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CA 2947904 A1 2017/05/12

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(12) DEMANDE DE BREVET CANADIEN
CANADIAN PATENT APPLICATION

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A61K 47/54 (2017.01), *C07H 15/08* (2006.01),
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C12N 15/00 (2006.01), *C12N 15/11* (2006.01),
C12N 15/113 (2010.01)

(71) Demandeurs/Applicants:
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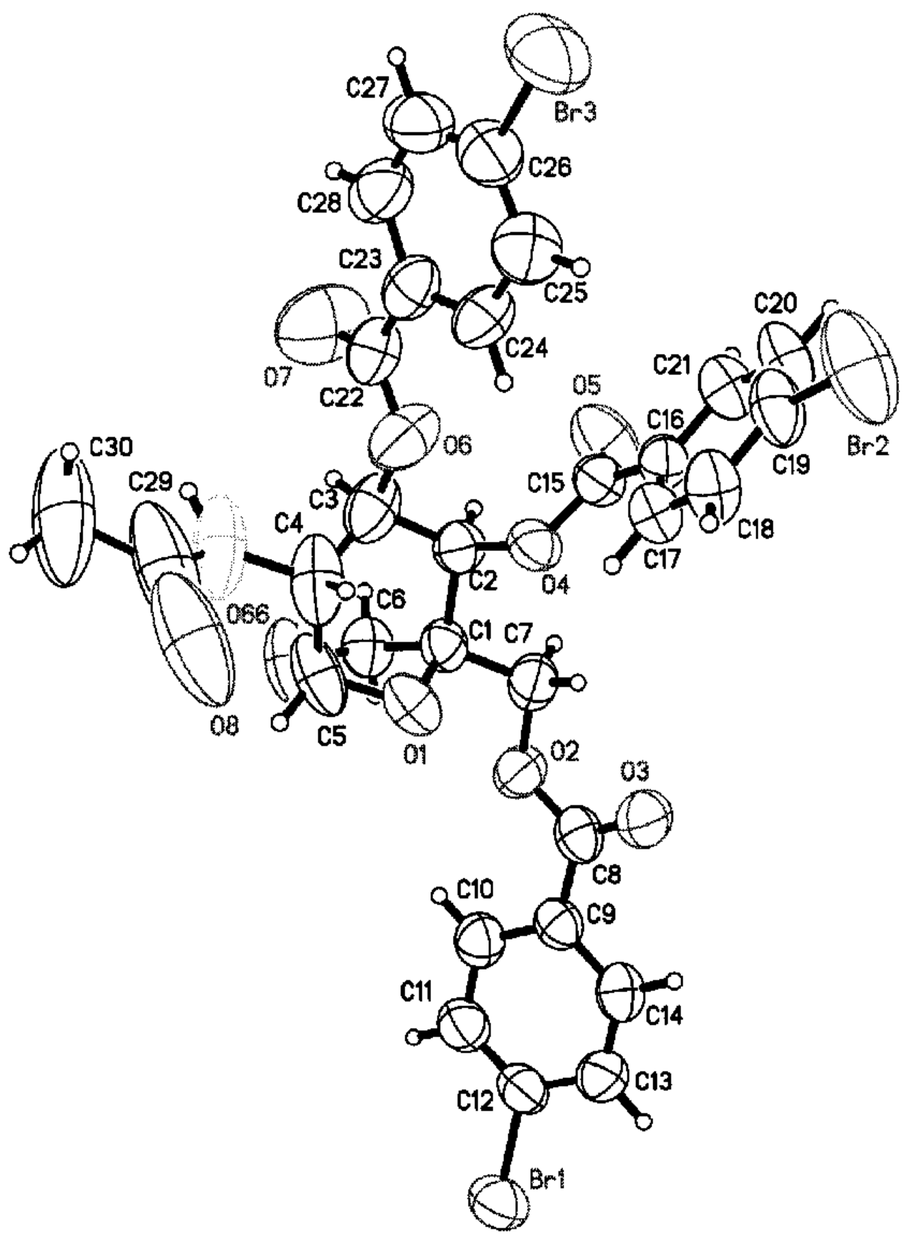
THUMA, BENJAMIN AARON, US;

(54) Titre : INGENIERIE DE GENOME SPECIFIQUE AU TISSU AU MOYEN DE CRISPR-CAS9
(54) Title: TISSUE-SPECIFIC GENOME ENGINEERING USING CRISPR-CAS9



(57) Abrégé/Abstract:
The present application provides compounds, compositions, and uses thereof as asialoglycoprotein receptor (ASGPR) targeting agents.

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(13) A1

(72) Inventeurs(suite)/Inventors(continued): DOUDNA, JENNIFER A., US; ROUET, ROMAIN, US

(74) Agent: SMART & BIGGAR

ABSTRACT

The present application provides compounds, compositions, and uses thereof as asialoglycoprotein receptor (ASGPR) targeting agents.

Ser	Ser	Ile	Phe	Gly	Lys	Gly	Trp	Ile	Asn	Phe	Ser	Val	Lys	Leu	Met
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Ile	Leu	Thr	Arg	Leu	Gly	Lys	Gln	Lys	Thr	Thr	Ser	Ser	Ser	Asn	Lys
	450					455					460				
Thr	Lys	Tyr	Ile	Asp	Glu	Lys	Leu	Leu	Thr	Glu	Glu	Ile	Tyr	Asn	Pro
465					470					475					480
Val	Val	Ala	Lys	Ser	Val	Arg	Gln	Ala	Ile	Lys	Ile	Val	Asn	Ala	Ala
				485					490					495	
Ile	Lys	Glu	Tyr	Gly	Asp	Phe	Asp	Asn	Ile	Val	Ile	Glu	Met	Ala	Arg
			500					505					510		
Glu	Thr	Asn	Glu	Asp	Asp	Glu	Lys	Lys	Ala	Ile	Gln	Lys	Ile	Gln	Lys
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Ala	Asn	Lys	Asp	Glu	Lys	Asp	Ala	Ala	Met	Leu	Lys	Ala	Ala	Asn	Gln
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Tyr	Asn	Gly	Lys	Ala	Glu	Leu	Pro	His	Ser	Val	Phe	His	Gly	His	Lys
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Gln	Leu	Ala	Thr	Lys	Ile	Arg	Leu	Trp	His	Gln	Gln	Gly	Glu	Arg	Cys
				565					570					575	
Leu	Tyr	Thr	Gly	Lys	Thr	Ile	Ser	Ile	His	Asp	Leu	Ile	Asn	Asn	Ser
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Asn	Gln	Phe	Glu	Val	Asp	His	Ile	Leu	Pro	Leu	Ser	Ile	Thr	Phe	Asp
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Asp	Ser	Leu	Ala	Asn	Lys	Val	Leu	Val	Tyr	Ala	Thr	Ala	Asn	Gln	Glu
	610					615					620				
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Trp	Ser	Phe	Arg	Glu	Leu	Lys	Ala	Phe	Val	Arg	Glu	Ser	Lys	Thr	Leu
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Phe	Asp	Val	Arg	Lys	Lys	Phe	Ile	Glu	Arg	Asn	Leu	Val	Asp	Thr	Arg
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Tyr	Ala	Ser	Arg	Val	Val	Leu	Asn	Ala	Leu	Gln	Glu	His	Phe	Arg	Ala
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His	Lys	Ile	Asp	Thr	Lys	Val	Ser	Val	Val	Arg	Gly	Gln	Phe	Thr	Ser
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Gln	Leu	Arg	Arg	His	Trp	Gly	Ile	Glu	Lys	Thr	Arg	Asp	Thr	Tyr	His
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His	His	Ala	Val	Asp	Ala	Leu	Ile	Ile	Ala	Ala	Ser	Ser	Gln	Leu	Asn
			740					745					750		
Leu	Trp	Lys	Lys	Gln	Lys	Asn	Thr	Leu	Val	Ser	Tyr	Ser	Glu	Asp	Gln
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Leu	Leu	Asp	Ile	Glu	Thr	Gly	Glu	Leu	Ile	Ser	Asp	Asp	Glu	Tyr	Lys
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Glu	Ser	Val	Phe	Lys	Ala	Pro	Tyr	Gln	His	Phe	Val	Asp	Thr	Leu	Lys
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Lys	Phe	Asn	Arg	Lys	Ile	Ser	Asp	Ala	Thr	Ile	Tyr	Ala	Thr	Arg	Gln
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Ala	Lys	Val	Gly	Lys	Asp	Lys	Ala	Asp	Glu	Thr	Tyr	Val	Leu	Gly	Lys
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Tyr Lys Lys Asp Lys Ser Lys Phe Leu Met Tyr Arg His Asp Pro Gln
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Thr Phe Glu Lys Val Ile Glu Pro Ile Leu Glu Asn Tyr Pro Asn Lys
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Gln Met Asn Glu Lys Gly Lys Glu Val Pro Cys Asn Pro Phe Leu Lys
900 905 910
Tyr Lys Glu Glu His Gly Tyr Ile Arg Lys Tyr Ser Lys Lys Gly Asn
915 920 925
Gly Pro Glu Ile Lys Ser Leu Lys Tyr Tyr Asp Ser Lys Lys Leu Gly Asn
930 935 940
His Ile Asp Ile Thr Pro Lys Asp Ser Asn Asn Lys Val Val Leu Gln
945 950 955 960
Ser Val Ser Pro Trp Arg Ala Asp Ile Tyr Phe Asn Asn Thr Thr Gly
965 970 975
Lys Tyr Glu Ile Leu Gly Leu Lys Tyr Ala Asp Leu Gln Phe Glu Lys
980 985 990
Gly Thr Gly Asn Tyr Lys Ile Ser Gln Glu Lys Tyr Asn Asp Ile Lys
995 1000 1005
Lys Lys Glu Gly Val Asp Ser Asp Ser Glu Phe Lys Phe Thr Leu
1010 1015 1020
Tyr Lys Asn Asp Leu Leu Leu Val Lys Glu Thr Glu Thr Lys Glu
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Gln Gln Leu Phe Arg Phe Leu Ser Arg Thr Met Pro Lys Gln Lys
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His Tyr Val Glu Leu Lys Pro Tyr Asp Lys Gln Lys Phe Glu Gly
1055 1060 1065
Gly Glu Ala Leu Ile Lys Val Leu Gly Asn Val Ala Asn Gly Gly
1070 1075 1080
Gln Cys Ile Lys Gly Leu Gly Lys Ser Asn Ile Ser Ile Tyr Lys
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35 40 45
Asn Arg Gln Gly Arg Arg Leu Thr Arg Arg Lys Lys His Arg Ile Val
50 55 60
Arg Leu Asn Arg Leu Phe Glu Glu Ser Gly Leu Ile Thr Asp Phe Thr
65 70 75 80
Lys Ile Ser Ile Asn Leu Asn Pro Tyr Gln Leu Arg Val Lys Gly Leu
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Thr Asp Glu Leu Ser Asn Glu Glu Leu Phe Ile Ala Leu Lys Asn Met
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Asn	Ser 130	Ser	Val	Gly	Asp	Tyr 135	Ala	Gln	Ile	Val	Lys 140	Glu	Asn	Ser	Lys
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Asp	Glu 210	Phe	Ile	Asn	Arg	Tyr 215	Leu	Glu	Ile	Leu	Thr 220	Gly	Lys	Arg	Lys
Tyr 225	Tyr	His	Gly	Pro	Gly 230	Asn	Glu	Lys	Ser	Arg 235	Thr	Asp	Tyr	Gly	Arg 240
Tyr	Arg	Thr	Ser	Gly 245	Glu	Thr	Leu	Asp	Asn 250	Ile	Phe	Gly	Ile	Leu 255	Ile
Gly	Lys	Cys	Thr 260	Phe	Tyr	Pro	Asp	Glu 265	Phe	Arg	Ala	Ala	Lys 270	Ala	Ser
Tyr	Thr	Ala 275	Gln	Glu	Phe	Asn	Leu 280	Leu	Asn	Asp	Leu	Asn 285	Leu	Asn	Leu
Val	Pro 290	Thr	Glu	Thr	Lys	Lys 295	Leu	Ser	Lys	Glu	Gln 300	Lys	Asn	Gln	Ile
Ile 305	Asn	Tyr	Val	Lys	Asn 310	Glu	Lys	Ala	Met	Gly 315	Pro	Ala	Lys	Leu	Phe 320
Lys	Tyr	Ile	Ala	Lys 325	Leu	Leu	Ser	Cys	Asp 330	Val	Ala	Asp	Ile	Lys 335	Glu
Tyr	Arg	Ile	Asp 340	Lys	Ser	Gly	Lys	Ala 345	Glu	Ile	His	Thr	Phe 350	Glu	Ala
Tyr	Arg	Lys 355	Met	Lys	Thr	Leu	Glu 360	Thr	Leu	Asp	Ile	Glu 365	Gln	Met	Asp
Arg	Glu 370	Thr	Leu	Asp	Lys	Leu 375	Ala	Tyr	Val	Leu	Thr 380	Leu	Asn	Thr	Glu
Arg 385	Glu	Gly	Ile	Gln	Glu 390	Ala	Leu	Glu	His	Glu 395	Phe	Ala	Asp	Gly	Ser 400
Phe	Ser	Gln	Lys	Gln 405	Val	Asp	Glu	Leu	Val 410	Gln	Phe	Arg	Lys	Ala 415	Asn
Ser	Ser	Ile	Phe 420	Gly	Lys	Gly	Trp	His 425	Asn	Phe	Ser	Val	Lys 430	Leu	Met
Met	Glu	Leu 435	Ile	Pro	Glu	Leu	Tyr 440	Glu	Thr	Ser	Glu	Glu 445	Gln	Met	Thr
Ile	Leu 450	Thr	Arg	Leu	Gly	Lys 455	Gln	Lys	Thr	Thr	Ser 460	Ser	Ser	Asn	Lys
Thr 465	Lys	Tyr	Ile	Asp	Glu 470	Lys	Leu	Leu	Thr	Glu 475	Glu	Ile	Tyr	Asn	Pro 480
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Glu	Thr	Asn 515	Glu	Asp	Asp	Glu	Lys 520	Lys	Ala	Ile	Gln	Lys 525	Ile	Gln	Lys
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580 585 590
Asn Gln Phe Glu Val Asp His Ile Leu Pro Leu Ser Ile Thr Phe Asp
595 600 605
Asp Ser Leu Ala Asn Lys Val Leu Val Tyr Ala Thr Ala Asn Gln Glu
610 615 620
Lys Gly Gln Arg Thr Pro Tyr Gln Ala Leu Asp Ser Met Asp Asp Ala
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645 650 655
Ser Asn Lys Lys Lys Glu Tyr Leu Leu Thr Glu Glu Asp Ile Ser Lys
660 665 670
Phe Asp Val Arg Lys Lys Phe Ile Glu Arg Asn Leu Val Asp Thr Arg
675 680 685
Tyr Ala Ser Arg Val Val Leu Asn Ala Leu Gln Glu His Phe Arg Ala
690 695 700
His Lys Ile Asp Thr Lys Val Ser Val Val Arg Gly Gln Phe Thr Ser
705 710 715 720
Gln Leu Arg Arg His Trp Gly Ile Glu Lys Thr Arg Asp Thr Tyr His
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740 745 750
Leu Trp Lys Lys Gln Lys Asn Thr Leu Val Ser Tyr Ser Glu Asp Gln
755 760 765
Leu Leu Asp Ile Glu Thr Gly Glu Leu Ile Ser Asp Asp Glu Tyr Lys
770 775 780
Glu Ser Val Phe Lys Ala Pro Tyr Gln His Phe Val Asp Thr Leu Lys
785 790 795 800
Ser Lys Glu Phe Glu Asp Ser Ile Leu Phe Ser Tyr Gln Val Asp Ser
805 810 815
Lys Phe Asn Arg Lys Ile Ser Asp Ala Thr Ile Tyr Ala Thr Arg Gln
820 825 830
Ala Lys Val Glu Lys Asp Lys Ala Asp Glu Thr Tyr Val Leu Gly Lys
835 840 845
Ile Lys Asp Ile Tyr Thr Gln Asp Gly Tyr Asp Ala Phe Met Lys Ile
850 855 860
Tyr Lys Lys Asp Lys Ser Lys Phe Leu Met Tyr Arg His Asp Pro Gln
865 870 875 880
Thr Phe Glu Lys Val Ile Glu Pro Ile Leu Glu Asn Tyr Pro Asn Lys
885 890 895
Gln Ile Asn Glu Lys Gly Lys Glu Val Pro Cys Asn Pro Phe Leu Lys
900 905 910
Tyr Lys Glu Glu His Gly Tyr Ile Arg Lys Tyr Ser Lys Lys Gly Asn
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Gly Pro Glu Ile Lys Ser Leu Lys Tyr Tyr Asp Ser Lys Leu Gly Asn
930 935 940
His Ile Asp Ile Thr Pro Lys Asp Ser Asn Asn Lys Val Val Leu Gln
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Ser Val Ser Pro Trp Arg Ala Asp Val Tyr Phe Asn Lys Thr Thr Gly
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Lys Tyr Glu Ile Leu Gly Leu Lys Tyr Ala Asp Leu Gln Phe Glu Lys
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Gly Thr Gly Thr Tyr Lys Ile Ser Gln Glu Lys Tyr Asn Asp Ile Lys
995 1000 1005

Lys	Lys	Glu	Gly	Val	Asp	Ser	Asp	Ser	Glu	Phe	Lys	Phe	Thr	Leu	
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Tyr	Lys	Asn	Asp	Leu	Leu	Leu	Val	Lys	Asp	Thr	Glu	Thr	Lys	Glu	
	1025					1030					1035				
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Gln	Cys	Lys	Lys	Gly	Leu	Gly	Lys	Ser	Asn	Ile	Ser	Ile	Tyr	Lys	
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Thr	Tyr	Gly	Gln	Leu	Arg	Gly	Asp	Phe	Thr	Val	Glu	Lys	Asp	Gly	Lys
				165					170					175	
Lys	His	Arg	Leu	Ile	Asn	Val	Phe	Pro	Thr	Ser	Ala	Tyr	Arg	Ser	Glu
			180					185					190		
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Tyr	Arg	Thr	Asn	Gly	Glu	Thr	Leu	Asp	Asn	Ile	Phe	Gly	Ile	Leu	Ile
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Glu	Thr	Asn 515	Glu	Asp	Asp	Glu	Lys 520	Lys	Ala	Ile	Gln	Lys 525	Ile	Gln	Lys
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755 760 765
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930 935 940
His Ile Asp Ile Thr Pro Lys Asp Ser Asn Asn Lys Val Val Leu Gln
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Ser Val Ser Pro Trp Arg Ala Asp Val Tyr Phe Asn Lys Thr Thr Gly
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Lys Lys Glu Gly Val Asp Ser Asp Ser Glu Phe Lys Phe Thr Leu
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Gln Gln Leu Phe Arg Phe Leu Ser Arg Thr Met Pro Lys Gln Lys
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Gly Glu Ala Leu Ile Lys Val Leu Gly Asn Val Ala Asn Ser Gly
1070 1075 1080
Gln Cys Lys Lys Gly Leu Gly Lys Ser Asn Ile Ser Ile Tyr Lys
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Lys	Ile	Ser	Ile	Asn	Leu	Asn	Pro	Tyr	Gln	Leu	Arg	Val	Arg	Gly	Leu
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Glu	Thr	Asn 515	Glu	Asp	Asp	Glu	Lys 520	Lys	Ala	Ile	Gln	Lys 525	Ile	Gln	Lys
Ala	Asn 530	Lys	Asp	Glu	Lys	Asp 535	Ala	Ala	Met	Leu	Lys 540	Ala	Ala	Asn	Gln
Tyr 545	Asn	Gly	Lys	Ala	Glu 550	Leu	Pro	His	Ser	Val 555	Phe	His	Gly	His	Lys 560
Gln	Leu	Ala	Thr	Lys 565	Ile	Arg	Leu	Trp	His 570	Gln	Gln	Gly	Glu	Arg 575	Cys
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Ser	Asn	Lys	Lys 660	Lys	Glu	Tyr	Leu	Leu 665	Thr	Glu	Glu	Asp	Ile 670	Ser	Lys
Phe	Asp	Val 675	Arg	Lys	Lys	Phe	Ile 680	Glu	Arg	Asn	Leu	Val 685	Asp	Thr	Arg
Tyr	Ala 690	Ser	Arg	Val	Val	Leu 695	Asn	Ala	Leu	Gln	Glu 700	His	Phe	Arg	Ala
His 705	Lys	Ile	Asp	Thr	Lys 710	Val	Ser	Val	Val	Arg 715	Gly	Gln	Phe	Thr	Ser 720
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His	His	Ala	Val 740	Asp	Ala	Leu	Ile	Ile 745	Ala	Ala	Ser	Ser	Gln 750	Leu	Asn
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Glu	Ser	Val	Phe	Lys	Ala	Pro	Tyr	Gln	His	Phe	Val	Asp	Thr	Leu	Lys
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Lys	Phe	Asn	Arg 820	Lys	Leu	Ser	Asp	Ala 825	Thr	Ile	Tyr	Ala	Thr 830	Arg	Gln
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Tyr Lys Lys Asp Lys Ser Lys Phe Leu Met Tyr Arg Ile Asp Pro Glu
865 870 875 880
Thr Phe Glu Lys Val Ile Glu Pro Ile Leu Glu Asn Tyr Pro Asn Lys
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Glu Met Asn Glu Lys Gly Lys Glu Val Pro Cys Asn Pro Phe Leu Lys
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Gln Ser Leu Lys Pro Trp Arg Ala Asp Val Tyr Phe Asn Lys Thr Thr
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Gly Lys Tyr Glu Ile Leu Gly Leu Lys Tyr Ala Asp Leu Gln Phe Glu
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Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Leu
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Tyr Leu Gln Glu Ile Phe Ser Thr Glu Met Ala Thr Leu Asp Asp Ala
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Asp	Ser	Lys 11[illegible]	Tyr	Pro	Ile	Phe	Gly 12(	Asn	Leu	Val	Glu	Glu 12[illegible]	Lys	Ala	Tyr
His	Asp 13(	Glu	Phe	Pro	Thr	Ile 13[illegible]	Tyr	His	Leu	Arg	Lys 14(	Tyr	Leu	Ala	Asp
Ser 14[illegible]	Thr	Lys	Lys	Ala	Asp 15(	Leu	Arg	Leu	Val	Tyr 15[illegible]	Leu	Ala	Leu	Ala	His 16(
Met	Ile	Lys	Tyr	Arg 16[illegible]	Gly	His	Phe	Leu	Ile 17(	Glu	Gly	Glu	Phe	Asn 17[illegible]	Ser
Lys	Asn	Asn	Asp 18(	Ile	Gln	Lys	Asn	Phe 18[illegible]	Gln	Asp	Phe	Leu	Asp 19(	Thr	Tyr
Asn	Ala	Ile 19[illegible]	Phe	Glu	Ser	Asp	Leu 20(	Ser	Leu	Glu	Asn	Ser 20[illegible]	Lys	Gln	Leu
Glu	Glu 21(	Ile	Val	Lys	Asp	Lys 21[illegible]	Ile	Ser	Lys	Leu	Glu 22(	Lys	Lys	Asp	Arg
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Phe	Leu	Lys	Leu	Ile 24[illegible]	Val	Gly	Asn	Gln	Ala 25(	Asp	Phe	Arg	Lys	Cys 25[illegible]	Phe
Asn	Leu	Asp	Glu 26(	Lys	Ala	Ser	Leu	His 26[illegible]	Phe	Ser	Lys	Glu	Ser 27(	Tyr	Asp
Glu	Asp	Leu 27[illegible]	Glu	Thr	Leu	Leu	Gly 28(	Tyr	Ile	Gly	Asp	Asp 28[illegible]	Tyr	Ser	Asp
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Phe 30[illegible]	Leu	Thr	Val	Thr	Asp 31(	Asn	Glu	Thr	Glu	Ala 31[illegible]	Pro	Leu	Ser	Ser	Ala 32(
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Glu	Tyr	Ile	Arg 34(	Asn	Ile	Ser	Leu	Lys 34[illegible]	Thr	Tyr	Asn	Glu	Val 35(	Phe	Lys
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Gln	Glu 37(	Asp	Phe	Tyr	Val	Tyr 37[illegible]	Leu	Lys	Asn	Leu	Leu 38(	Ala	Glu	Phe	Glu
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Lys	Gln	Arg	Thr	Phe 40[illegible]	Asp	Asn	Gly	Ser	Ile 41(	Pro	Tyr	Gln	Ile	His 41[illegible]	Leu
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Leu	Leu	Tyr 51[illegible]	Glu	Thr	Phe	Asn	Val 52(	Tyr	Asn	Glu	Leu	Thr 52[illegible]	Lys	Val	Arg
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Ile	Glu	Leu	Lys 580	Gly	Ile	Glu	Lys	Gln 585	Phe	Asn	Ser	Ser	Leu 590	Ser	Thr
Tyr	His	Asp 595	Leu	Leu	Asn	Ile	Ile 600	Asn	Asp	Lys	Glu	Phe 605	Leu	Asp	Asp
Ser	Ser 610	Asn	Glu	Ala	Ile	Ile 615	Glu	Glu	Ile	Ile	His 620	Thr	Leu	Thr	Ile
Phe	Glu	Asp	Arg	Glu	Met 630	Ile	Lys	Gln	Arg	Leu 635	Ser	Lys	Phe	Glu	Asn 640
Ile	Phe	Asp	Lys	Ser 645	Val	Leu	Lys	Lys	Leu 650	Ser	Arg	Arg	His	Tyr 655	Thr
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Lys	Ser	Gly 675	Asn	Thr	Ile	Leu	Asp 680	Tyr	Leu	Ile	Asp	Asp 685	Gly	Ile	Ser
Asn	Arg 690	Asn	Phe	Met	Gln	Leu 695	Ile	His	Asp	Asp	Ala 700	Leu	Ser	Phe	Lys
Lys 705	Lys	Ile	Gln	Lys	Ala 710	Gln	Ile	Ile	Gly	Asp 715	Glu	Asp	Lys	Gly	Asn 720
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Gln	Tyr 770	Thr	Asn	Gln	Gly	Lys 775	Ser	Asn	Ser	Gln	Gln 780	Arg	Leu	Lys	Arg
Leu 785	Glu	Lys	Ser	Leu	Lys 790	Glu	Leu	Gly	Ser	Lys 795	Ile	Leu	Lys	Glu	Asn 800
Ile	Pro	Ala	Lys	Leu 805	Ser	Lys	Ile	Asp	Asn 810	Asn	Ala	Leu	Gln	Asn 815	Asp
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Lys	Leu	Ile	Ser 900	Gln	Arg	Lys	Phe	Asp 905	Asn	Leu	Thr	Lys	Ala 910	Glu	Arg
Gly	Gly	Leu 915	Leu	Pro	Glu	Asp	Lys 920	Ala	Gly	Phe	Ile	Gln 925	Arg	Gln	Leu
Val	Glu	Thr	Arg	Gln	Ile	Thr	Lys	His	Val	Ala	Arg	Leu	Leu	Asp	Glu

