc tgcctaatac
agctggggtg 1860

cagctggaag atcctgagtt tcaggcatct aacatcatgc atagtattaa
tggctacgtg 1920

ttcgacagtt tgcagctgag cgtgtgcctg cacgaggtcg cttactggta
tattctgagc 1980

attggggcac agacagattt cctgagcgtg ttcttttccg gctacacttt
taagcataaa 2040

atggtctatg aggacacact gactctgttc cccttcagcg gcgaaaccgt
gttttatgagc 2100

atggagaatc ccggactgtg gattctgggg tgccacaaca gcgatttcag
aaatcgcgga 2160

atgactgccc tgctgaaagt gtcaagctgt gacaagaaca ccggggacta
ctatgaagat 2220

tcatacgagg acatcagcgc atatctgctg tccaaaaaca atgccattga
accccggtct 2280

tttagtcaga atcctccagt gctgaagagg caccagaggg agatcacccg
cactaccctg 2340

cagagtgatc aggaagagat cgactacgac gatacaattt ctgtggaaat
gaagaaagag 2400

gacttcgata tctatgacga agatgagaac cagagtcctc gatcattcca
gaagaaaacc 2460

aggcattact ttattgccgc agtggagcgg ctgtgggatt atggcatgtc
ctctagtcct 2520

cacgtgctgc gaaatagggc ccagtcagga agcgtcccac agttcaagaa
agtggctctc 2580

caggagttta cagacgggtc ctttactcag ccactgtaca ggggcgaact
gaacgagcac 2640

ctgggactgc tggggcccta tatcagagca gaagtggagg ataacattat
ggtcaccttc 2700

agaaatcagg cctctcggcc ttacagtttt tattcaagcc tgatctctta
cgaagaggac 2760

cagcgacagg gagctgaacc acgaaaaaac ttcgtgaagc ctaatgagac
caaacatac 2820

ttttggaagg tgcagcacca tatggcccca acaaagacg agttcgattg
caaggcatgg 2880

gcctatTTTT ctgacgtgga tctggagaag gacgtgcaca gtggcctgat
tggccactg 2940

ctggtgtgcc atactaacac cctgaatcca gccacgggc ggcaggtcac
tgtccaggag 3000

ttcgctctgt tctttaccat ctttgatgag acaaagagct ggtacttcac
cgaaaacatg 3060

gagcgaaatt gcagggctcc atgtaacatt cagatggaag accccacatt
caaggagaac 3120

taccgctttc atgctatcaa tggatacatc atggatactc tgcccgggct
ggtcattggca 3180

caggaccaga gaatccggtg gtatctgctg agcatgggca gcaacgagaa
tatccactca 3240

attcatttca gcgggcacgt gtttactgtc aggaagaaag aagagtacaa
gatggccctg 3300

tacaacctgt atcccggcgt gttcgaaacc gtcgagatgc tgcctagcaa
ggccggaatc 3360

tggagagtgg aatgcctgat tggagagcac ctgcatgctg ggatgtctac
cctgtttctg 3420

gtgtacagta ataagtgtca gacaccctg ggaatggcat ccgggcatat
cagggatttc 3480

cagattaccg catctggaca gtacggacag tgggcaccta agctggctag
actgcactat 3540

tccggatcta tcaacgcttg gtccacaaaa gagcctttct cttggattaa
ggtggacctg 3600

ctggcccaaa tgatcattca tggcatcaaa actcaggag ctcggcagaa
gttctcctct 3660

ctgtacatct cacagtttat catcatgtac agcctggatg ggaagaaatg
gcagacatac 3720

cgcggaata gcacaggaac tctgatggtg ttctttggca acgtggacag
cagcgaatc 3780

aagcacaaca ttttcaatcc ccctatcatt gctagataca tccggctgca
cccaacccat 3840

tattctattc gaagtacact gaggatggaa ctgatgggat gcgatctgaa
cagttggtca 3900

atgcccctgg ggatggagtc caaggcaatc tctgacgcc agattaccgc
cagctcctac 3960

ttcactaata tgtttgctac ctggagccct tccaaagcaa gactgcacct
gcaaggccgc 4020

agcaacgcat ggcgaccaca ggtgaacaat cccaaggagt ggttgcaggt
cgattttcag 4080

aaaactatga aggtgaccgg ggtcacaact cagggcgtga aaagtctgct
gacctcaatg 4140

tacgtcaagg agttcctgat ctctagttca caggacggac atcagtggac
actgttcttt 4200

cagaacggga aggtgaaagt cttccagggc aatcaggatt cctttacacc
tgtggtcaac 4260

agtctagacc ctccactgct gaccagatac ctgagaatcc accctcagtc
ctgggtgcac 4320

cagattgccc tgagaatgga agtgctggga tgcgaggccc aggatctgta ctga
4374

<210> 69

<211> 577

<212> ADN

<213> Secuencia artificial

<220>

<223> Promotor ET, secuencia de ADN

<400> 69

ctcgaggtca attcacgcga gttaataatt accagcgcgg gccaaataaa
taatccgcga 60

ggggcaggtg acgtttgccc agcgcgcgct ggtaattatt aacctcgcga
atattgattc 120

gaggccgcga ttgccgcaat cgcgaggggc aggtgacctt tgcccagcgc
gcgttcgccc 180

cgccccggac ggtatcgata agcttaggag cttgggctgc aggtcgaggg
cactgggagg 240

atgttgagta agatggaaaa ctactgatga cccttcgaga gacagagtat
taggacatgt 300

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ctccacgcgg ggatgtccac cctcttcctg gtgtactcga ataagtgcc
gaccccgctg 3900