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Phe	Glu	Leu	Tyr 980	Lys	Val	Cys	Glu	Ile 985	Asn	Asp	Phe	His	His 990	Ala	His

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Tyr Ser Asn Ile Met Asn Ile Phe Lys Lys Ser Ile Ser Leu Ala
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Asp Gly Arg Val Ile Glu Arg Pro Leu Ile Glu Val Asn Glu Glu
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Thr Gly Glu Ser Val Trp Asn Lys Glu Ser Asp Leu Ala Thr Val
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Arg Arg Val Leu Ser Tyr Pro Gln Val Asn Val Val Lys Lys Val
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Glu Glu Gln Asn His Gly Leu Asp Arg Gly Lys Pro Lys Gly Leu
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Phe Asn Ala Asn Leu Ser Ser Lys Pro Lys Pro Asn Ser Asn Glu
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Asn Leu Val Gly Ala Lys Glu Tyr Leu Asp Pro Lys Lys Tyr Gly
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Gly Tyr Ala Gly Ile Ser Asn Ser Phe Ala Val Leu Val Lys Gly
        1145                1150                1155

Thr Ile Glu Lys Gly Ala Lys Lys Lys Ile Thr Asn Val Leu Glu
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Phe Gln Gly Ile Ser Ile Leu Asp Arg Ile Asn Tyr Arg Lys Asp
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Lys Leu Asn Phe Leu Leu Glu Lys Gly Tyr Lys Asp Ile Glu Leu
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Ile Ile Glu Leu Pro Lys Tyr Ser Leu Phe Glu Leu Ser Asp Gly
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Ser Arg Arg Met Leu Ala Ser Ile Leu Ser Thr Asn Asn Lys Arg
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Gly Glu Ile His Lys Gly Asn Gln Ile Phe Leu Ser Gln Lys Phe
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Val Lys Leu Leu Tyr His Ala Lys Arg Ile Ser Asn Thr Ile Asn
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Glu Asn His Arg Lys Tyr Val Glu Asn His Lys Lys Glu Phe Glu
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Glu Leu Phe Tyr Tyr Ile Leu Glu Phe Asn Glu Asn Tyr Val Gly
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Ala Lys Lys Asn Gly Lys Leu Leu Asn Ser Ala Phe Gln Ser Trp
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Gln Asn His Ser Ile Asp Glu Leu Cys Ser Ser Phe Ile Gly Pro
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Thr Gly Ser Glu Arg Lys Gly Leu Phe Glu Leu Thr Ser Arg Gly
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Ser Ala Ala Asp Phe Glu Phe Leu Gly Val Lys Ile Pro Arg Tyr
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Arg Asp Tyr Thr Pro Ser Ser Leu Leu Lys Asp Ala Thr Leu Ile
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Lys Leu Gly Glu Gly
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Phe	Phe	Gln	Arg	Leu	Asp	Asp	Ser	Phe	Leu	Val	Pro	Asp	Asp	Lys	Arg
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225					230					235					240
Phe	Leu	Lys	Leu	Ile	Val	Gly	Asn	Gln	Ala	Asp	Phe	Arg	Lys	Cys	Phe
				245					250					255	
Asn	Leu	Asp	Glu	Lys	Ala	Ser	Leu	His	Phe	Ser	Lys	Glu	Ser	Tyr	Asp
			260					265					270		
Glu	Asp	Leu	Glu	Thr	Leu	Leu	Gly	Tyr	Ile	Gly	Asp	Asp	Tyr	Ser	Asp
		275					280					285			
Val	Phe	Leu	Lys	Ala	Lys	Lys	Leu	Tyr	Asp	Ala	Ile	Leu	Leu	Ser	Gly
	290					295					300				
Phe	Leu	Thr	Val	Thr	Asp	Asn	Glu	Thr	Glu	Ala	Pro	Leu	Ser	Ser	Ala
305					310					315					320
Met	Ile	Lys	Arg	Tyr	Asn	Glu	His	Lys	Glu	Asp	Leu	Ala	Leu	Leu	Lys
				325					330					335	
Glu	Tyr	Ile	Arg	Asn	Ile	Ser	Leu	Lys	Thr	Tyr	Asn	Glu	Val	Phe	Lys
								345					350		
Asp	Asp	Thr	Lys	Asn	Gly	Tyr	Ala	Gly	Tyr	Ile	Asp	Gly	Lys	Thr	Asn
		355					360					365			
Gln	Glu	Asp	Phe	Tyr	Val	Tyr	Leu	Lys	Asn	Leu	Leu	Ala	Glu	Phe	Glu
	370					375					380				
Gly	Ala	Asp	Tyr	Phe	Leu	Glu	Lys	Ile	Asp	Arg	Glu	Asp	Phe	Leu	Arg
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Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro Tyr Gln Ile His Leu
405 410 415
Gln Glu Met Arg Ala Ile Leu Asp Lys Gln Ala Lys Phe Tyr Pro Phe
420 425 430
Leu Ala Lys Asn Lys Glu Arg Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Asp Phe Ala Trp
450 455 460
Ser Ile Arg Lys Arg Asn Glu Lys Ile Thr Pro Trp Asn Phe Glu Asp
465 470 475 480
Val Ile Asp Lys Glu Ser Ser Ala Glu Ala Phe Ile Asn Arg Met Thr
485 490 495
Ser Phe Asp Leu Tyr Leu Pro Glu Glu Lys Val Leu Pro Lys His Ser
500 505 510
Leu Leu Tyr Glu Thr Phe Asn Val Tyr Asn Glu Leu Thr Lys Val Arg
515 520 525
Phe Ile Ala Glu Ser Met Arg Asp Tyr Gln Phe Leu Asp Ser Lys Gln
530 535 540
Lys Lys Asp Ile Val Arg Leu Tyr Phe Lys Asp Lys Arg Lys Val Thr
545 550 555 560
Asp Lys Asp Ile Ile Glu Tyr Leu His Ala Ile Tyr Gly Tyr Asp Gly
565 570 575
Ile Glu Leu Lys Gly Ile Glu Lys Gln Phe Asn Ser Ser Leu Ser Thr
580 585 590
Tyr His Asp Leu Leu Asn Ile Ile Asn Asp Lys Glu Phe Leu Asp Asp
595 600 605
Ser Ser Asn Glu Ala Ile Ile Glu Glu Ile Ile His Thr Leu Thr Ile
610 615 620
Phe Glu Asp Arg Glu Met Ile Lys Gln Arg Leu Ser Lys Phe Glu Asn
625 630 635 640
Ile Phe Asp Lys Ser Val Leu Lys Lys Leu Ser Arg Arg His Tyr Thr
645 650 655
Gly Trp Gly Lys Leu Ser Ala Lys Leu Ile Asn Gly Ile Arg Asp Glu
660 665 670
Lys Ser Gly Asn Thr Ile Leu Asp Tyr Leu Ile Asp Asp Gly Ile Ser
675 680 685
Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ala Leu Ser Phe Lys
690 695 700
Lys Lys Ile Gln Lys Ala Gln Ile Ile Gly Asp Glu Asp Lys Gly Asn
705 710 715 720
Ile Lys Glu Val Val Lys Ser Leu Pro Gly Ser Pro Ala Ile Lys Lys
725 730 735
Gly Ile Leu Gln Ser Ile Lys Ile Val Asp Glu Leu Val Lys Val Met
740 745 750
Gly Gly Arg Lys Pro Glu Ser Ile Val Val Glu Met Ala Arg Glu Asn
755 760 765
Gln Tyr Thr Asn Gln Gly Lys Ser Asn Ser Gln Gln Arg Leu Lys Arg
770 775 780
Leu Glu Lys Ser Leu Lys Glu Leu Gly Ser Lys Ile Leu Lys Glu Asn
785 790 795 800
Ile Pro Ala Lys Leu Ser Lys Ile Asp Asn Asn Ala Leu Gln Asn Asp
805 810 815
Arg Leu Tyr Leu Tyr Tyr Leu Gln Asn Gly Lys Asp Met Tyr Thr Gly
820 825 830
Asp Asp Leu Asp Ile Asp Arg Leu Ser Asn Tyr Asp Ile Asp His Ile
835 840 845

Ile Pro Gln Ala Phe Leu Lys Asp Asn Ser Ile Asp Asn Lys Val Leu
850 855 860
Val Ser Ser Ala Ser Asn Arg Gly Lys Ser Asp Asp Phe Pro Ser Leu
865 870 875 880
Glu Val Val Lys Lys Arg Lys Thr Phe Trp Tyr Gln Leu Leu Lys Ser
885 890 895
Lys Leu Ile Ser Gln Arg Lys Phe Asp Asn Leu Thr Lys Ala Glu Arg
900 905 910
Gly Gly Leu Leu Pro Glu Asp Lys Ala Gly Phe Ile Gln Arg Gln Leu
915 920 925
Val Glu Thr Arg Gln Ile Thr Lys Asn Val Ala Arg Leu Leu Asp Glu
930 935 940
Lys Phe Asn Asn Lys Lys Asp Glu Asn Asn Arg Ala Val Arg Thr Val
945 950 955 960
Lys Ile Ile Thr Leu Lys Ser Thr Leu Val Ser Gln Phe Arg Lys Asp
965 970 975
Phe Glu Leu Tyr Lys Val Arg Glu Ile Asn Asp Phe His His Ala His
980 985 990
Asp Ala Tyr Leu Asn Ala Val Ile Ala Ser Ala Leu Leu Lys Lys Tyr
995 1000 1005
Pro Lys Leu Glu Pro Glu Phe Val Tyr Gly Asp Tyr Pro Lys Tyr
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Tyr Ser Asn Ile Met Asn Ile Phe Lys Lys Ser Ile Ser Leu Ala
1040 1045 1050
Asp Gly Arg Val Ile Glu Arg Pro Leu Ile Glu Val Asn Glu Glu
1055 1060 1065
Thr Gly Glu Ser Val Trp Asn Lys Glu Ser Asp Leu Ala Thr Val
1070 1075 1080
Arg Arg Val Leu Ser Tyr Pro Gln Val Asn Val Val Lys Lys Val
1085 1090 1095
Glu Glu Gln Asn His Gly Leu Asp Arg Gly Lys Pro Lys Gly Leu
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Phe Asn Ala Asn Leu Ser Ser Lys Pro Lys Pro Asn Ser Asn Glu
1115 1120 1125
Asn Leu Val Gly Ala Lys Glu Tyr Leu Asp Pro Lys Lys Tyr Gly
1130 1135 1140
Gly Tyr Ala Gly Ile Ser Asn Ser Phe Ala Val Leu Val Lys Gly
1145 1150 1155
Thr Ile Glu Lys Gly Ala Lys Lys Lys Ile Thr Asn Val Leu Glu
1160 1165 1170
Phe Gln Gly Ile Ser Ile Leu Asp Arg Ile Asn Tyr Arg Lys Asp
1175 1180 1185
Lys Leu Asn Phe Leu Leu Glu Lys Gly Tyr Lys Asp Ile Glu Leu
1190 1195 1200
Ile Ile Glu Leu Pro Lys Tyr Ser Leu Phe Glu Leu Ser Asp Gly
1205 1210 1215
Ser Arg Arg Met Leu Ala Ser Ile Leu Ser Thr Asn Asn Lys Arg
1220 1225 1230
Gly Glu Ile His Lys Gly Asn Gln Ile Phe Leu Ser Gln Lys Phe
1235 1240 1245
Val Lys Leu Leu Tyr His Ala Lys Arg Ile Ser Asn Thr Ile Asn
1250 1255 1260
Glu Asn His Arg Lys Tyr Val Glu Asn His Lys Lys Glu Phe Glu
1265 1270 1275

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Glu Leu Phe Tyr Tyr Ile Leu Glu Phe Asn Glu Asn Tyr Val Gly
        1260                1295                1330
Ala Lys Lys Asn Gly Lys Leu Leu Asn Ser Ala Phe Gln Ser Trp
    1265                1300                1335
Gln Asn Phe Ser Ile Asp Glu Leu Cys Ser Ser Phe Ile Gly Pro
        1310                1345                1380
Thr Gly Ser Glu Arg Lys Gly Leu Phe Glu Leu Thr Ser Arg Gly
    1315                1350                1385
Ser Ala Ala Asp Phe Glu Phe Leu Gly Val Lys Ile Pro Arg Tyr
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Arg Asp Tyr Thr Pro Ser Ser Leu Leu Lys Asp Ile Thr Leu Ile
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Lys Leu Gly Glu Gly
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<213> Streptococcus thermophilus

<400> 765

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Glu Thr Ser Glu Glu Gln Met Thr Ile Leu Lys Arg Leu Gly Lys Gln
        35                  40                  45
Lys Thr Thr Ser Ser Ser Asn Lys Thr Lys Tyr Ile Asp Glu Lys Leu
    50                  55                  60
Leu Thr Glu Glu Ile Tyr Asn Pro Val Val Ala Lys Ser Val Arg Gln
65                  70                  75                  80
Ala Ile Lys Ile Val Asn Ala Ala Ile Lys Glu Tyr Gly Asp Phe Asp
                85                  90                  95
Asn Ile Val Ile Glu Met Ala Arg Glu Thr Asn Glu Asp Asp Glu Lys
            100                 105                 110
Lys Ala Ile Gln Lys Ile Gln Lys Ala Asn Lys Asp Glu Lys Asp Ala
        115                 120                 125
Ala Met Leu Lys Ala Ala Asn Gln Tyr Asn Gly Lys Ala Glu Leu Pro
    130                 135                 140
His Ser Val Phe His Gly His Lys Gln Leu Ala Thr Lys Ile Arg Leu
145                 150                 155                 160
Trp His Gln Gln Gly Glu Arg Cys Leu Tyr Thr Gly Lys Thr Ile Ser
                165                 170                 175
Ile His Asp Leu Ile Asn Asn Pro Asn Gln Phe Glu Val Asp His Ile
            180                 185                 190
Leu Pro Leu Ser Ile Thr Phe Asp Asp Ser Leu Ala Asn Lys Val Leu
        195                 200                 205
Val Tyr Ala Thr Ala Asn Gln Glu Lys Gly Gln Arg Thr Pro Tyr Gln
    210                 215                 220
Ala Leu Asp Ser Met Asp Asp Ala Trp Ser Phe Arg Glu Leu Lys Ala
225                 230                 235                 240
Phe Val Arg Glu Ser Lys Thr Leu Ser Asn Lys Lys Lys Glu Tyr Leu
                245                 250                 255
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Leu Thr Glu Glu Asp Ile Ser Lys Phe Asp Val Arg Lys Lys Phe Ile
260 265 270
Glu Arg Asn Leu Val Asp Thr Arg Tyr Ala Ser Arg Val Val Leu Asn
275 280 285
Ala Leu Gln Glu His Phe Arg Ala His Lys Ile Asp Thr Lys Val Ser
290 295 300
Val Val Arg Gly Gln Phe Thr Ser Gln Leu Arg Arg His Trp Gly Ile
305 310 315 320
Glu Lys Thr Arg Asp Thr Tyr His His His Ala Val Asp Ala Leu Ile
325 330 335
Ile Ala Ala Ser Ser Ser Gln Leu Asn Leu Trp Lys Lys Gln Lys Asn
340 345 350
Leu Val Ser Tyr Ser Glu Asp Gln Phe Leu Asp Ile Glu Thr Gly Glu
355 360 365
Leu Ile Ser Asp Asp Glu Tyr Lys Glu Ser Val Phe Lys Ala Pro Tyr
370 375 380
Gln His Phe Val Asp Thr Leu Lys Ser Lys Glu Phe Glu Asp Ser Ile
385 390 395 400
Leu Phe Ser Tyr Gln Val Asp Ser Lys Phe Asn Arg Lys Ile Ser Asp
405 410 415
Ala Thr Ile Tyr Ala Thr Arg Lys Ala Lys Leu Asp Lys Glu Lys Lys
420 425 430
Glu Tyr Thr Tyr Thr Leu Gly Lys Ile Lys Asp Ile Tyr Thr Gln Ala
435 440 445
Gly Tyr Asp Ala Phe Ile Lys Ile Tyr Lys Lys Asp Lys Ser Lys Phe
450 455 460
Leu Met Tyr His His Asp Pro Gln Thr Phe Glu Lys Val Ile Glu Pro
465 470 475 480
Ile Leu Glu Asn Tyr Pro Asn Lys Glu Ile Asn Glu Lys Gly Lys Glu
485 490 495
Val Pro Cys Asn Pro Phe Leu Lys Tyr Lys Glu Glu His Gly Tyr Ile
500 505 510
Arg Lys Tyr Ser Lys Lys Gly Asn Gly Pro Glu Ile Lys Ser Leu Lys
515 520 525
Tyr Tyr Asp Asn Leu Leu Gly Arg His Ile Asp Ile Thr Pro Lys Asn
530 535 540
Ser Lys Asn Ile Val Ala Leu Arg Lys Leu Asn Pro Trp Arg Thr Asp
545 550 555 560
Val Tyr Phe Asn His Glu Thr Met Lys Tyr Glu Phe Leu Gly Leu Lys
565 570 575
Tyr Ala Asp Ile Ser Tyr Lys Lys Ser Lys Asn Lys Ala Gly Asp Phe
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Leu Pro Lys
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<212> PRT
<213> Streptococcus thermophilus

<400> 786
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Gly Trp Ala Val Ile Thr Asp Asn Tyr Lys Val Pro Ser Lys Lys Met
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		35					40					45			
Gly	Val	Leu	Leu	Phe	Asp	Ser	Gly	Ile	Thr	Ala	Glu	Gly	Arg	Arg	Leu
	50					55					60				
Lys	Arg	Thr	Ala	Arg	Arg	Arg	Tyr	Thr	Arg	Arg	Arg	Asn	Arg	Ile	Leu
65					70					75					80
Tyr	Leu	Gln	Glu	Ile	Phe	Ser	Thr	Glu	Met	Ala	Thr	Leu	Asp	Asp	Ala
				85					90					95	
Phe	Phe	Gln	Arg	Leu	Asp	Asp	Ser	Phe	Leu	Val	Pro	Asp	Asp	Lys	Arg
			100					105					110		
Asp	Ser	Lys	Tyr	Pro	Ile	Phe	Gly	Asn	Leu	Val	Glu	Glu	Lys	Val	Tyr
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His	Asp	Glu	Phe	Pro	Thr	Ile	Tyr	His	Leu	Arg	Lys	Tyr	Leu	Ala	Asp
	130					135					140				
Ser	Thr	Lys	Lys	Ala	Asp	Leu	Arg	Leu	Val	Tyr	Leu	Ala	Leu	Ala	His
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Met	Ile	Lys	Tyr	Arg	Gly	His	Phe	Leu	Ile	Glu	Gly	Glu	Phe	Asn	Ser
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Lys	Asn	Asn	Asp	Ile	Gln	Lys	Asn	Phe	Gln	Asp	Phe	Leu	Asp	Thr	Tyr
			180					185					190		
Asn	Ala	Ile	Phe	Glu	Ser	Asp	Leu	Ser	Leu	Glu	Asn	Ser	Lys	Gln	Leu
		195					200					205			
Glu	Glu	Ile	Val	Lys	Asp	Lys	Ile	Ser	Lys	Leu	Glu	Lys	Lys	Asp	Arg
	210					215					220				
Ile	Leu	Lys	Leu	Phe	Pro	Gly	Glu	Lys	Asn	Ser	Gly	Ile	Phe	Ser	Glu
225					230					235					240
Phe	Leu	Lys	Leu	Ile	Val	Gly	Asn	Gln	Ala	Asp	Phe	Arg	Lys	Cys	Phe
				245					250					255	
Asn	Leu	Asp	Glu	Lys	Ala	Ser	Leu	His	Phe	Ser	Lys	Glu	Ser	Tyr	Asp
			260					265					270		
Glu	Asp	Leu	Glu	Thr	Leu	Leu	Gly	Tyr	Ile	Gly	Asp	Asp	Tyr	Ser	Asp
		275					280					285			
Val	Phe	Leu	Lys	Ala	Lys	Lys	Leu	Tyr	Asp	Ala	Ile	Leu	Leu	Ser	Gly
	290					295					300				
Phe	Leu	Thr	Val	Thr	Asp	Asn	Glu	Thr	Glu	Ala	Pro	Leu	Ser	Ser	Ala
305					310					315					320
Met	Ile	Lys	Arg	Tyr	Asn	Glu	His	Lys	Glu	Asp	Leu	Ala	Leu	Leu	Lys
				325					330					335	
Glu	Tyr	Ile	Arg	Asn	Ile	Ser	Leu	Lys	Thr	Tyr	Asn	Glu	Val	Phe	Lys
			340					345					350		
Asp	Asp	Thr	Lys	Asn	Gly	Tyr	Ala	Gly	Tyr	Ile	Asp	Gly	Lys	Thr	Asn
		355					360					365			
Gln	Glu	Asp	Phe	Tyr	Val	Tyr	Leu	Lys	Asn	Leu	Leu	Ala	Glu	Phe	Glu
	370					375					380				
Gly	Ala	Asp	Tyr	Phe	Leu	Glu	Lys	Ile	Asp	Arg	Glu	Asp	Phe	Leu	Arg
385					390					395					400
Lys	Gln	Arg	Thr	Phe	Asp	Asn	Gly	Ser	Ile	Pro	Tyr	Gln	Ile	His	Leu
				405					410					415	
Gln	Glu	Met	Arg	Ala	Ile	Leu	Asp	Lys	Gln	Ala	Lys	Phe	Tyr	Pro	Phe
			420					425					430		
Leu	Ala	Lys	Asn	Lys	Glu	Arg	Ile	Glu	Lys	Ile	Leu	Thr	Phe	Arg	Ile
		435					440					445			
Pro	Tyr	Tyr	Val	Gly	Pro	Leu	Ala	Arg	Gly	Asn	Ser	Asp	Phe	Ala	Trp
	450					455					460				
Ser	Ile	Arg	Lys	Arg	Asn	Glu	Lys	Ile	Thr	Pro	Trp	Asn	Phe	Glu	Asp
465					470					475					480

Val	Ile	Asp	Lys	Glu 485	Ser	Ser	Ala	Glu	Ala 490	Phe	Ile	Asn	Arg	Met 495	Thr
Ser	Phe	Asp	Leu 500	Tyr	Leu	Pro	Glu	Glu 505	Lys	Val	Leu	Pro	Lys 510	His	Ser
Leu	Leu	Tyr 515	Glu	Thr	Phe	Asn	Val 520	Tyr	Asn	Glu	Leu	Thr 525	Lys	Val	Arg
Phe	Ile 530	Ala	Glu	Ser	Met	Arg 535	Asp	Tyr	Gln	Phe	Leu 540	Asp	Ser	Lys	Glu
Lys 545	Lys	Asp	Ile	Val	Arg 550	Leu	Tyr	Phe	Lys	Asp 555	Lys	Arg	Lys	Val	Thr 560
Asp	Lys	Asp	Ile	Ile 565	Glu	Tyr	Leu	His	Ala 570	Ile	Tyr	Gly	Tyr	Asp 575	Gly
Ile	Glu	Leu	Lys 580	Gly	Ile	Glu	Lys	Gln 585	Phe	Asn	Ser	Ser	Leu 590	Ser	Thr
Tyr	His	Asp 595	Leu	Leu	Asn	Ile	Ile 600	Asn	Asp	Lys	Glu	Phe 605	Leu	Asp	Asp
Ser	Ser 610	Asn	Glu	Ala	Ile	Ile 615	Glu	Glu	Ile	Ile	His 620	Thr	Leu	Thr	Ile
Phe 625	Glu	Asp	Arg	Glu	Met 630	Ile	Lys	Gln	Arg	Leu 635	Ser	Lys	Phe	Glu	Asn 640
Ile	Phe	Asp	Lys	Ser 645	Val	Leu	Lys	Lys	Leu 650	Ser	Arg	Arg	His	Tyr 655	Thr
Gly	Trp	Gly	Lys 660	Leu	Ser	Ala	Lys	Leu 665	Ile	Asn	Gly	Ile	Arg 670	Asp	Glu
Lys	Ser	Gly 675	Asn	Thr	Ile	Leu	Asp 680	Tyr	Leu	Ile	Asp	Asp 685	Gly	Ile	Ser
Asn	Arg 690	Asn	Phe	Met	Gln	Leu 695	Ile	His	Asp	Asp	Ala 700	Leu	Ser	Phe	Lys
Lys 705	Lys	Ile	Gln	Lys	Ala 710	Gln	Ile	Ile	Gly	Asp 715	Glu	Asp	Lys	Gly	Asn 720
Ile	Lys	Glu	Val	Val 725	Lys	Ser	Leu	Pro	Gly 730	Ser	Pro	Ala	Ile	Lys 735	Lys
Gly	Ile	Leu	Gln 740	Ser	Ile	Lys	Ile	Val 745	Asp	Glu	Leu	Val	Lys 750	Val	Met
Gly	Gly	Arg 755	Lys	Pro	Glu	Ser	Ile 760	Val	Val	Glu	Met	Ala 765	Arg	Glu	Asn
Gln	Tyr 770	Thr	Asn	Gln	Gly	Lys 775	Ser	Asn	Ser	Gln	Gln 780	Arg	Leu	Lys	Arg
Leu 785	Glu	Lys	Ser	Leu	Lys 790	Glu	Leu	Gly	Ser	Lys 795	Ile	Leu	Lys	Glu	Asn 800
Ile	Pro	Ala	Lys	Leu 805	Ser	Lys	Ile	Asp	Asn 810	Asn	Ala	Leu	Gln	Asn 815	Asp
Arg	Leu	Tyr	Leu 820	Tyr	Tyr	Leu	Gln	Asn 825	Gly	Lys	Asp	Met	Tyr 830	Thr	Gly
Asp	Asp	Leu 835	Asp	Ile	Asp	Arg	Leu 840	Ser	Asn	Tyr	Asp	Ile 845	Asp	His	Ile
Ile	Pro 850	Gln	Ala	Phe	Leu	Lys 855	Asp	Asn	Ser	Ile	Asp 860	Asn	Lys	Val	Leu
Val 865	Ser	Ser	Ala	Ser	Asn 870	Arg	Gly	Lys	Ser	Asp 875	Asp	Phe	Pro	Ser	Leu 880
Glu	Val	Val	Lys	Lys 885	Arg	Lys	Thr	Phe	Trp 890	Tyr	Gln	Leu	Leu	Lys 895	Ser
Lys	Leu	Ile	Ser 900	Gln	Arg	Lys	Phe	Asp 905	Asn	Leu	Thr	Lys	Ala 910	Glu	Arg
Gly	Gly	Leu 915	Leu	Pro	Glu	Asp	Lys 920	Ala	Gly	Phe	Ile	Gln 925	Arg	Gln	Leu

Val Glu Thr Arg Gln Ile Thr Lys His Val Ala Arg Leu Leu Asp Glu
930 935 940

Lys Phe Asn Asn Lys Lys Asp Glu Asn Asn Arg Ala Val Arg Thr Val
945 950 955 960

Lys Ile Ile Thr Leu Lys Ser Thr Leu Val Ser Gln Phe Arg Lys Asp
965 970 975

Phe Glu Leu Tyr Lys Val Arg Glu Ile Asn Asp Phe His His Ala His
980 985 990

Asp Ala Tyr Leu Asn Ala Val Ile Ala Ser Ala Leu Leu Lys Lys Tyr
995 1000 1005

Pro Lys Leu Glu Pro Glu Phe Val Tyr Gly Asp Tyr Pro Lys Tyr
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Asn Ser Phe Arg Glu Arg Lys Ser Ala Thr Glu Lys Val Tyr Phe
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Tyr Ser Asn Ile Met Asn Ile Phe Lys Lys Ser Ile Ser Leu Ala
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Thr Gly Glu Ser Val Trp Asn Lys Glu Ser Asp Leu Ala Thr Val
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Arg Arg Val Leu Ser Tyr Pro Gln Val Asn Val Val Lys Lys Val
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Glu Glu Gln Asn His Gly Leu Asp Arg Gly Lys Pro Lys Gly Leu
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Phe Asn Ala Asn Leu Ser Ser Lys Pro Lys Pro Asn Ser Asn Glu
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Asn Leu Val Gly Ala Lys Glu Tyr Leu Asp Pro Lys Lys Tyr Gly
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Gly Tyr Ala Gly Ile Ser Asn Ser Phe Ala Val Leu Val Lys Gly
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Thr Ile Glu Lys Gly Ala Lys Lys Lys Ile Thr Asn Val Leu Glu
1160 1165 1170

Phe Gln Gly Ile Ser Ile Leu Asp Arg Ile Asn Tyr Arg Lys Asp
1175 1180 1185

Lys Leu Asn Phe Leu Leu Glu Lys Gly Tyr Lys Asp Ile Glu Leu
1190 1195 1200

Ile Ile Glu Leu Pro Lys Tyr Ser Leu Phe Glu Leu Ser Asp Gly
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Ser Arg Arg Met Leu Ala Ser Ile Leu Ser Thr Asn Asn Lys Arg
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Gly Glu Ile His Lys Gly Asn Gln Ile Phe Leu Ser Gln Lys Phe
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Val Lys Leu Leu Tyr His Ala Lys Arg Ile Ser Asn Thr Ile Asn
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Glu Asn His Arg Lys Tyr Val Glu Asn His Lys Lys Glu Phe Glu
1265 1270 1275

Glu Leu Phe Tyr Tyr Ile Leu Glu Phe Asn Glu Asn Tyr Val Gly
1280 1285 1290

Ala Lys Lys Asn Glu Lys Leu Leu Asn Ser Ala Phe Gln Ser Trp
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Gln Asn His Ser Ile Asp Glu Leu Cys Ser Ser Phe Ile Gly Pro
1310 1315 1320

Thr Gly Ser Glu Arg Lys Gly Leu Phe Glu Leu Thr Ser Arg Gly
1325 1330 1335

Ser Ala Ala Asp Phe Glu Phe Leu Gly Val Lys Ile Pro Arg Tyr
1340 1345 1350

Arg	Asp 1355	Tyr	Thr	Pro	Ser	Ser 1360	Leu	Leu	Lys	Asp	Ala 1365	Thr	Leu	Ile
His	Gln 1370	Ser	Val	Thr	Gly	Leu 1375	Tyr	Glu	Thr	Arg	Ile 1380	Asp	Leu	Ala
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<212> PRT
<213> Streptococcus vestibularis

<400> 787

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Gly	Asn	Ser 35	Ser	Val	Gly	Asp	Tyr 40	Ala	Gln	Ile	Val	Lys 45	Glu	Asn	Ser
Lys	Gln 50	Leu	Glu	Thr	Lys	Thr 55	Pro	Gly	Gln	Ile	Gln 60	Leu	Glu	Arg	Tyr
Gln 65	Lys	Tyr	Gly	Gln	Leu 70	Arg	Gly	Asp	Phe	Thr 75	Val	Glu	Glu	Asp	Gly 80
Lys	Lys	His	Arg	Leu 85	Ile	Asn	Val	Phe	Pro 90	Thr	Ser	Ala	Tyr	Arg 95	Ala
Glu	Ala	Leu	Arg 100	Ile	Leu	Gln	Thr	Gln 105	Gln	Glu	Phe	Asn	Ser 110	Gln	Ile
Thr	Asp	Glu 115	Phe	Ile	Asn	Arg	Tyr 120	Leu	Glu	Ile	Leu	Thr 125	Gly	Lys	Arg
Lys	Tyr 130	Tyr	His	Gly	Pro	Gly 135	Asn	Glu	Lys	Ser	Arg 140	Thr	Asp	Tyr	Gly
Arg 145	Tyr	Arg	Thr	Ser	Gly 150	Glu	Thr	Leu	Asp	Asn 155	Ile	Phe	Gly	Ile	Leu 160
Ile	Gly	Lys	Cys	Thr 165	Phe	Tyr	Pro	Glu	Glu 170	Phe	Arg	Ala	Ala	Lys 175	Ala
Ser	Tyr	Thr	Ala 180	Gln	Glu	Phe	Asn	Leu 185	Leu	Asn	Asp	Leu	Asn 190	Asn	Leu
Thr	Val	Pro 195	Thr	Glu	Thr	Lys	Lys 200	Leu	Ser	Glu	Glu	Gln 205	Lys	Asn	Gln
Ile	Ile 210	Asn	Tyr	Val	Lys	Asn 215	Glu	Lys	Ala	Met	Gly 220	Pro	Ala	Lys	Leu
Phe 225	Lys	Tyr	Ile	Ala	Lys 230	Leu	Leu	Ser	Cys	Asp 235	Ile	Ala	Asp	Ile	Lys 240
Gly	Tyr	Arg	Ile	Asp 245	Lys	Ser	Asp	Lys	Ala 250	Glu	Ile	His	Thr	Phe 255	Glu
Ala	Tyr	Arg	Lys 260	Met	Lys	Thr	Leu	Glu 265	Thr	Ile	Asp	Ile	Glu 270	Lys	Met
Ser	Arg	Glu 275	Glu	Leu	Asp	Lys	Leu 280	Ala	Tyr	Val	Leu	Thr 285	Leu	Asn	Thr
Glu	Arg 290	Glu	Gly	Ile	Gln	Glu 295	Ala	Leu	Glu	His	Glu 300	Phe	Val	Asp	Gly
Asn 305	Phe	Ser	Gln	Glu	Gln 310	Ile	Asp	Glu	Leu	Val 315	Gln	Phe	Arg	Lys	Ala 320
Asn	Ser	Ser	Ile	Phe 325	Gly	Lys	Gly	Trp	His 330	Asn	Phe	Ser	Val	Lys 335	Leu

Met	Met	Glu	Leu 340	Ile	Pro	Glu	Leu	Tyr 345	Ala	Thr	Ser	Glu	Glu 350	Gln	Met
Thr	Ile	Leu 355	Thr	Arg	Leu	Gly	Lys 360	Gln	Lys	Thr	Thr	Ser 365	Ser	Ser	Asn
Lys	Thr 370	Lys	Tyr	Ile	Asp	Glu 375	Lys	Leu	Leu	Thr	Glu 380	Glu	Ile	Tyr	Asn
Pro 385	Val	Val	Ala	Lys	Ser 390	Val	Arg	Gln	Ala	Ile 395	Lys	Ile	Val	Asn	Ala 400
Ala	Ile	Lys	Glu	Tyr 405	Gly	Asp	Phe	Asp	Asn 410	Ile	Val	Ile	Glu	Met 415	Ala
Arg	Ala	Thr	Asn 420	Glu	Asp	Asp	Glu	Lys 425	Lys	Ala	Ile	Gln	Lys 430	Ile	Gln
Lys	Ala	Asn 435	Lys	Asp	Glu	Lys	Asp 440	Ala	Ala	Met	Leu	Lys 445	Ala	Ala	Asn
Gln	Tyr 450	Asn	Gly	Lys	Ala	Glu 455	Leu	Pro	His	Ser	Val 460	Phe	His	Gly	His
Lys 465	Gln	Leu	Ala	Thr	Lys 470	Ile	Arg	Leu	Trp	His 475	Gln	Gln	Gly	Glu	Arg 480
Cys	Leu	Tyr	Thr	Gly 485	Lys	Thr	Ile	Ser	Ile 490	His	Asp	Leu	Ile	Asn 495	Asn
Pro	Asn	Gln	Phe 500	Glu	Ile	Asp	His	Ile 505	Leu	Pro	Leu	Ser	Ile 510	Thr	Phe
Asp	Asp	Ser 515	Leu	Ala	Asn	Lys	Val 520	Leu	Val	Tyr	Ala	Thr 525	Ala	Asn	Gln
Glu	Lys 530	Gly	Gln	Arg	Thr	Pro 535	Tyr	Gln	Ala	Leu	Asp 540	Ser	Met	Asp	Asp
Ala 545	Trp	Ser	Phe	Arg	Glu 550	Leu	Lys	Ala	Phe	Val 555	Arg	Glu	Ser	Lys	Thr 560
Leu	Ser	Asn	Lys	Lys 565	Lys	Glu	Tyr	Leu	Leu 570	Thr	Glu	Glu	Asp	Ile 575	Ser
Lys	Phe	Asp	Val 580	Arg	Lys	Lys	Phe	Ile 585	Glu	Arg	Asn	Leu	Val 590	Asp	Thr
Arg	Tyr	Ala 595	Ser	Arg	Val	Val	Leu 600	Asn	Ala	Leu	Gln	Glu 605	His	Phe	Arg
Ala	His 610	Lys	Ile	Asp	Thr	Lys 615	Val	Ser	Val	Val	Arg 620	Gly	Gln	Phe	Thr
Ser 625	Gln	Leu	Arg	Arg	His 630	Trp	Gly	Ile	Glu	Lys 635	Thr	Arg	Asp	Thr	Tyr 640
His	His	His	Ala	Val 645	Asp	Ala	Leu	Ile	Ile 650	Ala	Ala	Ser	Ser	Gln 655	Leu
Asn	Leu	Trp	Lys 660	Lys	Gln	Lys	Asn	Thr 665	Leu	Val	Asn	Tyr	Ser 670	Glu	Asn
Gln	Leu	Leu 675	Asp	Ile	Glu	Thr	Gly 680	Glu	Leu	Ile	Ser	Asp 685	Asp	Glu	Tyr
Lys	Glu 690	Ser	Val	Phe	Lys	Ala 695	Pro	Tyr	Gln	His	Phe 700	Val	Asp	Thr	Leu
Lys 705	Ser	Lys	Glu	Phe	Glu 710	Asp	Ser	Ile	Leu	Phe 715	Ser	Tyr	Gln	Val	Asp 720
Ser	Lys	Phe	Asn	Arg 725	Lys	Ile	Ser	Asp	Ala 730	Thr	Ile	Tyr	Ala	Thr 735	Arg
Lys	Ala	Lys	Leu 740	Asp	Lys	Glu	Lys	Lys 745	Glu	Tyr	Thr	Tyr	Thr 750	Leu	Gly
Lys	Ile	Lys 755	Asp	Ile	Tyr	Ala	Leu 760	Gly	Thr	Lys	Thr	Pro 765	Ser	Lys	Thr
Gly	Phe 770	Tyr	Lys	Phe	Leu	Asp 775	Leu	Tyr	Lys	Lys	Asn 780	Lys	Ser	Gln	Phe

Leu Met Tyr Gln Lys Asp Arg Lys Thr Trp Asp Glu Val Ile Glu Lys
765 770 775 780
Ile Leu Glu Gln Tyr Arg Pro Phe Lys Glu Lys Asp Lys Asn Gly Lys
785 790 795 800
Glu Val Asp Phe Asn Pro Phe Glu Lys Tyr Arg Ile Glu Asn Gly Pro
805 810 815
Ile Arg Lys Ser Arg Asn Thr Gly Ser Trp Asp Thr Lys Leu Lys Tyr
820 825 830
Lys Tyr Tyr Asp Asn Leu Leu Gly Arg Phe Val Asp Ile Lys Pro Ser
835 840 845
Glu Ser Lys Asn Pro Val Ala Leu Leu Ser Leu Asn Pro Trp Arg Thr
850 855 860
Asp Val Tyr Tyr Asp Ser Lys Thr Arg Lys Tyr Glu Phe Leu Gly Leu
865 870 875 880
Lys Tyr Ala Asp Leu Ser Phe Glu Lys Gly Ser Gly Thr Tyr Lys Ile
885 890 895
Ser Lys Val Lys Tyr Asn Leu Leu Met Ile Ala Leu Gly Lys Gly Glu
900 905 910
Ser Val Lys Phe Lys Ser Ile Ile Glu Arg Asn Ile Phe Asp Glu Lys
915 920 925
Ser Glu Phe Lys Phe Thr Leu Tyr Lys Asn Asp Leu Ile Leu Ile Lys
930 935 940
Asp Thr Glu Thr Asn Glu Ile Ile Glu Arg Ala Glu Ile Phe Leu Lys
945 950 955 960
Gly Lys Asp Asn Pro Lys Arg Phe Glu Lys Ile Lys Ile Glu Leu Lys
965 970 975
Pro Tyr Glu Lys Ala Arg Phe Glu Lys Gly Glu Glu Leu Glu Val Leu
980 985 990
Gly Lys Val Pro Pro Ser Ser Asn Gln Leu Gln Lys Asn Met Gln Ile
995 1000 1005
Glu Asn Leu Ser Ile Phe Lys Val Arg Thr Asp Val Leu Gly Asn
1010 1015 1020
Gln His Ile Ile Lys Asn Glu Gly Asp Lys Pro Lys Leu Asp Phe
1025 1030 1035

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<211> 97
<212> PRT
<213> Streptococcus vestibularis

<400> 788
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Val Gly Ile Leu Asn Lys Val Thr Gly Glu Ile Ile His Lys Asn Ser
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Arg Ile Phe Pro Ala Ala Gln Ala Glu Asn Asn Val Glu Arg Arg Thr
35 40 45
Asn Arg Gln Gly Arg Arg Leu Thr Arg Arg Lys Lys His Arg Arg Val
50 55 60
Arg Leu Asn His Leu Phe Glu Glu Ser Gly Leu Ile Thr Asp Phe Thr
65 70 75 80
Lys Val Ser Ile Asn Leu Asn Pro Tyr Gln Leu Arg Val Lys Ile Asp
85 90 95
Arg

<210> 789
<211> 1084

<211> PRT
<213> Subdoligranulum sp.