ggcatggcct cgggccacat cagagacttc cagatcacag caagcggaca
atacggccaa 3960

tgggcgccga agctggcccg cttgcactac tccggatcga tcaacgcatg
gtccaccaag 4020

gaaccgttct cgtggattaa ggtggacctc ctggccccta tgattatcca
cggaattaag 4080

accagggcg ccaggcagaa gttctcctcc ctgtacatct cgcaattcat
catcatgtac 4140

agcctggacg ggaagaagtg gcagacttac aggggaaact ccaccggcac
cctgatggtc 4200

tttttcggca acgtggattc ctccggcatt aagcacaaca tcttcaaccc
accgatcata 4260

gccagatata ttaggctcca cccactcac tactcaatcc gctcaactct
tcggatggaa 4320

ctcatggggg gcgacctgaa ctcttgctcc atgccgttgg ggatggaatc
aaaggctatt 4380

agcgacgccc agatcaccgc gagctcctac ttcactaaca tggtcggccac
ctggagcccc 4440

tccaaggcca ggctgcactt gcagggacgg tcaaatgcct ggcggccgca
agtgaacaat 4500

ccgaaggaat ggcttcaagt ggatttccaa aagaccatga aagtgaccgg
agtcaccacc 4560

caggagagtga agtcccttct gacctcgatg tatgtgaagg agttcctgat
tagcagcagc 4620

caggacgggc accagtggac cctgttcttc caaaacggaa aggtcaaggt
gttccagggg 4680

aaccaggact cgttcacacc cgtggtgaac tccctggacc cccactgct
gacgcggtac 4740

ttgaggattc atcctcagtc ctgggtccat cagattgcat tgcgaatgga
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<213> Secuencia artificial

<220>

<223> Motivo AD

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

<210> 74

<211> 12

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<213> Secuencia artificial

<220>

<223> Motivo AD

<400> 74

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

<210> 75

<211> 12

<212> PRT

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<220>

<223> Motivo AD

<400> 75

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

<210> 76

<211> 12

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<213> Secuencia artificial

<220>

<223> Motivo AD

<400> 76

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

<210> 77

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> Motivo AE, AM

<400> 77

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

<210> 78
<211> 12
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<220>
<223> Motivo AE, AM, AQ

<400> 78

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

<210> 79
<211> 12
<212> PRT
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<220>
<223> Motivo AE, AM, AQ

<400> 79

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

<210> 80
<211> 12
<212> PRT
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<220>

<223> Motivo AE, AM, AQ

<400> 80

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

<210> 81

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> Motivo AF, AM

<400> 81

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

<210> 82

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> Motivo AF, AM

<400> 82

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

<210> 83

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> Motivo AF, AM

<400> 83

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

<210> 84

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> Motivo AF, AM

<400> 84

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

<210> 85

<211> 12
<212> PRT
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<220>

<223> Motivo AG, AM

<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>

<223> Motivo AG, AM

<400> 86

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

<210> 87
<211> 12
<212> PRT
<213> Secuencia artificial

<220>

<223> Motivo AG, AM

<400> 87

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

<210> 88

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> Motivo AG, AM

<400> 88

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

<210> 89

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> Motivo AQ

<400> 89

Gly	Glu	Pro	Ala	Gly	Ser	Pro	Thr	Ser	Thr	Ser	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1 5 10

<210> 90
<211> 12
<212> PRT
<213> Secuencia artificial

<220>
<223> Motivo AQ

<400> 90

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

<210> 91
<211> 12
<212> PRT
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<220>
<223> Motivo AQ

<400> 91

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

<210> 92
<211> 12

<212> PRT
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<220>
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<400> 92

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

<210> 93
<211> 12
<212> PRT
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<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
<213> Secuencia artificial

<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

<213> Secuencia artificial

<220>

<223> Motivo BC

<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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<400> 96

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

<210> 97
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<212> PRT
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<400> 97

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

<210> 98
<211> 12
<212> PRT
<213> Secuencia artificial

<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

<213> Secuencia artificial

<220>

<223> Motivo BD

<400> 99

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

<210> 100

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> Motivo BD

<400> 100

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

<210> 101

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> Motivo BD

<400> 101

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

<210> 102

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> Motivo BD

<400> 102

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

<210> 103

<211> 1607

<212> PRT

<213> Secuencia artificial

<220>

<223> coFVIII-6-XTEN secuencia de proteínas

<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
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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		