<220>
<223> Subdoligranulum sp. 4_3_54A2FAA

<400> 789

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Val Gly Trp Ala Val Val Gly Leu Asn Gly Thr Gly Glu Pro Val Gly
20 25 30
Leu Ala Arg Leu Gly Val Arg Ile Phe Asp Lys Ala Glu Gln Pro Lys
35 40 45
Thr Gly Glu Ser Leu Ala Ala Pro Arg Arg Met Ala Arg Gly Met Arg
50 55 60
Arg Arg Leu Arg Arg Lys Ala Leu Arg Arg Ala Asp Val Tyr Ala Leu
65 70 75 80
Leu Glu Arg Ser Gly Leu Ser Thr Arg Glu Glu Leu Ala Gln Met Phe
85 90 95
Glu Ala Gly Gly Leu Glu Asp Ile Tyr Ala Leu Arg Thr Arg Ala Leu
100 105 110
Asp Glu Pro Val Gly Lys Ala Glu Phe Ser Arg Ile Leu Leu His Leu
115 120 125
Ala Gln Arg Arg Gly Phe Lys Ser Asn Arg Arg Thr Ala Ser Asp Gly
130 135 140
Glu Asp Gly Arg Leu Leu Ala Ala Val Asn Glu Asn Arg Arg Arg Met
145 150 155 160
Ala Gln Gly Gly Trp Arg Thr Val Gly Glu Met Leu Tyr Arg His Glu
165 170 175
Ala Phe Ala Leu His Lys Arg Asn Lys Ala Asp Asp Tyr Leu Ser Thr
180 185 190
Val Gly Arg Asp Met Val Ala Glu Ala Ser Ile Leu Phe Glu Arg
195 200 205
Gln Arg Ala Met Gly Cys Ser Trp Ala Ala Pro Glu Leu Gln Ala Glu
210 215 220
Tyr Leu Ser Ile Leu Leu Arg Gln Arg Ser Phe Asp Glu Gly Pro Gly
225 230 235 240
Gly Asn Ser Pro Tyr Gly Gly Asn Gln Val Glu Lys Met Val Gly Arg
245 250 255
Cys Thr Phe Glu Pro Asp Glu Pro Arg Ala Ala Lys Ala Ala Tyr Ser
260 265 270
Phe Glu Tyr Phe Ser Leu Leu Gln Lys Leu Asn His Ile Arg Leu Ala
275 280 285
Glu Asn Gly Glu Thr Arg Pro Leu Thr Gln Pro Gln Arg Gln Gln Leu
290 295 300
Leu Ser Leu Ala His Lys Thr Pro Asp Ile Ser Leu Ala Arg Ile Arg
305 310 315 320
Lys Glu Leu Ala Leu Pro Glu Thr Val Gln Phe Asn Gly Val Arg Cys
325 330 335
Arg Ala Asn Glu Thr Leu Glu Glu Ser Glu Lys Lys Glu Lys Phe Ala
340 345 350
Cys Leu Pro Ala Tyr His Lys Met Arg Lys Ala Leu Asp Gly Val Val
355 360 365
Lys Gly Arg Ile Ser Ser Leu Ser Ile Ser Gln Arg Asp Ala Ala Ala
370 375 380
Thr Ala Leu Ser Leu Tyr Lys Asn Glu Asp Thr Leu Arg Ala Lys Leu
385 390 395 400

Thr	Glu	Ala	Gly	Phe 405	Gln	Ala	Pro	Glu	Ile 410	Asp	Ala	Leu	Ala	Gly 415	Leu
Thr	Gly	Phe	Ser 420	Lys	Phe	Gly	His	Leu 425	Ser	Leu	Lys	Ala	Cys 430	Arg	Lys
Leu	Ile	Pro 435	His	Leu	Glu	Gln	Gly 440	Leu	Thr	Tyr	Asp	Gln 445	Ala	Cys	Thr
Ala	Ala 450	Gly	Tyr	Asp	Phe	Lys 455	Gly	His	Gly	Ala	Gly 460	Glu	Arg	Ala	Phe
Thr 465	Leu	Pro	Ala	Ala	Ala 470	Pro	Glu	Met	Glu	Gln 475	Ile	Thr	Ser	Pro	Val 480
Val	Arg	Arg	Ala	Val 485	Ala	Gln	Thr	Ile	Lys 490	Val	Val	Asn	Gly	Ile 495	Ile
Arg	Glu	Met	Asp 500	Ala	Ser	Pro	Ala	Trp 505	Val	Arg	Ile	Glu	Leu 510	Ala	Arg
Glu	Leu	Ser 515	Lys	Thr	Phe	Gly	Glu 520	Arg	Gln	Glu	Met	Asp 525	Arg	Ser	Met
Arg	Glu 530	Asn	Ala	Ala	Gln	Asn 535	Glu	Arg	Leu	Met	Gln 540	Glu	Leu	Arg	Asp
Thr 545	Phe	His	Leu	Leu	Ser 550	Pro	Thr	Gly	Gln	Asp 555	Leu	Val	Lys	Tyr	Arg 560
Leu	Trp	Lys	Glu	Gln 565	Asp	Gly	Val	Cys	Ala 570	Tyr	Ser	Leu	Arg	Arg 575	Leu
Asp	Val	Glu	Arg 580	Leu	Phe	Glu	Pro	Gly 585	Tyr	Val	Asp	Val	Asp 590	His	Ile
Val	Pro	Tyr 595	Ser	Leu	Ser	Phe	Asp 600	Asp	Arg	Arg	Ser	Asn 605	Lys	Val	Leu
Val	Leu 610	Ser	Ser	Glu	Asn	Arg 615	Gln	Lys	Gly	Asn	Arg 620	Leu	Pro	Leu	Gln
Tyr 625	Leu	Gln	Gly	Lys	Arg 630	Arg	Glu	Asp	Phe	Ile 635	Val	Trp	Thr	Asn	Ser 640
Ser	Val	His	Asp	Tyr 645	Arg	Lys	Arg	Gln	Asn 650	Leu	Leu	Arg	Glu	Lys 655	Leu
Ser	Gly	Asp	Glu 660	Ala	Glu	Gly	Phe	Arg 665	Gln	Arg	Asn	Leu	Gln 670	Asp	Thr
Gln	His	Met 675	Ala	Arg	Phe	Leu	Tyr 680	Asn	Tyr	Ile	Ser	Asp 685	His	Leu	Ala
Phe	Ala 690	Gln	Ser	Glu	Ala	Leu 695	Gly	Lys	Lys	Arg	Val 700	Phe	Ala	Val	Ser
Gly 705	Ala	Val	Thr	Ser	His 710	Leu	Arg	Lys	Arg	Trp 715	Gly	Leu	Ser	Lys	Val 720
Arg	Ala	Asp	Gly	Asp 725	Leu	His	His	Ala	Leu 730	Asp	Ala	Ala	Val	Val 735	Ala
Cys	Thr	Thr	Asp 740	Gly	Met	Ile	Arg	Arg 745	Ile	Ser	Gly	Tyr	Tyr 750	Gly	His
Ile	Glu	Gly 755	Glu	Tyr	Leu	Gln	Asp 760	Ala	Asp	Gly	Ala	Gly 765	Ser	Gln	His
Ala	Arg 770	Thr	Lys	Glu	Arg	Phe 775	Pro	Ala	Pro	Trp	Pro 780	Arg	Phe	Arg	Asp
Glu 785	Leu	Ile	Val	Arg	Leu 790	Ser	Glu	Gln	Pro	Ala 795	Glu	Pro	Leu	Leu	Asp 800
Ile	Asn	Pro	Glu	Phe 805	Tyr	Cys	Glu	Tyr	Gly 810	Thr	Glu	His	Ile	Arg 815	Pro
Val	Phe	Val	Ser 820	Arg	Met	Pro	Arg	Arg 825	Lys	Val	Thr	Gly	Pro 830	Gly	His
Lys	Glu	Thr 835	Ile	Lys	Gly	Ala	Ala 840	Ala	Ala	Asp	Glu	Gly 845	Leu	Leu	Thr

Val	Arg	Lys	Ala	Leu	Thr	Glu	Leu	Lys	Leu	Asp	Lys	Asp	Gly	Glu	Ile
	855					860									
Lys	Asp	Tyr	Tyr	Met	Pro	Ser	Ser	Asp	Thr	Leu	Leu	Tyr	Glu	Ala	Leu
865					870					875					880
Lys	Ala	Gln	Leu	Arg	Arg	Phe	Gly	Gly	Asp	Gly	Lys	Lys	Ala	Phe	Ala
				885					890					895	
Glu	Pro	Phe	Tyr	Lys	Pro	Lys	Ala	Asp	Gly	Thr	Pro	Gly	Pro	Leu	Val
			900					905					910		
Arg	Lys	Val	Lys	Thr	Thr	Glu	Lys	Ala	Thr	Leu	Thr	Val	Pro	Val	Ala
		915					920					925			
Gly	Gly	Ala	Ala	Ser	Asn	Asp	Thr	Met	Val	Arg	Val	Asp	Val	Phe	Leu
	930					935					940				
Val	Pro	Gly	Asp	Gly	Tyr	Tyr	Thr	Val	Pro	Val	Tyr	Thr	Ala	Asp	Thr
945					950					955					960
Leu	Lys	Pro	Glu	Leu	Pro	Asn	Arg	Ala	Val	Val	Gln	Gly	Lys	Pro	Tyr
				965					970					975	
Ser	Glu	Trp	Lys	Glu	Met	Arg	Glu	Glu	Asp	Phe	Ile	Phe	Ser	Leu	Tyr
			980					985					990		
Pro	Asn	Asp	Leu	Val	Tyr	Val	Glu	His	Lys	Ser	Gly	Leu	Lys	Phe	Thr
		995					1000					1005			
Leu	Gln	Asn	Ala	Asp	Ser	Thr	Leu	Glu	Lys	Thr	Arg	Thr	Gln	Thr	
	1010					1015					1020				
Ser	Ala	Phe	Ala	Tyr	Phe	Val	Ser	Gly	Ser	Ile	Ser	Thr	Ala	Ser	
	1025					1030					1035				
Ile	Thr	Ile	Arg	Thr	His	Asp	Asn	Ala	Tyr	Gly	Ile	Pro	Ser	Leu	
	1040					1045					1050				
Gly	Val	Lys	Thr	Leu	Lys	Thr	Phe	His	Lys	Tyr	Gln	Val	Asp	Val	
	1055					1060					1065				
Leu	Gly	Asn	Val	Phe	Pro	Val	His	Lys	Glu	Thr	Arg	Gln	Lys	Phe	
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Arg

<210> 790
<211> 951
<212> PRT
<213> Sutterella parvirubra

<400> 790

Met	Pro	Thr	Val	Arg	Pro	Val	Phe	His	Ser	Ser	Ala	Ser	Phe	Asp	Leu
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Gly	Ala	Lys	Asn	Thr	Gly	Leu	Phe	Leu	Val	Asn	His	Pro	Ala	Gly	Ala
			20					25					30		
Ala	Pro	Ser	Ala	Glu	Tyr	Ala	Ala	Ala	Tyr	Thr	Ile	Val	Gln	Pro	Ala
		35					40					45			
Asp	Gly	Asp	Gly	Leu	Asn	Tyr	Ser	Thr	Thr	Asn	Arg	Arg	Ala	Val	Arg
	50					55					60				
His	Arg	Leu	Arg	Gly	Gly	Lys	Arg	Phe	Lys	Leu	Ala	Arg	Arg	Leu	Val
65					70					75					80
Leu	Gln	Val	Ile	Asp	Ala	Leu	Arg	Lys	Leu	Lys	Pro	Gly	Leu	Ile	Arg
				85					90					95	
Asp	Glu	Glu	Met	Arg	Arg	Thr	Val	Glu	Ala	Leu	Ser	Ser	Leu	Leu	Lys
			100					105					110		
Arg	Arg	Gly	Phe	Thr	Arg	Ile	Glu	Ser	Glu	Ala	Gln	Val	Asp	Pro	Thr
		115					120					125			
Thr	Leu	Asp	Ser	Val	Asp	Pro	Ala	Val	Phe	Ala	Asp	His	Glu	Thr	Leu
	130					135					140				

Gly	Gly	Phe	Phe	Ser	Leu	Gly	Ile	Pro	Ile	Ser	Thr	Gln	Trp	Asp	Ala
145					150					155					160
Leu	Ser	Gln	Asn	Pro	Gly	Ala	Val	Glu	Gln	Leu	Phe	Lys	Ala	Leu	Pro
				165					170					175	
Ser	Ala	Lys	Asp	Phe	Gly	Lys	Tyr	Val	Thr	Glu	Gln	Phe	Pro	Glu	Phe
			180					185					190		
Ala	Glu	Gln	Lys	Lys	Leu	Tyr	Ala	Asp	Ala	Ile	Lys	Val	Leu	Ser	Ser
		195					200					205			
Glu	Ala	Lys	Ser	Ile	Val	Met	Gln	Leu	Gly	Leu	Gly	His	His	His	Arg
	210					215					220				
Ser	Lys	Tyr	Phe	Glu	Met	Ile	Ala	His	Asp	Met	Leu	Arg	Asp	Pro	Arg
225					230					235					240
Leu	Gln	Gly	Val	Phe	Glu	Leu	Phe	Gly	Ser	Glu	Glu	Arg	Phe	Lys	Thr
				245					250					255	
Phe	Ile	Cys	Asn	Val	Ser	Asn	Leu	Gln	Leu	Arg	Ala	Leu	Arg	Trp	Tyr
			260					265					270		
Phe	Asp	Glu	Pro	Asn	Pro	Glu	Val	Ala	Asn	Gln	Trp	Asn	Pro	Glu	Lys
		275					280					285			
Phe	Gln	Val	Val	Trp	Leu	Arg	Gly	Leu	Lys	Tyr	Phe	His	Pro	Asp	Ala
	290					295					300				
Glu	Arg	Lys	Ala	Asp	Met	Lys	Lys	Leu	Ile	Asp	Glu	Leu	Thr	Ala	Ser
305					310					315					320
Lys	Asp	Ile	Leu	Asp	Ala	Leu	Cys	Thr	Thr	Asp	Pro	Arg	Arg	Thr	Ile
				325					330					335	
Pro	Pro	Tyr	Glu	Asp	Gln	Asn	Asn	Arg	Arg	Pro	Pro	Phe	Asp	Gln	Thr
			340					345					350		
Leu	Trp	Leu	Ser	Ala	Ala	Glu	Leu	Thr	Arg	Arg	Tyr	Gly	Asp	Lys	Trp
		355					360					365			
Arg	Ile	Trp	Ser	Gln	Lys	Phe	Glu	Arg	Ala	Asp	Arg	Ala	Leu	Ser	Thr
	370					375					380				
Gly	Leu	Asp	Glu	Ile	Leu	Leu	Tyr	Thr	Asp	Arg	Arg	Ser	Arg	Met	Phe
385					390					395					400
Asn	Arg	Asn	Gln	Asp	Pro	Ser	Val	Tyr	Ala	Asp	Ser	Tyr	Val	Leu	Gln
				405					410					415	
Arg	Val	Leu	Asp	Arg	Ser	Ser	Lys	Leu	Asp	Arg	Tyr	Ala	Leu	Arg	Ala
			420					425					430		
Leu	Ala	Ala	Gly	Tyr	Arg	Thr	Gln	Glu	Leu	His	Glu	Pro	Leu	Ala	Thr
		435					440					445			
Leu	Ser	Asp	Thr	Leu	Gly	Thr	Gln	His	Val	Glu	Thr	Phe	Leu	Thr	Phe
	450					455					460				
Ala	Ala	Glu	Tyr	Tyr	Glu	Glu	Val	Ala	Ala	Ala	Lys	Asn	Gly	Leu	Trp
465					470					475					480
Leu	Asp	Gly	Pro	Ser	Arg	Leu	Leu	Glu	Arg	Ala	Asp	Ile	His	Pro	Pro
				485					490					495	
Met	Lys	Lys	Lys	Val	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Ile	Leu	Asp	Ala
			500					505					510		
Thr	Pro	Glu	Ile	Gly	Arg	Ile	Leu	Arg	Thr	Val	Leu	Trp	Asn	Arg	His
		515					520					525			
Val	His	Glu	Lys	Ser	Arg	Ser	Thr	Pro	Ala	Ser	Leu	Cys	Arg	Ser	Ile
	530					535					540				
Glu	Ala	Ile	Arg	Lys	Asp	Phe	Gly	Gly	Glu	Phe	Arg	Met	Arg	Tyr	Asp
545					550					555					560
Ala	Leu	Asp	Ala	Lys	Ile	Arg	Ala	Ala	Glu	Asp	Gln	Lys	Lys	Lys	Phe
				565					570					575	
Lys	Pro	Thr	Asn	Ala	Glu	Glu	Lys	Asp	Leu	Phe	Lys	Ala	Trp	Asn	Ala
			580					585					590		

Thr Lys Thr Met His Ala Phe Leu Arg Asp Val Leu Gln Leu Thr Pro
595 600 605
Lys Gln Leu Glu Arg Thr Ala Ser Pro Tyr Val Phe Ala Gln Leu His
610 615 620
Thr Leu Ile Asp Thr Glu Arg Asp Gly Phe Thr Ser Thr Ser Leu Ala
625 630 635 640
Ala His Leu Glu Asn Ile Trp Arg Met Arg Ala Asn Ala Ala Gly Met
645 650 655
Ala Gln Cys Ser Arg Leu Pro Ala Asp Ala Val Arg Pro Phe Asp Gly
660 665 670
Val Leu Ser Lys Ala Leu Asp Arg Gln Ala Phe Glu Ala Ala Lys Leu
675 680 685
Ala Ala Gln His Leu Met Ser Arg Lys Glu Leu Thr Asp Thr Asp Ile
690 695 700
Arg Tyr Ser Ile Ile Ile Glu Ser Asn Arg Phe Ala Phe Ser Ala Ser
705 710 715 720
Thr Ala Glu Leu Lys Lys Asn Thr Leu Ala Lys Lys Asn Ala Glu Lys
725 730 735
Gly Leu Asn Phe Glu Leu Lys Arg Trp Gln Asp Lys Asp Ser Arg Ile
740 745 750
Arg Glu Ala Ser Arg Gly Ile Cys Ala Tyr Thr Gly Ala Lys Leu Gly
755 760 765
Asp Val Val Glu Tyr Asp His Ile Ile Pro Arg Ala Phe Thr Thr Ser
770 775 780
Ala Met Gly Ser Val Phe Asn Ser Glu Ala Asn Leu Ile Cys Val Ser
785 790 795 800
Arg Pro Gly Asn Gln Thr Lys Ala Asp Lys Arg Tyr Gly Leu Asn Lys
805 810 815
Leu His Lys Thr Tyr Leu Thr Ala Val Phe Gly Thr Ala Asp Val Thr
820 825 830
Thr Ile Ala Ala Ser Ile Glu Asp Ile Val Gly Lys Leu Ala Ser Ala
835 840 845
Asn Arg Leu Arg His Phe Glu Leu Leu Asn Glu Lys Glu Gln Asp Ala
850 855 860
Val Arg His Ala Leu Phe Leu Asp Asp Glu Ser Asp Ala Arg Arg Ile
865 870 875 880
Val Leu Arg Glu Leu Ala Ala Gln Asn Lys Ser Arg Val Asn Gly Thr
885 890 895
Gln Ala Trp Phe Val Arg Ala Phe Met Thr Lys Leu Leu Glu Ile Thr
900 905 910
Lys Asp Trp Arg Glu Arg Thr Gly Asn Thr Leu Asp Ile Arg Ser Trp
915 920 925
Lys Thr Asp Ala Glu Val Ala Ser Arg Leu Arg Ser Ala Leu Asn Phe
930 935 940
His Ala Glu Ile Thr Leu Thr
945 950

<210> 791
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<212> PRT
<213> Sutterella parvirubra

<400> 791
Ser Asn Leu Phe Arg Glu Glu Val Pro Tyr Gly Asp His Phe Leu Pro
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Ile	Ile	Gln	Met	Lys	Asn	Arg	Ile	Tyr	Ile	Gly	Tyr	Gln	Leu	Pro	Lys
			20					25					30		
Ala	Asp	Gly	Thr	Gly	Gly	Asn	Ala	Val	Ala	Val	Leu	Gly	Lys	Asp	Pro
		35					40					45			
Leu	Glu	Leu	Leu	Glu	Thr	Leu	Lys	Pro	Phe	Leu	Asp	Arg	Glu	Pro	Gln
	50					55					60				
Ala	Phe	Ser	Asp	His	Pro	Val	Thr	Tyr	Lys	Met	Ile	Asn	Glu	Arg	Ala
65					70					75					80
Tyr	Glu	Leu	Leu	Thr	Lys	Cys	Ala	Leu	Thr	Pro	Asp	Gln	Thr	Thr	Glu
				85					90					95	
Leu	Glu	Arg	Thr	Gln	Ala	Glu	Val	Leu	Arg	Ser	Leu	Asn	Tyr	Gln	Thr
			100					105					110		
Ser	Arg	Ala	Ala	Val	Leu	Gly	Arg	Leu	Val	Asp	Asp	Lys	Asn	Lys	Phe
		115					120					125			
Val	Ala	Lys	Asp	Ala	Val	Trp	Lys	Glu	Lys	Asp	Phe	Val	Ile	Ser	Phe
	130					135					140				
Lys	Leu	Ser	Pro	Lys	Lys	Ser	Ala	Phe	Lys	Ala	Ser	Gly	Gln	Leu	Glu
145					150					155					160
Leu	Pro	Ala	Lys	Ser	Asp	Trp	Lys	Ala	Leu	Val	Asp	Ser	Pro	Glu	Leu
				165					170					175	
Ala	Ile	Asn	Trp	Gly	Gln	Pro	Ala	Asp	Asp	Thr	Phe	Ser	Gln	Arg	Ile
			180					185					190		
Glu	Arg	Lys	Val	Arg	Met	Asn	Ser	Ser	His	Leu	Glu	His	Thr	Pro	Lys
		195					200					205			
Lys	Arg	Val	Val	Ser	Leu	Pro	Val	Val	Asp	Lys	Pro	Ser	Gly	Gly	Phe
	210					215					220				
Arg	Ile	Arg	Arg	His	Asn	Leu	Asp	Gly	Ser	Ala	Val	Phe	Gln	Val	His
225					230					235					240
Thr	Val	Ala	Asn	Asn	Lys	Tyr	Gly	Gly	Phe	Ser	Ala	Asp	Ser	Ala	Gly
				245					250					255	
Lys	Val	Asp	Trp	Ser	Thr	Pro	Val	Leu	Cys	Gly	His	Leu	Gln	His	Ala
			260					265					270		
Asn	Leu	Val	Pro	Leu	Asp	Pro	Glu	Thr	Ala	Ser	Ala	Glu	Gln	Leu	Val
		275					280					285			
Arg	Met	Ser	Glu	Trp	Arg	Val	Val	Glu	Thr	Thr	Ser	Asp	Ile	Arg	Leu
	290					295					300				
Glu	Val	Cys	Pro	Gly	Thr	Ser	Gly	Arg	Arg	Tyr	Val	Arg	Val	Glu	Leu
305					310					315					320
Pro	Phe	Thr	Leu	Leu	Gln	Glu	Trp	Leu	Thr	Ala	Gly	Lys	Val	Ala	Asp
				325					330					335	
Val	Pro	Val	Ser	Pro	Leu	His	Leu	Pro	Gly	Ser	Ile	Lys	Leu	Thr	Asp
			340					345					350		
Pro	Lys	Thr	Phe	Cys	Ala	Glu	Ala	Gln	Lys	Thr	Leu	Ser	Ile	Phe	Ala
		355					360					365			
Gln	Pro	Arg	Ala	Thr	Ile	Phe	Phe	Glu	Gln	Leu	Gly	Asp	Arg	Val	Arg
	370					375					380				
Phe	Arg	Phe	Glu	Ala	Ser	Gly	Gly	Pro	Ala	Thr	Met	Asn	Ala	Ala	Tyr
385					390					395					400
Asn	Ala	Ala	Gly	Arg	Ser										
					405										

<211> 792
<211> 369
<212> PRT
<213> Sutterella wadsworthensis

<400> 791

Met	Lys	Ala	Cys	Asp	Leu	Glu	Glu	Lys	Thr	Asn	His	Leu	Gln	Ala	Cys
1				5					10					15	
Val	Ala	Ile	Asp	Leu	Gly	Ala	Arg	Tyr	Thr	Gly	Thr	Phe	Ser	Ile	Leu
			20					25					30		
His	Lys	Ser	Ser	His	Leu	Pro	Ser	Lys	Asp	Asp	Cys	Arg	Ala	Ala	Thr
		35					40					45			
Tyr	Val	Leu	Pro	Glu	Asp	Gly	Gly	Lys	Met	Thr	Tyr	Ser	Gln	Arg	Asn
	50					55					60				
Arg	Thr	Ala	Val	Arg	His	Arg	Ile	Arg	Gly	Lys	Lys	Arg	Phe	Ala	Leu
65					70					75					80
Ala	Arg	Arg	Met	Ala	Met	Leu	Ile	Ile	Arg	Glu	Lys	Leu	Ala	Ala	Lys
				85					90					95	
Ser	Val	Thr	Leu	Thr	Ser	Ser	Glu	Thr	Arg	Arg	Leu	Ala	Glu	Ala	Val
			100					105					110		
Gly	Ser	Leu	Leu	Arg	Arg	Arg	Gly	Tyr	Asn	Arg	Leu	Glu	Thr	Glu	Thr
		115					120					125			
Asp	Asn	Asp	Leu	Thr	Val	Leu	Glu	Asn	Ile	Glu	Pro	Glu	Val	Phe	Ser
	130					135					140				
Glu	His	Glu	Ile	Leu	Gly	Lys	Tyr	Phe	Tyr	Ala	Gly	Thr	Asp	Leu	Ala
145					150					155					160
Ile	Gln	Trp	Glu	Thr	Leu	Ser	Gln	Asp	Leu	Ser	Lys	Ile	Ser	Ser	Leu
				165					170					175	
Leu	Ala	Glu	Arg	Leu	Ser	Glu	Lys	Asp	Phe	Lys	Lys	Tyr	Leu	Thr	Gly
			180					185					190		
Leu	Ile	Pro	Asp	Asp	Lys	Asn	Lys	Ile	Lys	His	Ile	Ile	Ser	Val	Phe
		195					200					205			
Lys	Met	Leu	Ile	Asp	Glu	Ala	Glu	Ser	Ile	Asn	Met	Gln	Cys	Val	Leu
	210					215					220				
Gly	His	Lys	His	Arg	Thr	Gln	Tyr	Leu	Ser	Asp	Ile	His	Ala	Asp	Met
225					230					235					240
His	Arg	Asp	Thr	Arg	Leu	Ser	Lys	Ala	Ala	Glu	Ala	Phe	Gly	Gly	Val
				245					250					255	
Asp	Arg	Leu	Trp	Arg	Leu	Leu	Gly	Asn	Leu	Ser	Asn	Leu	Gln	Leu	Arg
			260					265					270		
Ala	His	Arg	Trp	Tyr	Phe	Asn	Ala	Pro	His	Leu	Phe	Asp	Asp	Gln	Ala
		275					280					285			
Leu	Glu	Pro	Ala	Arg	Leu	Gln	Lys	Thr	Leu	Val	Arg	Ala	Phe	Lys	Tyr
	290					295					300				
Leu	His	Cys	Pro	Gln	Gly	Val	Glu	Ser	Arg	Ala	Gln	Ala	Glu	Leu	Val
305					310					315					320
Lys	Glu	Leu	Glu	Glu	Ala	Asp	Asp	Ile	Ile	Asp	Ala	Leu	Cys	Thr	Ile
				325					330					335	
Asp	Pro	Val	Arg	Thr	Ile	Pro	Pro	Tyr	Glu	Asn	Gln	Gln	Asn	Arg	Arg
			340					345					350		
Pro	Pro	Phe	Asp	Gln	Thr	Leu	Tyr	Leu	Ser	Pro	Asp	Leu	Gly	Val	Ser
		355					360					365			
Gly	Phe	Leu	Cys	Leu	Gly	Arg	Leu	Phe	Gln	Gly	Gln	Pro	Asn	Glu	Ala
	370					375					380				
Ala	Leu	Cys	Phe	Leu											
385															

<210> 793
<211> 976
<212> PRT
<213> Tannerella sp.

<210>
<211> Tannerella sp. 6_1_58FAA_CT1

<400> 798

Met Lys Lys Ile Leu Gly Leu Asp Leu Gly Ser Asn Ser Ile Gly Trp
1 5 10 15
Ala Leu Val Asn Glu Ala Glu Asn Arg Asp Glu Ala Ser Ser Ile Ile
20 25 30
Lys Leu Gly Val Arg Val Asn Pro Leu Thr Val Asp Glu Met Gln Asn
35 40 45
Phe Glu Lys Gly Lys Ser Ile Thr Thr Asn Ala Asp Arg Thr Leu Lys
50 55 60
Arg Ser Met Arg Arg Asn Leu Gln Arg Tyr Lys Leu Arg Arg Asp Ala
65 70 75 80
Leu Ile Lys Leu Leu Lys Val Gly Phe Ile Thr Asp Gly Thr Ile
85 90 95
Leu Ser Glu Gln Gly Asn Arg Thr Thr Phe Glu Thr Tyr Arg Leu Arg
100 105 110
Ala Lys Ala Ala Pro Asp Glu Glu Ile Ser Leu Gln Glu Leu Ala Arg Val
115 120 125
Leu Leu Met Ile Asn Lys Arg Gly Tyr Lys Ser Ser Arg Lys Ile
130 135 140
Lys Glu Lys Glu Ala Gly Thr Leu Leu Ile Asp Gly Met Glu Val Ala Lys
145 150 155 160
Lys Leu Tyr Asp Glu Asp Leu Thr Pro Gly Gln Leu Cys Leu Gln Leu
165 170 175
Leu Glu Ser Gly Lys Lys Ser Leu Pro Asp Phe Tyr Ser Ser Asp Leu
180 185 190
Gln Glu Glu Phe Asp Arg Ile Trp Asn Phe Gln Lys Gln Phe Asn Pro
195 200 205
Lys Ala Phe Cys Asp Thr Ala Lys Glu Glu Ile Lys Gly Lys Asn Lys
210 215 220
Ser Gln Thr Trp Ala Ile Leu Ala Lys Tyr Phe Ile Trp Met Glu Glu
225 230 235 240
Met Asp Val Trp Asn Glu Lys Glu Ser Lys Thr Glu Arg Val Glu Lys
245 250 255
Glu Cys Lys Leu Val Gly Leu Lys Arg Thr Val Lys Lys Glu Glu Gln
260 265 270
Arg Lys Glu Asn Tyr Cys Trp Arg Val Gln Ala Leu Thr Glu Gln Leu
275 280 285
Asp Leu Glu Lys Val Ala Val Val Leu Gln Glu Ile Asn Gly Gln Ile
290 295 300
Ser Thr Ser Ser Gly Tyr Leu Gly Ala Ile Ser Asp Arg Ser Lys Val
305 310 315 320
Leu Tyr Phe Asn Arg Gln Thr Val Gly Gln Tyr Gln Met Ala Glu Leu
325 330 335
Glu Lys Asn Pro Asn Thr Ser Leu Arg Asn Met Val Phe Tyr Arg Gln
340 345 350
Asp Tyr Leu Asp Glu Phe Asp Lys Ile Trp Glu Lys Gln Ala Glu Phe
355 360 365
His Lys Glu Leu Thr Val Glu Leu Lys Lys Glu Ile Arg Asp Ile Ile
370 375 380
Ile Phe Tyr Gln Arg Arg Leu Lys Ser Gln Lys Gly Leu Ile Gly Phe
385 390 395 400
Cys Glu Phe Glu Asn Arg Glu Ile Met Val Glu Lys Asn Gly Lys Met
405 410 415

Gln	Ala	Lys	Val 420	Val	Gly	Cys	Lys	Val 425	Ile	Pro	Arg	Ser	His 430	Pro	Leu
Phe	Gln	Glu 435	Phe	Lys	Ile	Trp	Gln 440	Thr	Leu	Asn	Asn	Val 445	Glu	Val	Phe
Ala	Gly 450	Glu	Lys	Lys	Cys	Lys 455	Arg	Lys	Arg	Thr	Asp 460	Ala	Phe	Pro	Gly
Leu 465	Phe	Asp	Gly	Thr	Glu 470	Asp	Thr	Leu	Met	Val 475	Glu	Gly	Trp	Arg	Tyr 480
Leu	Tyr	Gln	Glu	Glu 485	Lys	Glu	Ile	Leu	Ala 490	Lys	Glu	Leu	Ser	Val 495	Lys
Lys	Ser	Leu	Lys 500	Lys	Glu	Tyr	Ile	Leu 505	Lys	Leu	Leu	Phe	Asp 510	Asn	Pro
Gln	Asp	Leu 515	Asp	Met	Asn	Phe	Glu 520	Gln	Ile	Glu	Gly	Asn 525	Asp	Thr	Gly
Asn	Val 530	Leu	Phe	Ser	Ala	Tyr 535	Ser	Lys	Met	Ile	Glu 540	Lys	Tyr	Gly	Tyr
Glu 545	Pro	Leu	Asp	Phe	Gly 550	Lys	Pro	Thr	Asp	Lys 555	Ile	Ile	Glu	Gln	Leu 560
Gln	Val	Ile	Phe	Ala 565	Asp	Leu	Gly	Trp	Asn 570	Thr	Asp	Leu	Leu	Phe 575	Val
Asp	Leu	Asn	Lys 580	Glu	Gly	Lys	Asp	Leu 585	Glu	Lys	Gln	Pro	Tyr 590	Phe	Lys
Leu	Trp	His 595	Leu	Leu	Tyr	Ser	Phe 600	Glu	Gly	Asp	Asn	Thr 605	Pro	Thr	Gly
Asn	Gly 610	Lys	Leu	Val	Glu	Lys 615	Leu	Met	Glu	Leu	Cys 620	His	Val	Gly	Lys
Glu 625	Cys	Ala	Leu	Glu	Leu 630	Val	Asn	Ile	Ser	Phe 635	Gln	Asn	Asp	Tyr	Gly 640
Ser	Leu	Ser	Ala	Lys 645	Ala	Ile	Lys	Lys	Ile 650	Leu	Pro	Tyr	Leu	Lys 655	Glu
Gly	Asn	Arg	Tyr 660	Asp	Val	Ala	Cys	Gly 665	Tyr	Ala	Gly	Tyr	Arg 670	His	Ser
Lys	Ser	Ser 675	Leu	Thr	Lys	Glu	Glu 680	Ile	Glu	Asn	Lys	Val 685	Leu	Lys	Asp
Lys	Leu 690	Asp	Ile	Leu	Pro	Lys 695	Asn	Ser	Leu	Arg	Asn 700	Pro	Val	Val	Glu
Lys 705	Ile	Leu	Asn	Gln	Met 710	Val	Asn	Val	Ile	Asn 715	Ala	Ile	Ile	Asp	Thr 720
Tyr	Gly	Lys	Pro	Asp 725	Glu	Ile	Arg	Val	Glu 730	Leu	Ala	Arg	Glu	Leu 735	Lys
Lys	Ser	Ala	Lys 740	Glu	Arg	Glu	Glu	Leu 745	Thr	Lys	Ala	Ile	Ala 750	Lys	Ser
Thr	Arg	Glu 755	His	Glu	Glu	Ile	Arg 760	Lys	Val	Leu	Gln	Glu 765	Glu	Phe	Gly
Met	Ile 770	Asn	Val	Ser	Arg	Asn 775	Asp	Ile	Ile	Arg	Tyr 780	Lys	Leu	Tyr	Lys
Glu 785	Leu	Lys	Asp	Asn	Gly 790	Tyr	Lys	Thr	Leu	Tyr 795	Ser	Asn	Gln	Asp	Ile 800
Pro	Lys	Glu	Lys	Val	Phe	Ser	Lys	Glu	Ile	Asp	Ile	Glu	His	Ile	Ile
				805					810					815	
Pro	Gln	Ala	Arg	Leu	Phe	Asp	Asp	Ser	Leu	Ser	Asn	Lys	Thr	Leu	Glu
			820					825					830		
Tyr	Lys	Ala	Ile	Asn	Ile	Glu	Lys	Gly	Asn	Lys	Thr	Ala	Tyr	Asp	Phe
		835					840					845			
Val	Lys	Glu	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Gln	Gln	Tyr	Leu	Asn	Arg
	850					855					860				

Cys 865	Glu	Ser	Leu	Phe	Lys 870	Gly	His	Arg	Thr	Lys 875	Leu	Arg	Lys	Leu	Lys 880
Met	Gly	Gln	Glu	Asn 885	Ile	Pro	Glu	Gly	Phe 890	Ile	Asn	Arg	Asp	Leu 895	Arg
Asn	Thr	Gln	Tyr 900	Ile	Ala	Lys	Lys	Ala 905	Leu	Ala	Met	Leu	Asn 910	Glu	Ile
Cys	Arg	Arg 915	Val	Val	Ala	Thr	Thr 920	Gly	Ser	Ile	Thr	Asp 925	Arg	Leu	Arg
Glu	Asp 930	Trp	Gln	Leu	Val	Asp 935	Val	Leu	Lys	Glu	Leu 940	Arg	Cys	Phe	Arg
Tyr 945	Phe	Lys	Asp	Thr	Lys 950	Met	Lys	Ala	Asn	His 955	Asn	Lys	Asn	Ile	Phe 960
Tyr	Thr	Ser	Ile	Lys 965	Val	Asp	Val	Ser	Asp 970	Thr	Ser	Lys	Ile	Leu 975	Lys

<210> 794
<211> 1049
<212> PRT
<213> Pistrella mobilis

<400> 794

Met 1	Ile	Asn	Glu	Arg 5	Leu	Thr	Phe	Gly	Ile 10	Asp	Leu	Gly	Ile	Gly 15	Ser
Cys	Gly	Trp	Ala 20	Val	Leu	Arg	His	Ala 25	Asp	Ala	Ala	Gly	Glu 30	Pro	Gly
Val	Ile	Glu 35	Gly	Leu	Gly	Ser	Trp 40	Cys	Phe	Asp	Val	Pro 45	Glu	Thr	Ser
Lys	Glu 50	Arg	Ile	Pro	Thr	Asn 55	Gln	Val	Arg	Arg	Ser 60	Asn	Arg	Leu	Leu
Arg	Arg	Val	Ile	Arg	Arg	Arg	Arg	Asn	Arg	Met	Ala	Glu	Ile	Arg	Arg
65					70					75					80
Leu	Phe	His	Ala	Gln 85	Gly	Leu	Leu	Pro	Ser 90	Ala	Asp	Glu	Asp	Ala 95	Leu
Lys	Arg	Pro	Arg 100	Leu	Asp	Pro	Trp	Glu 105	Leu	Arg	Ala	Arg	Gly 110	Leu	Asp
Gln	Cys	Leu 115	Ser	Ala	Glu	Glu	Phe 120	Ala	Val	Ala	Leu	Gly 125	His	Ile	Ala
Arg	His 130	Arg	Gly	Phe	Arg	Ser 135	Ser	Ala	Lys	Arg	Lys 140	Ala	Ala	Asn	Thr
Ser 145	Gly	Glu	Asp	Ser	Lys 150	Met	Leu	Ser	Ala	Leu 155	Leu	Val	Thr	Arg	Glu 160
Arg	Thr	Ala	Arg	Tyr 165	Arg	Thr	Val	Gly	Glu 170	Met	Phe	Ala	Arg	Asp 175	Pro
Glu	Tyr	Ser	Ala 180	Arg	Arg	Arg	Asn	Arg 185	Asp	Gly	Ile	Phe	Asp 190	Arg	Thr
Val	Ala	Arg 195	Asp	Asp	Leu	Ile	His 200	Glu	Val	Gly	Lys	Leu 205	Phe	Glu	Ala
Gln	Arg	Ala 210	Arg	Gly	Ser	Ala	Phe 215	Ala	Ser	Pro	Asp	Leu 220	Glu	Ala	Asp
Phe 225	Asn	Ala	Ile	Ala	Phe 230	Arg	Gln	Ala	Glu	Met 235	Gln	Asp	Ser	Glu	Arg 240
Leu	Val	Gly	Asn	Cys 245	Pro	Phe	Glu	Arg	Asp 250	Glu	Lys	Arg	Ala	Ala 255	Arg
Trp	Ala	Pro	Ser 260	Phe	Glu	Arg	Phe	Arg 265	Leu	Leu	Thr	Arg	Leu 270	Ile	Asn

Leu Arg Ile Ala Thr Ala Glu Gly Glu Arg Arg Phe Thr Pro Glu Asp
175 280 285

Leu Ala Arg Val Ser Ala Glu Leu Gly Ala Thr Ala Lys Leu Pro Val
190 295 300

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

Thr Ile Arg Val Glu Asp Glu Asp Arg Asp Ile Val Ala Arg Thr Gly
325 330 335

Glu Ala Ala Pro Gly Thr Trp Arg Leu Arg Arg Lys Thr Leu Gly Glu Ala
340 345 350

Leu Trp Ala Glu Met Gln Ala Arg Pro Asp Gln Leu Asp Ala Leu Ile Ala
355 360 365

His Val Leu Ser Phe Phe Glu Ala Thr Ala Lys Ile Arg Ser Glu Leu
370 375 380

Asp Arg Leu Gly Leu Pro Ala Ala Val Ile Glu Ala Leu Asp Arg Gly
385 390 395 400

Leu Glu Asp Gly Phe Ala Lys Phe Lys Phe Lys Gly Ala Gly His Ile Ser
405 410 415

Ala Lys Ala Cys Arg Asn Leu Leu Pro His Leu Gln Gln Gly His Arg
420 425 430

Tyr Asp Gln Ala Cys Arg Leu Ala Gly Tyr Asp His Ala Ala Ser Thr
435 440 445

Leu Ser His Thr Ala Gln Val Val Ser Lys Ala Gly Phe Asn Ala Leu
450 455 460

Val Thr Glu Leu Gly Glu Ser Ile Ala Asn Pro Ile Ala Arg Lys Ala
465 470 475 480

Leu Thr Glu Gly Leu Lys Gln Ile Arg Ala Met Cys Ala Arg Thr Gly
485 490 495

Leu Pro Gly Ala Ile His Ile Glu Leu Ala Arg Glu Val Gly Asn Ser
500 505 510

Ile Glu Lys Arg Arg Glu Leu Glu Ser Gln Arg Glu Thr Thr Thr Lys
515 520 525

Arg Arg Gln Thr Glu Arg Asp Glu Ile Arg Gly Leu Leu Ala Leu Glu
530 535 540

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

Gly Gly Lys Cys Leu Tyr Thr Gly Lys Asp Ile His Val Arg Gln Leu
565 570 575

Ile Ala Thr Asp Asn Ser Val Gln Val Asp His Ile Leu Pro Trp Ser
580 585 590

Arg Phe Gly Asp Asp Ser Phe Asn Asn Lys Thr Leu Cys Leu Ala Ser
595 600 605

Ala Asn Gln Arg Lys Arg Gly Gln Thr Pro Trp Glu Trp Phe Ser Leu
610 615 620

Thr Gly Thr Pro Glu Ala Trp Glu Val Phe Ala Ser Arg Val Glu Thr
625 630 635 640

Ser Lys Asp Leu Arg Gly Phe Lys Lys Arg Asn Leu Leu Leu Lys Asn
645 650 655

Ala Asp Glu Val Ala Gln Arg Phe Arg Ser Arg Asn Leu Asn Asp Thr
660 665 670

Arg Tyr Ala Ala Arg Leu Leu Ala Gln Ala Ala Lys Leu Phe Tyr Pro
675 680 685

Ala Gly Asp Arg Gln Glu Lys Asp Gly Arg Arg Arg Val Leu Thr Arg
690 695 700

Pro Gly Leu Thr Ala Leu Leu Arg His Ala Trp Gly Leu Glu Ser
705 710 715

Leu Lys Lys Ala Asp Gly Lys Arg Val Ser Asp Asp Arg His His Ala
                    730   735
Leu Asp Ala Leu Ala Val Ala Ala Ile Ser Glu Arg Glu Val Gln Arg
                740   745   750
Leu Thr Arg Ser Phe Gln Glu Trp Glu Gln Gln Gly Leu Ala Arg Pro
            755   760   765
Leu Arg His Val Ala Pro Pro Trp Pro Gly Phe Arg Gly Asp Val Leu
        770   775   780
Ala Ala Tyr Ala Gln Phe Val Ala Arg Pro Glu Arg Arg Arg Ala Ala
    785   790   795   800
Arg Gly Lys Gly His Asp Ala Ser Ile Arg Gln Val Val Gly Glu Gly
                805   810   815
Pro Glu Ala Gln Val Phe Glu Arg Arg Gly Leu Ala Asp Leu Ser Lys Glu
            820   825   830
Ala Asp Leu Asp Arg Val Lys Asp Pro Glu Arg Asn Gln Ala Ile Ile
        835   840   845
Glu Ala Val Arg Ala Trp Ile Leu Leu Ala Gly Arg Pro Ala Asp Ala Pro
    850   855   860
Pro Arg Ser Pro Arg Gly Asp Val Ile Val Lys Leu Arg Thr Ala Pro
865   870   875   880
Ala Lys Lys Ile Lys Pro Ala Val Pro Val Arg Gly Gly Thr Ala Asp
                885   890   895
Arg Gly Asp Met Val Arg Ile Asp Val Phe Thr Arg Pro Asn Arg Lys
            900   905   910
Gly Arg Asp Glu Trp Tyr Leu Val Pro Ile Tyr Pro His Gln Val Met
        915   920   925
Asn Arg Lys Ala Trp Pro His Pro Pro Pro Met Arg Ser Val Val Ala Tyr
    930   935   940
Lys Asp Glu Ala Gly Trp Thr Glu Ile Gly Ala Glu His Ser Phe Arg
945   950   955   960
Phe Ser Leu Tyr Pro Arg Ser Tyr Val Gln Leu Val Lys Ser Asn Gly
                965   970   975
Asp Val Ile Glu Gly Tyr Leu Val Ser Met Asp Arg Ser Thr Gly Ala
            980   985   990
Phe Arg Val Phe Val His Asn Pro Ala Glu Met Ala Lys Gly Ile
        995   1000   1005
Gly Ala Lys Thr Leu Leu Asn Leu Arg Lys Phe Asn Val Asp Arg
    1010   1015   1020
Phe Gly Val Arg Thr Glu Val Lys Ser Glu Val Arg Thr Trp His
    1025   1030   1035
Gly Glu Val Cys Thr Ser Pro Val Pro Pro Asp
    1040   1045

<210> 795
<211> 1395
<212> PRT
<213> Treponema denticola

<400> 795
Met Lys Lys Glu Ile Lys Asp Tyr Phe Leu Gly Leu Asp Val Gly Thr
1   5   10   15
Gly Ser Val Gly Trp Ala Val Thr Asp Thr Asp Tyr Lys Leu Leu Lys
            20   25   30
Ala Asn Arg Lys Asp Leu Trp Gly Met Arg Cys Phe Glu Thr Ala Glu
        35   40   45

Thr	Ala	Glu	Val	Arg	Arg	Leu	His	Arg	Gly	Ala	Arg	Arg	Arg	Ile	Glu
	50					55					60				
Arg	Arg	Lys	Lys	Arg	Ile	Lys	Leu	Leu	Gln	Glu	Leu	Phe	Ser	Gln	Glu
65					70					75					80
Ile	Ala	Lys	Ile	Asp	Glu	Gly	Phe	Phe	Gln	Arg	Met	Lys	Glu	Ser	Pro
				85					90					95	
Phe	Tyr	Ala	Glu	Asp	Lys	Thr	Ile	Leu	Gln	Glu	Asn	Ala	Leu	Phe	Asn
			100					105					110		
Asp	Lys	Asp	Phe	Thr	Asp	Lys	Thr	Tyr	His	Lys	Ala	Tyr	Pro	Thr	Ile
		115					120					125			
Asn	His	Leu	Ile	Lys	Ala	Trp	Ile	Glu	Asn	Lys	Val	Lys	Pro	Asp	Pro
	130					135					140				
Arg	Leu	Leu	Tyr	Leu	Ala	Cys	His	Asn	Ile	Ile	Lys	Lys	Arg	Gly	His
145					150					155					160
Phe	Leu	Phe	Glu	Gly	Asp	Phe	Asp	Ser	Glu	Asn	Gln	Phe	Asp	Thr	Ser
				165					170					175	
Ile	Gln	Ala	Leu	Phe	Glu	Tyr	Leu	Arg	Glu	Asp	Met	Glu	Val	Asp	Ile
			180					185					190		
Asp	Ala	Asp	Ser	Gln	Lys	Val	Lys	Glu	Ile	Leu	Lys	Asp	Ser	Ser	Leu
		195					200					205			
Lys	Asn	Ser	Glu	Lys	Gln	Ser	Arg	Leu	Asn	Lys	Ile	Leu	Gly	Leu	Lys
	210					215					220				
Pro	Ser	Asp	Lys	Gln	Lys	Lys	Ala	Ile	Thr	Asn	Leu	Ile	Ser	Gly	Asn
225					230					235					240
Lys	Ile	Asn	Phe	Ala	Asp	Leu	Tyr	Asp	Asn	Pro	Asp	Leu	Lys	Asp	Ala
				245					250					255	
Glu	Lys	Asn	Ser	Ile	Ser	Phe	Ser	Lys	Asp	Asp	Phe	Asp	Ala	Leu	Ser
			260					265					270		
Asp	Asp	Leu	Ala	Ser	Ile	Leu	Gly	Asp	Ser	Phe	Glu	Leu	Leu	Leu	Lys
		275					280					285			
Ala	Lys	Ala	Val	Tyr	Asn	Cys	Ser	Val	Leu	Ser	Lys	Val	Ile	Gly	Asp
	290					295					300				
Glu	Gln	Tyr	Leu	Ser	Phe	Ala	Lys	Val	Lys	Ile	Tyr	Glu	Lys	His	Lys
305					310					315					320
Thr	Asp	Leu	Thr	Lys	Leu	Lys	Ala	Val	Ile	Lys	Lys	His	Phe	Pro	Asn
				325					330					335	
Asn	Tyr	Lys	Lys	Val	Phe	Gly	Tyr	Asn	Gln	Asp	Asn	Glu	Ser	Lys	Asn
			340					345					350		
Asn	Tyr	Ser	Gly	Tyr	Val	Gly	Val	Cys	Lys	Thr	Lys	Asn	Lys	Lys	Leu
		355					360					365			
Val	Ile	Asn	Asn	Ser	Val	Asn	Gln	Glu	Asp	Phe	Tyr	Lys	Phe	Leu	Lys
	370					375					380				
Pro	Ile	Leu	Ser	Ala	Lys	Ser	Glu	Ile	Lys	Glu	Val	Asn	Asp	Ile	Leu
385					390					395					400
Ala	Glu	Ile	Glu	Thr	Gly	Asn	Phe	Leu	Pro	Lys	Gln	Ile	Ser	Lys	Ser
				405					410					415	
Asn	Ala	Glu	Ile	Pro	Tyr	Gln	Leu	Arg	Lys	Met	Glu	Leu	Glu	Lys	Ile
			420					425					430		
Leu	Ser	Asn	Ala	Glu	Lys	His	Phe	Ser	Phe	Leu	Lys	Gln	Lys	Asp	Glu
		435					440					445			
Lys	Gly	Leu	Ser	His	Ser	Glu	Lys	Ile	Ile	Met	Leu	Leu	Thr	Phe	Lys
	450					455					460				
Ile	Pro	Tyr	Tyr	Ile	Gly	Pro	Ile	Asn	Asp	Asn	His	Lys	Lys	Ser	Phe
465					470					475					480
Pro	Asp	Arg	Cys	Trp	Val	Val	Lys	Lys	Glu	Lys	Ser	Pro	Ser	Gly	Lys
				485					490					495	

Thr	Thr	Pro	Trp 500	Asn	Phe	Phe	Asp	His 505	Ile	Asp	Lys	Glu	Lys 510	Thr	Ala
Glu	Glu	Phe 515	Ile	Thr	Ser	Arg	Thr 520	Asn	Phe	Cys	Thr	Tyr 525	Leu	Ile	Gly
Glu	Ser 530	Val	Leu	Pro	Lys	Asn 535	Ser	Leu	Leu	Tyr	Ser 540	Glu	Tyr	Thr	Val
Leu 545	Asn	Glu	Ile	Asn	Asn 550	Leu	Gln	Ile	Ile	Ile 555	Asp	Gly	Lys	Asn	Ile 560
Cys	Asp	Thr	Lys	Leu 565	Lys	Gln	Lys	Ile	Tyr 570	Glu	Asp	Leu	Phe	Lys 575	Lys
Tyr	Lys	Lys	Ile 580	Thr	Gln	Lys	Gln	Ile 585	Ser	Thr	Phe	Ile	Lys 590	His	Glu
Gly	Ile	Cys 595	Asn	Lys	Thr	Asp	Glu 600	Val	Ile	Ile	Leu	Gly 605	Ile	Asp	Lys
Glu	Cys 610	Thr	Ser	Ser	Leu	Lys 615	Ser	Tyr	Ile	Glu	Leu 620	Lys	Asn	Ile	Phe
Gly 625	Lys	Gln	Val	Asp	Glu 630	Ile	Ser	Thr	Lys	Asn 635	Met	Leu	Glu	Glu	Ile 640
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Lys	Thr	Lys	Ile 660	Lys	Ala	Glu	Tyr	Gly 665	Lys	Tyr	Cys	Ser	Asp 670	Glu	Gln
Ile	Lys	Lys 675	Ile	Leu	Asn	Leu	Lys 680	Phe	Ser	Gly	Trp	Gly 685	Arg	Leu	Ser
Arg	Lys 690	Phe	Leu	Glu	Thr	Val 695	Thr	Ser	Glu	Met	Pro 700	Gly	Phe	Ser	Glu
Pro 705	Val	Asn	Ile	Ile	Thr 710	Ala	Met	Arg	Glu	Thr 715	Gln	Asn	Asn	Leu	Met 720
Glu	Leu	Leu	Ser	Ser 725	Glu	Phe	Lys	Phe	Thr 730	Glu	Asn	Ile	Lys	Lys 735	Ile
Asn	Ser	Gly	Phe 740	Glu	Asp	Ala	Glu	Lys 745	Gln	Phe	Ser	Tyr	Asp 750	Gly	Leu
Val	Lys	Pro 755	Leu	Phe	Leu	Ser	Pro 760	Ser	Val	Lys	Lys	Met 765	Leu	Trp	Gln
Thr	Leu 770	Lys	Leu	Val	Lys	Glu 775	Ile	Ser	His	Ile	Thr 780	Gln	Ala	Pro	Pro
Lys 785	Lys	Ile	Phe	Ile	Glu 790	Met	Ala	Lys	Gly	Ala 795	Glu	Leu	Glu	Pro	Ala 800
Arg	Thr	Lys	Thr	Arg 805	Leu	Lys	Ile	Leu	Gln 810	Asp	Leu	Tyr	Ser	Ser 815	Cys
Lys	Asn	Asp	Ala 820	Asp	Ala	Phe	Ser	Ser 825	Glu	Ile	Gln	Tyr	Leu 830	Ser	Gly
Lys	Ile	Glu 835	Asn	Glu	Asp	Asn	Leu 840	Arg	Leu	Arg	Ser	Asp 845	Lys	Leu	Tyr
Leu	Tyr 850	Tyr	Thr	Gln	Leu	Gly 855	Lys	Cys	Met	Tyr	Cys 860	Gly	Lys	Pro	Ile
Glu 865	Ile	Gly	His	Val	Phe 870	Asp	Thr	Ser	Asn	Tyr 875	Asp	Ile	Asp	His	Ile 880
Tyr	Pro	Gln	Ser	Lys	Ile	Lys	Asp	Asp	Ser	Ile	Ser	Asn	Arg	Val	Leu
				885					890					895	
Val	Cys	Ser	Ser 900	Cys	Asn	Lys	Asn	Lys 905	Glu	Asp	Lys	Tyr	Pro 910	Leu	Lys
Ser	Glu	Ile 915	Gln	Ser	Lys	Gln	Arg 920	Gly	Phe	Trp	Asn	Phe 925	Leu	Gln	Arg
Asn	Asn 930	Phe	Ile	Ser	Leu	Glu 935	Lys	Leu	Asn	Arg	Leu 940	Thr	Arg	Thr	Thr

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945                 950                 955                 960
Glu Thr Arg Gln Ala Thr Lys Val Ala Ala Lys Val Leu Glu Lys Met
                965                 970                 975
Phe Pro Glu Thr Lys Ile Val Tyr Ser Lys Ala Glu Thr Val Ser Met
            980                 985                 990
Phe Arg Asn Lys Phe Asp Ile Ile Lys Lys Arg Glu Ile Asn Asp Phe
        995                1000                1005
His His Ala His Asp Ala Tyr Leu Asn Ile Val Val Gly Asn Val
    1010                1015                1020
Tyr Asn Thr Lys Phe Thr Asn Asn Pro Trp Asn Phe Ile Lys Glu
1025                1030                1035
Lys Arg Asp Asn Pro Lys Ile Ala Asp Thr Tyr Asn Tyr Tyr Lys
            1040                1045                1050
Val Phe Asp Tyr Asp Val Lys Arg Asn Asn Ile Thr Ala Trp Glu
        1055                1060                1065
Lys Gly Lys Thr Ile Ile Thr Val Lys Asp Met Leu Lys Arg Asn
    1070                1075                1080
Thr Pro Ile Tyr Thr Arg Gln Ala Ala Cys Lys Lys Gly Gly Leu
1085                1090                1095
Phe Asp Gln Thr Ile Met Lys Lys Gly Leu Gly Gln His Pro Leu
            1100                1105                1110
Lys Lys Glu Gly Pro Phe Ser Asn Ile Ser Lys Tyr Gly Gly Tyr
        1115                1120                1125
Asn Lys Val Ser Ala Ala Tyr Thr Leu Ile Glu Tyr Glu Glu
    1130                1135                1140
Lys Gly Asn Lys Ile Arg Ser Leu Glu Thr Ile Pro Leu Tyr Leu
1145                1150                1155
Val Lys Asp Ile Gln Lys Asp Gln Asp Val Leu Lys Ser Tyr Leu
            1160                1165                1170
Thr Asp Leu Leu Gly Lys Lys Glu Phe Lys Ile Leu Val Pro Lys
        1175                1180                1185
Ile Lys Ile Asn Ser Leu Leu Lys Ile Asn Gly Phe Pro Cys His
    1190                1195                1200
Ile Thr Gly Lys Thr Asn Asp Ser Phe Leu Leu Arg Pro Ala Val
1205                1210                1215
Gln Phe Cys Cys Ser Asn Asp Glu Val Leu Tyr Phe Lys Lys Ile
            1220                1225                1230
Ile Arg Phe Ser Glu Ile Arg Ser Gln Arg Glu Lys Ile Gly Lys
        1235                1240                1245
Thr Ile Ser Pro Tyr Glu Asp Leu Ser Phe Arg Ser Tyr Ile Lys
    1250                1255                1260
Glu Asn Leu Cys Lys Lys Thr Lys Asn Asp Glu Ile Gly Glu Lys
1265                1270                1275
Glu Phe Tyr Asp Leu Leu Gln Lys Lys Asn Leu Glu Ile Tyr Asp
            1280                1285                1290
Met Leu Leu Thr Lys His Lys Asp Thr Ile Tyr Lys Lys Arg Pro
        1295                1300                1305
Asn Ser Ala Thr Ile Asp Ile Leu Val Lys Gly Lys Glu Lys Phe
    1310                1315                1320
Lys Ser Leu Ile Ile Glu Asn Gln Phe Glu Val Ile Leu Glu Ile
1325                1330                1335
Leu Lys Leu Phe Ser Ala Thr Arg Asn Val Ser Glu Leu Gln Ile
            1340                1345                1350
Ile Gly Gly Ser Lys Tyr Ser Gly Val Ala Lys Ile Gly Asn Lys
        1355                1360                1365
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Ile Ser  Ser Leu Asp Asn Cys  Ile Leu Ile Tyr Gln  Ser Ile Thr
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Gly Ile  Phe Glu Lys Arg Ile  Asp Leu Leu Lys Val
     1385                 1390                 1395
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<213> Treponema denticola

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Gly	Ser	Val	Gly 20	Trp	Ala	Val	Thr	Asp 25	Thr	Asp	Tyr	Lys	Leu 30	Leu	Lys
Ala	Asn	Arg 35	Lys	Asp	Leu	Trp	Gly 40	Met	Arg	Cys	Phe	Glu 45	Thr	Ala	Glu
Thr	Ala 50	Glu	Val	Arg	Arg	Leu 55	His	Arg	Gly	Ala	Arg 60	Arg	Arg	Ile	Glu
Arg 65	Arg	Lys	Lys	Arg	Ile 70	Lys	Leu	Leu	Gln	Glu 75	Leu	Phe	Ser	Gln	Glu 80
Ile	Ala	Lys	Ile	Asp 85	Glu	Gly	Phe	Phe	Gln 90	Arg	Met	Lys	Glu	Ser 95	Pro
Phe	Tyr	Ala	Glu 100	Asp	Lys	Thr	Ile	Leu 105	Gln	Glu	Asn	Ala	Leu 110	Phe	Asn
Asp	Lys	Asp 115	Phe	Thr	Asp	Lys	Thr 120	Tyr	His	Lys	Ala	Tyr 125	Pro	Thr	Ile
Asn	His 130	Leu	Ile	Lys	Ala	Trp 135	Ile	Glu	Asn	Lys	Val 140	Lys	Pro	Asp	Pro
Arg 145	Leu	Leu	Tyr	Leu	Ala 150	Cys	His	Asn	Ile	Ile 155	Lys	Lys	Arg	Gly	His 160
Phe	Leu	Phe	Glu	Gly 165	Asp	Phe	Asp	Ser	Glu 170	Asn	Gln	Phe	Asp	Thr 175	Ser
Ile	Gln	Ala	Leu 180	Phe	Glu	Tyr	Leu	Arg 185	Glu	Asp	Met	Glu	Val 190	Asp	Ile
Asp	Ala	Asp 195	Ser	Gln	Lys	Val	Lys 200	Glu	Ile	Leu	Lys	Asp 205	Ser	Ser	Leu
Lys	Asn 210	Ser	Glu	Lys	Gln	Ser 215	Arg	Leu	Asn	Lys	Ile 220	Leu	Gly	Leu	Lys
Pro 225	Ser	Asp	Lys	Gln	Lys 230	Lys	Ala	Ile	Thr	Asn 235	Leu	Ile	Ser	Gly	Asn 240
Lys	Ile	Asn	Phe	Ala 245	Asp	Leu	Tyr	Asp	Asn 250	Pro	Asp	Leu	Lys	Asp 255	Ala
Glu	Lys	Asn	Ser 260	Ile	Ser	Phe	Ser	Lys 265	Asp	Asp	Phe	Asp	Ala 270	Leu	Ser
Asp	Asp	Leu 275	Ala	Ser	Ile	Leu	Gly 280	Asp	Ser	Phe	Glu	Leu 285	Leu	Leu	Lys
Ala	Lys 290	Ala	Val	Tyr	Asn	Cys 295	Ser	Val	Leu	Ser	Lys 300	Val	Ile	Gly	Asp
Glu 305	Gln	Tyr	Leu	Ser	Phe 310	Ala	Lys	Val	Lys	Ile 315	Tyr	Glu	Lys	His	Lys 320
Thr	Asp	Leu	Thr	Lys 325	Leu	Lys	Ala	Val	Ile 330	Lys	Lys	His	Phe	Ile 335	Asn
Asn	Tyr	Lys	Lys 340	Val	Phe	Gly	Tyr	Asn 345	Gln	Asp	Asn	Glu	Ser 350	Lys	Asn

Asn Tyr Ser Gly Tyr Val Gly Val Cys Lys Thr Lys Asn Lys Lys Leu
355 360 365
Val Ile Asn Asn Ser Val Asn Gln Glu Asp Phe Tyr Lys Phe Leu Lys
370 375 380
Pro Ile Leu Ser Ala Lys Ser Glu Ile Lys Glu Val Asn Asp Ile Leu
385 390 395 400
Ala Glu Ile Glu Thr Gly Asn Phe Leu Pro Lys Gln Ile Ser Lys Ser
405 410 415
Asn Ala Glu Ile Pro Tyr Gln Leu Arg Lys Met Glu Leu Glu Lys Ile
420 425 430
Leu Ser Asn Ala Glu Lys His Phe Ser Phe Leu Lys Gln Lys Asp Glu
435 440 445
Lys Gly Leu Ser His Ser Glu Lys Ile Ile Met Leu Leu Thr Phe Lys
450 455 460
Ile Pro Tyr Tyr Ile Gly Pro Ile Asn Asp Asn His Lys Lys Ser Phe
465 470 475 480
Pro Asp Arg Cys Trp Val Val Lys Lys Glu Ile Ser Pro Ser Gly Lys
485 490 495
Thr Thr Pro Trp Asn Phe Phe Asp His Ile Asn Lys Glu Lys Thr Ala
500 505 510
Glu Glu Phe Ile Thr Ser Arg Thr Asn Phe Cys Thr Tyr Leu Ile Gly
515 520 525
Glu Ser Val Leu Pro Lys Asn Ser Leu Leu Tyr Ser Glu Tyr Thr Val
530 535 540
Leu Asn Glu Ile Asn Leu Gln Ile Ile Ile Asp Gly Lys Asn Ile
545 550 560
Cys Asp Thr Lys Leu Lys Gln Lys Ile Tyr Glu Asp Leu Phe Lys Lys
565 570 575
Tyr Lys Lys Ile Thr Gln Lys Gln Ile Ser Thr Phe Ile Lys His Glu
580 585 590
Gly Ile Cys Asn Lys Thr Asp Glu Val Ile Ile Leu Gly Ile Asp Lys
595 600 605
Glu Cys Thr Ser Ser Leu Lys Ser Tyr Ile Glu Leu Lys Asn Ile Phe
610 615 620
Gly Lys Gln Val Asp Glu Ile Ser Thr Lys Asn Met Leu Glu Glu Ile
625 630 635 640
Ile Arg Trp Ala Thr Ile Tyr Asp Glu Gly Glu Gly Lys Thr Ile Leu
645 650 655
Lys Thr Lys Ile Lys Ala Glu Tyr Gly Lys Tyr Cys Ser Asp Glu Gln
660 665 670
Ile Lys Lys Ile Leu Asn Leu Lys Phe Ser Gly Trp Gly Arg Leu Ser
675 680 685
Arg Lys Phe Leu Glu Thr Val Thr Ser Glu Met Pro Gly Phe Ser Glu
690 695 700
Pro Val Asn Ile Ile Thr Ala Met Arg Glu Thr Gln Asn Asn Leu Met
705 710 715 720
Glu Leu Leu Ser Ser Glu Phe Lys Phe Thr Glu Asn Ile Lys Lys Ile
725 730 735
Asn Ser Gly Phe Glu Asp Ala Glu Lys Gln Phe Ser Tyr Asp Gly Leu
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Leu

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<110> DBT
<113> Treponema denticola

<400> 797

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			20					25					30		
Ala	Asn	Arg	Lys	Asp	Leu	Trp	Gly	Met	Arg	Cys	Phe	Glu	Thr	Ala	Glu
		35					40					45			
Thr	Ala	Glu	Val	Arg	Arg	Leu	His	Arg	Gly	Ala	Arg	Arg	Arg	Ile	Glu
	50					55					60				
Arg	Arg	Lys	Lys	Arg	Ile	Lys	Leu	Leu	Gln	Glu	Leu	Phe	Ser	Gln	Glu
65					70					75					80
Ile	Ala	Lys	Ile	Asp	Glu	Gly	Phe	Phe	Gln	Arg	Met	Lys	Glu	Ser	Pro
				85					90					95	
Phe	Tyr	Ala	Glu	Asp	Lys	Thr	Ile	Leu	Gln	Glu	Asn	Ala	Leu	Phe	Asn
			100					105					110		
Asp	Lys	Asp	Phe	Thr	Asp	Lys	Thr	Tyr	His	Lys	Ala	Tyr	Pro	Thr	Ile
		115					120					125			
Asn	His	Leu	Ile	Lys	Ala	Trp	Ile	Glu	Asn	Lys	Val	Lys	Pro	Asp	Pro
	130					135					140				
Arg	Leu	Leu	Tyr	Leu	Ala	Cys	His	Asn	Ile	Ile	Lys	Lys	Arg	Gly	His
145					150					155					160
Phe	Leu	Phe	Glu	Gly	Asp	Phe	Asp	Ser	Glu	Asn	Gln	Phe	Asp	Thr	Ser
				165					170					175	
Ile	Gln	Ala	Leu	Phe	Glu	Tyr	Leu	Arg	Glu	Asp	Met	Glu	Val	Asp	Ile
			180					185					190		
Asp	Ala	Asp	Ser	Gln	Lys	Val	Lys	Glu	Ile	Leu	Lys	Asp	Ser	Ser	Leu
		195					200					205			
Lys	Asn	Ser	Glu	Lys	Gln	Ser	Arg	Leu	Asn	Lys	Ile	Leu	Gly	Leu	Lys
	210					215					220				
Pro	Ser	Asp	Lys	Gln	Lys	Lys	Ala	Ile	Thr	Asn	Leu	Ile	Ser	Gly	Asn
225					230					235					240
Lys	Ile	Asn	Phe	Ala	Asp	Leu	Tyr	Asp	Asn	Pro	Asp	Leu	Lys	Asp	Ala
				245					250					255	
Glu	Lys	Asn	Ser	Ile	Ser	Phe	Ser	Lys	Asp	Asp	Phe	Asp	Ala	Leu	Ser
			260					265					270		
Asp	Asp	Leu	Ala	Ser	Ile	Leu	Gly	Asp	Ser	Phe	Glu	Leu	Leu	Leu	Lys
		275					280					285			
Ala	Lys	Ala	Val	Tyr	Asn	Cys	Ser	Val	Leu	Ser	Lys	Val	Ile	Gly	Asp
	290					295					300				
Glu	Gln	Tyr	Leu	Ser	Phe	Ala	Lys	Val	Lys	Ile	Tyr	Glu	Lys	His	Lys
305					310					315					320
Thr	Asp	Leu	Thr	Lys	Leu	Lys	Ala	Val	Ile	Lys	Lys	His	Phe	Pro	Asn
				325					330					335	
Asn	Tyr	Lys	Lys	Val	Phe	Gly	Tyr	Asn	Gln	Asp	Asn	Glu	Ser	Lys	Asn
			340					345					350		
Asn	Tyr	Ser	Gly	Tyr	Val	Gly	Val	Cys	Lys	Thr	Lys	Asn	Lys	Lys	Leu
		355					360					365			
Val	Ile	Asn	Asn	Ser	Val	Asn	Gln	Glu	Asp	Phe	Tyr	Lys	Phe	Leu	Lys
	370					375					380				
Pro	Ile	Leu	Ser	Ala	Lys	Ser	Glu	Ile	Lys	Glu	Val	Asn	Asp	Ile	Leu
385					390					395					400
Ala	Glu	Ile	Glu	Thr	Gly	Asn	Phe	Leu	Pro	Lys	Gln	Ile	Ser	Lys	Ser
				405					410					415	

Asn	Ala	Glu	Ile 420	Pro	Tyr	Gln	Leu	Arg 425	Lys	Met	Glu	Leu	Glu 430	Lys	Ile
Leu	Ser	Asn 435	Ala	Glu	Lys	His	Phe 440	Ser	Phe	Leu	Lys	Gln 445	Lys	Asp	Glu
Lys	Gly 450	Leu	Ser	His	Ser	Glu 455	Lys	Ile	Ile	Met	Leu 460	Leu	Thr	Phe	Lys
Ile 465	Pro	Tyr	Tyr	Ile	Gly 470	Pro	Ile	Asn	Asp	Asn 475	His	Lys	Lys	Ser	Phe 480
Pro	Asp	Arg	Cys	Trp 485	Val	Val	Lys	Lys	Glu 490	Lys	Ser	Pro	Ser	Gly 495	Lys
Thr	Thr	Pro	Trp 500	Asn	Phe	Phe	Asp	His 505	Ile	Asp	Lys	Glu	Lys 510	Thr	Ala
Glu	Glu	Phe 515	Ile	Thr	Ser	Arg	Thr 520	Asn	Phe	Cys	Thr	Tyr 525	Leu	Ile	Gly
Glu	Ser 530	Val	Leu	Pro	Lys	Asn 535	Ser	Leu	Leu	Tyr	Ser 540	Glu	Tyr	Thr	Val
Leu 545	Asn	Glu	Ile	Asn	Asn 550	Leu	Gln	Ile	Ile	Ile 555	Asp	Gly	Lys	Asn	Ile 560
Cys	Asp	Thr	Lys	Leu 565	Lys	Gln	Lys	Ile	Tyr 570	Glu	Asp	Leu	Phe	Lys 575	Lys
Tyr	Lys	Lys	Ile 580	Thr	Gln	Lys	Gln	Ile 585	Ser	Thr	Phe	Ile	Lys 590	His	Glu
Gly	Ile	Cys 595	Asn	Lys	Thr	Asp	Glu 600	Val	Ile	Ile	Leu	Gly 605	Ile	Asp	Lys
Glu	Cys 610	Thr	Ser	Ser	Leu	Lys 615	Ser	Tyr	Ile	Glu	Leu 620	Lys	Asn	Ile	Phe
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Ile	Arg	Trp	Ala	Thr 645	Ile	Tyr	Asp	Glu	Gly 650	Glu	Gly	Lys	Thr	Ile 655	Leu
Lys	Thr	Lys	Ile 660	Lys	Ala	Glu	Tyr	Gly 665	Lys	Tyr	Cys	Ser	Asp 670	Glu	Gln
Ile	Lys	Lys 675	Ile	Leu	Asn	Leu	Lys 680	Phe	Ser	Gly	Trp	Gly 685	Arg	Leu	Ser
Arg	Lys 690	Phe	Leu	Glu	Thr	Val 695	Thr	Ser	Glu	Met	Pro 700	Gly	Phe	Ser	Glu
Pro 705	Val	Asn	Ile	Ile	Thr 710	Ala	Met	Arg	Glu	Thr 715	Gln	Asn	Asn	Leu	Met 720
Glu	Leu	Leu	Ser	Ser 725	Glu	Phe	Lys	Phe	Thr 730	Glu	Asn	Ile	Lys	Lys 735	Ile
Asn	Ser	Gly	Phe 740	Glu	Asp	Ala	Glu	Lys 745	Gln	Phe	Ser	Tyr	Asp 750	Gly	Leu
Val	Lys	Pro 755	Leu	Phe	Leu	Ser	Pro 760	Ser	Val	Lys	Lys	Met 765	Leu	Trp	Gln
Thr	Leu 770	Lys	Leu	Val	Lys	Glu 775	Ile	Ser	His	Ile	Thr 780	Gln	Ala	Pro	Pro
Lys 785	Lys	Ile	Phe	Ile	Glu 790	Met	Ala	Lys	Gly	Ala 795	Glu	Leu	Glu	Pro	Ala 800
Arg	Thr	Lys	Thr	Arg	Leu	Lys	Ile	Leu	Gln	Asp	Leu	Tyr	Ser	Ser	Cys
				805					810					815	
Lys	Asn	Asp	Ala	Asp	Ala	Phe	Ser	Ser	Glu	Ile	Gln	Tyr	Leu	Ser	Gly
			820					825					830		
Lys	Ile	Glu	Asn	Glu	Asp	Asn	Leu	Arg	Leu	Arg	Ser	Asp	Lys	Leu	Tyr
		835					840					845			
Leu	Tyr	Tyr	Thr	Gln	Leu	Gly	Lys	Cys	Met	Tyr	Cys	Gly	Lys	Pro	Ile
	850					855					860				

Glu Ile Gly His Val Phe Asp Thr Ser Asn Tyr Asp Ile Asp His Ile
865 870 875 880

Tyr Pro Gln Ser Lys Ile Lys Asp Asp Ser Ile Ser Asn Arg Val Leu
885 890 895

Val Cys Ser Ser Cys Asn Lys Asn Lys Asn Glu Asp Lys Tyr Pro Leu Lys
900 905 910

Ser Glu Ile Gln Ser Lys Gln Arg Gly Phe Trp Asn Phe Leu Gln Arg
915 920 925

Asn Asn Phe Ile Ser Leu Glu Lys Leu Asn Arg Leu Asn Thr Arg Thr Thr
930 935 940

Pro Ile Ser Asp Asp Glu Thr Ala Lys Phe Ile Ala Arg Gln Leu Val
945 950 955 960

Glu Thr Arg Gln Ala Thr Lys Val Ala Ala Lys Val Leu Glu Lys Met
965 970 975

Phe Pro Glu Thr Lys Ile Val Tyr Ser Lys Ala Glu Thr Val Ser Met
980 985 990

Phe Arg Asn Lys Phe Asp Ile Ile Lys Cys Arg Glu Ile Asn Asp Phe
995 1000 1005

His His Ala His Asp Ala Tyr Leu Asn Ile Val Val Gly Asn Val
1010 1015 1020

Tyr Asn Thr Lys Phe Thr Asn Asn Pro Trp Asn Phe Ile Lys Glu
1025 1030 1035

Lys Arg Asp Asn Pro Lys Ile Ala Asp Thr Tyr Asn Tyr Tyr Lys
1040 1045 1050

Val Phe Asp Tyr Asp Val Lys Arg Asn Asn Ile Thr Ala Trp Glu
1055 1060 1065

Lys Gly Lys Thr Ile Ile Thr Val Lys Asp Met Leu Lys Arg Asn
1070 1075 1080

Thr Pro Ile Tyr Thr Arg Gln Ala Ala Cys Lys Gly Glu Leu
1085 1090 1095

Phe Asn Gln Thr Ile Met Lys Lys Gly Leu Gly Gln His Pro Leu
1100 1105 1110

Lys Lys Glu Gly Pro Phe Ser Asn Ile Ser Lys Tyr Gly Gly Tyr
1115 1120 1125

Asn Lys Val Ser Ala Ala Tyr Tyr Thr Leu Ile Glu Tyr Glu Glu
1130 1135 1140

Lys Val Asn Lys Ile Arg Ser Leu Glu Thr Ile Pro Leu Tyr Leu
1145 1150 1155

Val Lys Asp Ile Gln Lys Asp Gln Asp Val Leu Lys Ser Tyr Leu
1160 1165 1170

Thr Asp Leu Leu Gly Lys Lys Glu Ile Lys Ile Leu Val Pro Lys
1175 1180 1185

Ile Lys Ile Asn Ser Leu Leu Lys Ile Asn Gly Phe Pro Cys His
1190 1195 1200

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

Ile Arg Phe Asn Glu Ile Arg Ser Gln Arg Glu Lys Met Gly Lys
1235 1240 1245

Thr Ile Ser Pro Tyr Glu Asp Leu Ser Phe Arg Ser Tyr Ile Lys
1250 1255 1260

Glu Asn Leu Cys Lys Lys Phe Lys Ala Asp Glu Ile Gly Glu Lys
1265 1270 1275

Glu Phe Tyr Asp Leu Leu Gln Lys Lys Asn Leu Glu Ile Tyr Asp
1280 1285 1290

Met	Leu	Leu	Thr	Lys	Ile	Lys	Asp	Thr	Ile	Tyr	Asn	Lys	Arg	Pro
	1295					1300					1305			
Asn	Ser	Thr	Thr	Leu	Gly	Met	Leu	Thr	Lys	Gly	Arg	Tyr	Glu	Phe
	1310					1315					1320			
Ile	Asn	Leu	Lys	Pro	Lys	Asp	Gln	Ile	Ile	Val	Met	Leu	Glu	Ile
	1325					1330					1335			
Leu	Lys	Leu	Phe	Cys	Thr	Thr	Arg	Glu	Ala	Ile	Asp	Leu	Gly	Leu
	1340					1345					1350			
Ile	Lys	Gly	Lys	Pro	Ala	Ala	Gly	Val	Ala	Thr	Leu	Gly	Lys	Lys
	1355					1360					1365			
Ile	Ser	Asn	Leu	Asp	Asn	Cys	Ile	Leu	Ile	Tyr	Gln	Ser	Ile	Thr
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Gly	Ile	Phe	Glu	Lys	Arg	Ile	Asp	Leu	Leu	Lys	Val			
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<213> Treponema denticola

<400> 138

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			20					25					30		
Ala	Asn	Arg	Lys	Asp	Leu	Trp	Gly	Met	Arg	Cys	Phe	Glu	Thr	Ala	Glu
		35					40					45			
Thr	Ala	Glu	Val	Arg	Arg	Leu	His	Arg	Gly	Ala	Arg	Arg	Arg	Ile	Glu
	50					55					60				
Arg	Arg	Lys	Lys	Arg	Ile	Lys	Leu	Leu	Gln	Glu	Leu	Phe	Ser	Gln	Glu
65					70					75					80
Ile	Ala	Lys	Ile	Asp	Glu	Gly	Phe	Phe	Gln	Arg	Met	Lys	Glu	Ser	Pro
				85					90					95	
Phe	Tyr	Ala	Glu	Asp	Lys	Thr	Ile	Leu	Gln	Glu	Asn	Thr	Leu	Phe	Asn
			100					105					110		
Asp	Lys	Asp	Phe	Thr	Asp	Lys	Thr	Tyr	His	Lys	Ala	Tyr	Pro	Thr	Ile
		115					120					125			
Asn	His	Leu	Ile	Lys	Ala	Trp	Ile	Glu	Asn	Lys	Val	Lys	Pro	Asp	Pro
	130					135					140				
Arg	Leu	Leu	Tyr	Leu	Ala	Cys	His	Asn	Ile	Ile	Lys	Lys	Arg	Gly	His
145					150					155					160
Phe	Leu	Phe	Glu	Gly	Asp	Phe	Asp	Ser	Glu	Asn	Gln	Phe	Asp	Thr	Ser
				165					170					175	
Ile	Gln	Ala	Leu	Phe	Glu	Tyr	Leu	Asn	Glu	Asp	Met	Glu	Val	Asp	Ile
			180					185					190		
Asp	Ala	Asp	Ser	Gln	Lys	Val	Lys	Glu	Ile	Leu	Lys	Asp	Ser	Ser	Leu
		195					200					205			
Lys	Asn	Ser	Glu	Lys	Gln	Ser	Arg	Leu	Asn	Lys	Ile	Leu	Gly	Leu	Lys
	210					215					220				
Pro	Ser	Asp	Lys	Gln	Lys	Lys	Ala	Ile	Thr	Asn	Leu	Ile	Ser	Gly	Asn
225					230					235					240
Lys	Ile	Asn	Phe	Ala	Asp	Leu	Tyr	Asp	Asn	Pro	Asp	Leu	Lys	Asp	Ala
				245					250					255	
Glu	Lys	Asn	Ser	Ile	Ser	Phe	Ser	Lys	Asp	Asp	Phe	Asp	Ala	Leu	Ser
			260					265					270		

Asp	Asp	Leu 275	Ala	Ser	Ile	Leu	Gly 280	Asp	Ser	Phe	Glu	Leu 285	Leu	Leu	Lys
Ala	Lys 290	Ala	Val	Tyr	Asn	Cys 295	Ser	Val	Leu	Ser	Lys 300	Val	Ile	Gly	Asp
Glu 305	Gln	Tyr	Leu	Ser	Phe 310	Ala	Lys	Val	Lys	Ile 315	Tyr	Glu	Lys	His	Lys 320
Thr	Asp	Leu	Thr	Lys 325	Leu	Lys	Asn	Val	Ile 330	Lys	Lys	His	Phe	Pro 335	Lys
Asp	Tyr	Lys	Lys 340	Val	Phe	Gly	Tyr	Asn 345	Lys	Asn	Glu	Lys	Asn 350	Asn	Asn
Asn	Tyr	Ser 355	Gly	Tyr	Val	Gly	Val 360	Cys	Lys	Thr	Lys	Ser 365	Lys	Lys	Leu
Ile	Ile 370	Asn	Asn	Ser	Val	Asn 375	Gln	Glu	Asp	Phe	Tyr 380	Lys	Phe	Leu	Lys
Thr 385	Ile	Leu	Ser	Ala	Lys 390	Ser	Glu	Ile	Lys	Glu 395	Val	Asn	Asp	Ile	Leu 400
Thr	Glu	Ile	Glu	Thr 405	Gly	Thr	Phe	Leu	Pro 410	Lys	Gln	Ile	Ser	Lys 415	Ser
Asn	Ala	Glu	Ile 420	Pro	Tyr	Gln	Leu	Arg 425	Lys	Met	Glu	Leu	Glu 430	Lys	Ile
Leu	Ser	Asn 435	Ala	Glu	Lys	His	Phe 440	Ser	Phe	Leu	Lys	Gln 445	Lys	Asp	Glu
Lys	Gly 450	Leu	Ser	His	Ser	Glu 455	Lys	Ile	Ile	Met	Leu 460	Leu	Thr	Phe	Lys
Ile 465	Pro	Tyr	Tyr	Ile	Gly 470	Pro	Ile	Asn	Asp	Asn 475	His	Lys	Lys	Ser	Phe 480
Pro	Asp	Arg	Cys	Trp 485	Val	Ile	Lys	Lys	Glu 490	Lys	Ser	Pro	Ser	Gly 495	Lys
Thr	Thr	Pro	Trp 500	Asn	Phe	Phe	Asp	His 505	Ile	Asp	Lys	Asp	Lys 510	Thr	Ala
Glu	Ala	Phe 515	Ile	Thr	Ser	Arg	Thr 520	Asn	Phe	Cys	Thr	Tyr 525	Leu	Val	Gly
Glu	Ser 530	Val	Leu	Pro	Lys	Ser 535	Ser	Leu	Leu	Tyr	Ser 540	Glu	Tyr	Thr	Val
Leu 545	Asn	Glu	Ile	Asn	Asn 550	Leu	Gln	Ile	Ile	Ile 555	Asp	Gly	Lys	Asn	Ile 560
Cys	Asp	Ile	Lys	Leu 565	Lys	Gln	Lys	Ile	Tyr 570	Glu	Glu	Leu	Phe	Lys 575	Lys
Tyr	Lys	Lys	Ile 580	Thr	Gln	Lys	Gln	Ile 585	Ser	Thr	Phe	Ile	Lys 590	His	Glu
Gly	Ile	Cys 595	Asn	Lys	Thr	Asp	Glu 600	Val	Ile	Ile	Leu	Gly 605	Ile	Asp	Lys
Glu	Cys 610	Thr	Ser	Ser	Leu	Lys 615	Ser	Tyr	Ile	Glu	Leu 620	Lys	Asn	Ile	Phe
Gly 625	Lys	Gln	Val	Asp	Glu 630	Ile	Ser	Thr	Lys	Asn 635	Met	Leu	Glu	Glu	Ile 640
Ile	Arg	Trp	Ala	Thr 645	Ile	Tyr	Asp	Glu	Gly 650	Glu	Gly	Lys	Thr	Ile 655	Leu
Lys	Thr	Lys	Ile 660	Lys	Ala	Glu	Tyr	Gly	Lys	Tyr	Cys	Ser	Asp	Glu	Gln
Ile	Lys	Lys 675	Ile	Leu	Asn	Leu	Lys 680	Phe	Ser	Gly	Trp	Gly 685	Arg	Leu	Ser
Arg	Lys 690	Phe	Leu	Glu	Thr	Val 695	Thr	Ser	Glu	Met	Pro 700	Gly	Phe	Ser	Glu
Pro 705	Val	Asn	Ile	Ile	Thr 710	Ala	Met	Arg	Glu	Thr 715	Gln	Asn	Asn	Leu	Met 720

Glu Leu Leu Ser Ser Glu Phe Lys Phe Thr Glu Asn Ile Lys Lys Ile
735 740 745 750 755 760
Asn Ser Gly Phe Glu Asp Ala Glu Lys Gln Phe Ser Tyr Asn Gly Leu
765 770 775 780
Val Lys Pro Leu Phe Leu Ser Pro Ser Val Lys Lys Met Leu Trp Gln
785 790 795 800
Thr Leu Lys Leu Val Lys Glu Ile Ser His Ile Thr Gln Ala Pro Pro
805 810 815 820
Lys Lys Ile Phe Ile Glu Met Ala Lys Gly Ala Glu Leu Glu Pro Ala
825 830 835 840
Arg Thr Lys Thr Arg Leu Lys Ile Leu Gln Asp Leu Tyr Asn Asn Cys
845 850 855 860
Lys Asn Asp Ala Asp Ala Phe Ser Ser Glu Ile Lys Asp Leu Ser Gly
865 870 875 880
Lys Ile Lys Ile Leu Glu Asp Asn Leu Ser Lys Met Ser Lys Asp Thr
885 890 895 900
Leu Tyr Tyr Thr Gln Leu Gly Lys Cys Met Tyr Cys Gly Lys Pro Ile
905 910 915 920
Glu Ile Gly His Val Phe Asp Thr Ser Asn Tyr Asp Ile Asp His Ile
925 930 935 940
Tyr Pro Gln Ser Lys Ile Lys Asp Asp Ser Ile Ser Asn Arg Val Leu
945 950 955 960
Val Cys Ser Ser Cys Asn Lys Asn Lys Glu Asp Lys Tyr Pro Leu Leu
965 970 975
Ser Glu Ile Gln Ser Lys Gln Arg Gly Phe Trp Asn Phe Leu Gln Arg
980 985 990
Asn Asn Phe Ile Ser Leu Glu Lys Leu Asn Arg Leu Thr Arg Thr Thr
995 1000 1005
Pro Ile Ser Asp Asp Glu Thr Ala Lys Phe Ile Ala Arg Gln Leu Val
1010 1015 1020
Glu Thr Arg Gln Ala Thr Lys Val Ala Ala Lys Val Leu Glu Lys Met
1025 1030 1035
Phe Pro Glu Thr Lys Ile Val Tyr Ser Lys Ala Glu Thr Val Ser Met
1040 1045 1050
Phe Arg Asn Lys Phe Asp Ile Ile Lys Cys Arg Glu Ile Asn Asp Phe
1055 1060 1065
His His Ala His Asp Ala Tyr Leu Asn Ile Val Val Gly Asn Val
1070 1075 1080
Tyr Asn Thr Lys Phe Thr Asn Asn Pro Trp Asn Phe Ile Lys Glu
1085 1090 1095
Lys Arg Asp Asn Pro Lys Ile Ala Asp Thr Tyr Asn Tyr Tyr Lys
1100 1105 1110
Val Phe Asp Tyr Asp Val Lys Arg Asn Asn Ile Thr Ala Trp Glu
1115 1120 1125
Lys Gly Lys Thr Ile Ile Thr Val Lys Asp Met Leu Lys Arg Asn
1130 1135 1140
Thr Pro Ile Tyr Thr Arg Gln Ala Ala Cys Lys Lys Gly Gly Leu
1145 1150 1155
Phe Asp Gln Thr Ile Met Lys Lys Gly Leu Gly Gln His Pro Leu
1160 1165 1170
Lys Lys Glu Gly Ala Phe Ser Asn Ile Ser Lys Tyr Gly Gly Tyr
1175 1180 1185
Asn Lys Val Ser Ala Ala Tyr Thr Val Leu Ile Glu Tyr Glu Glu
1190 1195 1200
Lys Gly Asn Lys Ile Arg Ser Leu Glu Thr Ile Pro Leu Tyr Leu
1205 1210 1215

Val Lys Asp Ile Gln Lys Asp Gln Asp Val Leu Lys Ser Tyr Leu
1160 1165 1170

Thr Asp Leu Leu Gly Lys Lys Glu Ile Lys Ile Leu Val Pro Lys
1175 1180 1185

Ile Lys Ile Asn Ser Leu Leu Lys Ile Asn Gly Phe Pro Cys His
1190 1195 1200

Ile Thr Gly Lys Thr Gly Asp Ser Phe Val Leu Arg Pro Ala Val
1205 1210 1215

Gln Phe Cys Cys Ser Asn Asp Glu Val Leu Tyr Phe Lys Lys Ile
1220 1225 1230

Ile Arg Phe Asn Glu Ile Arg Ser Gln Arg Glu Lys Met Gly Lys
1235 1240 1245

Thr Ile Ser Pro Tyr Glu Asp Leu Ser Phe Arg Ser Tyr Ile Lys
1250 1255 1260

Glu Asn Leu Cys Lys Lys Thr Lys Ala Asp Glu Ile Gly Glu Lys
1265 1270 1275

Glu Phe Tyr Asp Leu Leu Gln Lys Lys Asn Leu Glu Ile Tyr Asp
1280 1285 1290

Met Leu Leu Thr Lys His Lys Asp Thr Ile Tyr Asn Lys Arg Pro
1295 1300 1305

Asn Ser Thr Thr Leu Gly Met Leu Thr Lys Gly Arg Tyr Glu Phe
1310 1315 1320

Ile Asn Leu Lys Pro Lys Asp Gln Ile Ile Val Met Leu Glu Ile
1325 1330 1335

Leu Lys Leu Phe Cys Thr Thr Arg Glu Ala Ile Asp Leu Gly Leu
1340 1345 1350

Ile Lys Gly Lys Pro Ala Ala Gly Val Ala Thr Leu Gly Lys Lys
1355 1360 1365

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Gly Ile Phe Glu Lys Arg Ile Asp Leu Leu Lys Val
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<213> Treponema denticola

<400> 799

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

Thr Ala Glu Val Arg Arg Leu His Arg Gly Ala Arg Arg Arg Ile Glu
50 55 60

Arg Arg Lys Lys Arg Ile Lys Leu Leu Gln Glu Leu Phe Ser Gln Glu
65 70 75 80

Ile Ala Lys Ile Asp Glu Gly Phe Phe Gln Arg Met Lys Glu Ser Pro
85 90 95

Leu Tyr Ala Glu Asp Lys Thr Ile Leu Gln Glu Asn Thr Leu Phe Asn
100 105 110

Asp Lys Asp Phe Thr Asp Lys Thr Tyr His Lys Ala Tyr Pro Thr Ile
115 120 125

Asn His Leu Ile Lys Ala Trp Ile Glu Asn Lys Val Lys Pro Asp Pro
130 135 140
Arg Leu Leu Tyr Leu Ala Cys His Asn Ile Ile Lys Lys Arg Gly His
145 150 155 160
Phe Leu Phe Glu Gly Asp Phe Asp Ser Glu Asn Gln Phe Asp Thr Ser
165 170 175
Ile Gln Ala Leu Phe Glu Tyr Leu Arg Glu Asp Met Glu Leu Asp Ile
180 185 190
Asp Ala Asp Ser Gln Lys Val Lys Glu Ile Leu Lys Asp Ser Ser Leu
195 200 205
Lys Asn Ser Glu Lys Gln Ser Arg Leu Asn Lys Met Leu Gly Leu Lys
210 215 220
Pro Ser Asp Lys Lys Ala Ile Thr Asn Leu Ile Ser Gly Asn
225 230 235 240
Lys Ile Asn Phe Ala Asp Leu Tyr Asp Asn Pro Asp Leu Lys Asp Ala
245 250 255
Glu Lys Asn Ser Ile Ser Phe Ser Lys Asp Phe Asp Ala Leu Ser
260 265 270
Asp Asp Leu Ala Ser Ile Leu Gly Asp Ser Phe Glu Leu Leu Leu Lys
275 280 285
Ala Lys Ala Val Tyr Asn Cys Ser Val Leu Ser Lys Val Ile Gly Asp
290 295 300
Glu Gln Tyr Leu Ser Phe Ala Lys Val Lys Ile Tyr Glu Lys His Lys
305 310 315 320
Thr Asp Leu Thr Lys Leu Lys Asn Val Ile Lys Lys His Phe Pro Lys
325 330 335
Asp Tyr Lys Lys Val Phe Gly Tyr Asn Lys Asn Glu Asn Asn
340 345 350
Asn Tyr Ser Ala Tyr Val Gly Val Cys Lys Ile Thr His Lys Lys Leu
355 360 365
Val Ile Lys Asn Ser Ala Lys Ser Glu Asp Phe Tyr Lys Phe Leu Lys
370 375 380
Thr Ile Leu Ser Ala Lys Ser Glu Ile Lys Glu Val Asn Asp Ile Leu
385 390 395 400
Thr Glu Ile Glu Thr Gly Thr Phe Leu Pro Lys Gln Ile Ser Lys Ser
405 410 415
Asn Ala Glu Ile Pro Tyr Gln Leu Arg Lys Met Glu Leu Glu Lys Ile
420 425 430
Leu Ser Asn Ala Glu Lys His Phe Ser Phe Leu Lys Gln Lys Asp Glu
435 440 445
Lys Gly Leu Ser His Ser Glu Lys Ile Ile Met Leu Leu Thr Phe Lys
450 455 460
Ile Pro Tyr Tyr Ile Gly Pro Ile Asn Asp Asn His Lys Lys Ser Phe
465 470 475 480
Pro Asp Arg Cys Trp Val Val Lys Lys Glu Lys Ser Pro Ser Gly Lys
485 490 495
Thr Thr Pro Trp Asn Phe Phe Asp His Ile Asp Lys Glu Lys Thr Ala
500 505 510
Glu Glu Phe Ile Thr Ser Arg Thr Asn Phe Cys Thr Tyr Leu Ile Gly
515 520 525
Glu Ser Val Leu Pro Lys Ser Ser Leu Leu Tyr Ser Glu Tyr Thr Val
530 535 540
Leu Asn Glu Ile Asn Asn Leu Ile Ile Ile Asp Gly Lys Asn Ile
545 550 555 560
Cys Asp Ile Lys Leu Lys Thr Lys Ile Tyr Glu Glu Leu Phe Lys Lys
565 570 575

Tyr Lys Lys Ile Thr Gln Lys Gln Ile Ser Thr Phe Ile Lys His Glu
580 585 590
Gly Ile Cys Asn Lys Thr Asp Glu Val Ile Ile Leu Gly Ile Asp Lys
595 600
Glu Cys Thr Ser Ser Leu Lys Ser Tyr Ile Glu Leu Lys Asn Ile Phe
610 615 620
Gly Lys Gln Val Asp Glu Ile Ser Thr Lys Asn Met Leu Glu Glu Ile
625 630 640
Ile Arg Trp Ala Thr Ile Tyr Asp Glu Gly Glu Gly Lys Thr Ile Leu
645 650 655
Lys Thr Lys Ile Lys Ala Glu Tyr Gly Lys Tyr Cys Ser Asp Glu Gln
660 665 670
Ile Lys Lys Phe Leu Asn Leu Lys Phe Ser Gly Trp Gly Arg Leu Ser
675 680
Arg Lys Phe Leu Glu Thr Val Lys Met Met Pro Gly Phe Ser Glu
690 695 700
Pro Val Asn Ile Ile Thr Ala Met Arg Glu Thr Gln Asn Asn Leu Met
705 710 715 720
Glu Leu Leu Ser Ser Glu Phe Lys Phe Thr Glu Asn Ile Lys Lys Ile
725 730 735
Asn Ser Gly Phe Glu Asp Ala Glu Lys Gln Phe Ser Tyr Asn Gly Leu
740 745 750
Val Lys Pro Leu Phe Leu Ser Pro Ser Val Lys Lys Met Leu Trp Gln
755 760 765
Thr Leu Lys Leu Val Lys Glu Ile Ser His Ile Thr Gln Ala Pro Pro
770 775 780
Lys Lys Ile Phe Ile Glu Met Ala Lys Gly Ala Glu Leu Glu Pro Ala
785 790 795 800
Arg Thr Lys Thr Arg Leu Lys Ile Leu Gln Asp Leu Tyr Ser Ser Cys
805 810 815
Lys Asn Asp Ala Asp Ala Phe Ser Ser Glu Ile Gln Tyr Leu Ser Gly
820 825 830
Lys Ile Glu Asn Glu Asp Asn Leu Arg Leu Arg Ser Asp Lys Leu Tyr
835 840 845
Leu Tyr Tyr Thr Gln Leu Gly Lys Cys Met Tyr Cys Gly Lys Pro Ile
850 855 860
Glu Ile Gly His Val Phe Asp Thr Ser Asn Tyr Asp Ile Asp His Ile
865 870 875 880
Tyr Pro Gln Ser Lys Ile Lys Asp Asp Ser Ile Ser Asn Arg Val Leu
885 890 895
Val Cys Ser Ser Cys Asn Lys Asn Lys Glu Asp Lys Tyr Pro Leu Lys
900 905 910
Ala Glu Ile Gln Ser Lys Gln Arg Gly Phe Trp Asn Phe Leu Gln Arg
915 920 925
Asn Asn Phe Ile Ser Leu Glu Lys Leu Asn Arg Leu Thr Arg Thr Ser
930 935 940
Pro Ile Ser Asp Asp Glu Thr Ala Lys Phe Ile Ala Arg Gln Leu Val
945 950 955 960
Glu Thr Arg Gln Ala Thr Lys Val Ala Ala Lys Val Leu Glu Lys Met
965 970 975
Phe Pro Glu Thr Lys Ile Val Tyr Ser Lys Ala Glu Thr Val Ser Met
980 985 990
Phe Asp Asn Lys Phe Asp Ile Ile Lys Cys Arg Glu Ile Asn Asp Phe
995 1000 1005
His His Ala His Asp Ala Tyr Leu Asn Ile Val Val Gly Asn Val
1010 1015 1020

Tyr Asn Thr Lys Phe Thr Asn Asn Pro Trp Asn Phe Ile Lys Glu
1025 1030 1035
Lys Arg Asp Asn Pro Lys Ile Ala Asp Thr Tyr Asn Tyr Tyr Lys
1040 1045 1050
Val Phe Asp Tyr Asp Val Lys Arg Asn Asn Ile Thr Ala Trp Glu
1055 1060 1065
Lys Gly Lys Thr Ile Ile Thr Val Lys Asp Met Leu Lys Arg Asn
1070 1075 1080
Thr Pro Ile Tyr Thr Arg Gln Ala Ala Lys Lys Lys Gly Glu Leu
1085 1090 1095
Phe Asn Gln Thr Ile Met Lys Lys Gly Leu Gly Gln Ala Pro Leu
1100 1105 1110
Lys Lys Glu Gly Pro Leu Ser Asn Ile Ser Lys Tyr Gly Gly Tyr
1115 1120 1125
Asn Lys Val Ser Ala Ala Tyr Thr Val Leu Val Glu Tyr Thr Leu
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Lys Gly Ser Lys Ile Arg Ser Leu Glu Thr Ile Pro Leu Tyr Leu
1145 1150 1155
Val Lys Asp Ile Gln Lys Asn Gly Leu Lys Ser Tyr Leu
1160 1165 1170
Thr Asn Gln Ile Gly Lys Leu Ile Pro Lys
1175 1180
Ile Lys Ile Asn Ser Leu Leu Lys Ile Asn Gly Phe Pro Cys His
1190 1195 1200
Ile Thr Gly Lys Met Gly Glu Ala Phe Val Leu Arg Pro Ala Val
1205 1210 1215
Gln Phe Cys Cys Ser Asn Asp Glu Ala Leu Tyr Phe Lys Lys Ile
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Ile Arg Phe Asn Glu Ile Arg Lys Gln Arg Glu Lys Met Gly Lys
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Thr Ile Ser Pro Tyr Glu Asp Leu Ser Phe Arg Ser Tyr Ile Lys
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Asp Asn Leu Cys Lys Lys Thr Lys Ala Asp Glu Ile Glu Glu Lys
1265 1270 1275
Glu Phe Tyr Asp Leu Leu Gln Lys Lys Asn Leu Glu Ile Tyr Asp
1280 1285 1290
Met Leu Leu Thr Lys His Lys Asp Thr Ile Tyr Lys Lys Arg Pro
1295 1300 1305
Asn Ser Ala Thr Ile Asp Ile Leu Val Lys Gly Lys Glu Lys Phe
1310 1315 1320
Lys Ser Leu Ile Ile Glu Asn Gln Phe Glu Val Ile Leu Glu Ile
1325 1330 1335
Leu Lys Leu Phe Ser Ala Thr Arg Asn Val Ser Asp Leu Gln His
1340 1345 1350
Ile Gly Gly Ser Lys Asn Ala Gly Asn Ala Arg Val Gly Asn Lys
1355 1360 1365
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Gly Ile Phe Glu Lys Arg Ile Asp Leu Leu Lys Ile
1385 1390 1395

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<400> 80

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Ala	Asn	Arg 35	Lys	Asp	Leu	Trp	Gly 40	Met	Arg	Cys	Phe	Glu 45	Thr	Ala	Glu
Thr	Ala 50	Glu	Val	Arg	Arg	Leu 55	His	Arg	Gly	Ala	Arg 60	Arg	Arg	Ile	Glu
Arg 65	Arg	Lys	Lys	Arg	Ile 70	Lys	Leu	Leu	Gln	Glu 75	Leu	Phe	Ser	Gln	Glu 80
Ile	Ala	Lys	Ile	Asp	Glu	Gly	Phe	Phe	Gln	Arg	Met	Lys	Glu	Ser	Pro
				85					90					95	
Leu	Tyr	Ala	Glu 100	Asp	Lys	Thr	Ile	Leu 105	Gln	Glu	Asn	Thr	Leu 110	Phe	Asn
Asp	Lys	Asn 115	Phe	Thr	Asp	Lys	Thr 120	Tyr	His	Lys	Ala	Tyr 125	Pro	Thr	Ile
Asn	His 130	Leu	Ile	Lys	Ala	Trp 135	Ile	Glu	Asn	Lys	Val 140	Lys	Pro	Asp	Pro
Arg 145	Leu	Leu	Tyr	Leu	Ala 150	Cys	His	Asn	Ile	Ile 155	Lys	Lys	Arg	Gly	His 160
Phe	Leu	Phe	Glu	Gly 165	Asp	Phe	Asp	Ser	Glu 170	Asn	Gln	Phe	Asp	Thr 175	Ser
Ile	Gln	Ala	Leu 180	Phe	Glu	Tyr	Leu	Arg 185	Glu	Asp	Met	Glu	Val 190	Asp	Ile
Asp	Ala	Asp 195	Ser	Gln	Lys	Val	Lys 200	Glu	Ile	Leu	Lys	Asp 205	Ser	Ser	Leu
Lys	Asn 210	Ser	Glu	Lys	Gln	Ser 215	Arg	Leu	Asn	Lys	Met 220	Leu	Gly	Leu	Lys
Pro 225	Ser	Asp	Lys	Gln	Lys 230	Lys	Ala	Ile	Thr	Asn 235	Leu	Ile	Ser	Gly	Asn 240
Lys	Ile	Asn	Phe	Ala 245	Asp	Leu	Tyr	Asp	Asn 250	Pro	Asp	Leu	Lys	Asp 255	Ala
Glu	Lys	Asn	Ser 260	Ile	Ser	Phe	Ser	Lys 265	Asp	Asp	Phe	Asp	Ala 270	Leu	Ser
Asp	Asp	Leu 275	Ala	Ser	Ile	Leu	Gly 280	Asp	Ser	Phe	Glu	Leu 285	Leu	Leu	Lys
Ala	Lys 290	Ala	Val	Tyr	Asn	Cys 295	Ser	Val	Leu	Ser	Lys 300	Val	Ile	Gly	Asp
Glu 305	Gln	Tyr	Leu	Ser	Phe 310	Ala	Lys	Val	Lys	Ile 315	Tyr	Glu	Lys	His	Lys 320
Thr	Asp	Leu	Thr	Lys 325	Leu	Lys	Asn	Val	Ile 330	Lys	Lys	His	Phe	Pro 335	Lys
Asp	Tyr	Lys	Lys 340	Val	Phe	Gly	Tyr	Asn 345	Lys	Asn	Glu	Lys	Asn 350	Asn	Asn
Asn	Tyr	Ser 355	Gly	Tyr	Val	Gly	Val 360	Cys	Lys	Thr	Lys	Ser 365	Lys	Lys	Leu
Ile	Ile 370	Asn	Asn	Ser	Val	Asn 375	Gln	Glu	Asp	Phe	Tyr 380	Lys	Phe	Leu	Lys
Thr 385	Ile	Leu	Ser	Ala	Lys 390	Ser	Glu	Ile	Lys	Glu 395	Val	Asn	Asp	Ile	Leu 400
Thr	Glu	Ile	Glu	Thr 405	Gly	Thr	Phe	Leu	Pro 410	Lys	Gln	Ile	Ser	Lys 415	Ser
Asn	Ala	Glu	Ile 420	Pro	Tyr	Gln	Leu	Arg 425	Lys	Met	Glu	Leu	Glu 430	Lys	Ile
Leu	Ser	Asn 435	Ala	Glu	Lys	His	Phe 440	Ser	Phe	Leu	Lys	Gln 445	Lys	Asp	Glu

Lys	Gly 450	Leu	Ser	His	Ser	Glu 455	Lys	Ile	Ile	Met	Leu 460	Leu	Thr	Phe	Lys
Ile 465	Pro	Tyr	Tyr	Ile	Gly 470	Pro	Ile	Asn	Asn	Asn 475	His	Lys	Lys	Ser	Phe 480
Pro	Asp	Arg	Cys	Phe 485	Val	Val	Lys	Lys	Glu 490	Lys	Ser	Pro	Ser	Gly 495	Lys
Thr	Thr	Pro	Tyr 500	Asn	Phe	Phe	Asp	His 505	Ile	Asn	Lys	Glu	Lys 510	Thr	Ala
Glu	Glu	Phe 515	Ile	Thr	Ser	Arg	Thr 520	Asn	Phe	Cys	Thr	Tyr 525	Leu	Ile	Gly
Glu	Ser 530	Val	Leu	Pro	Lys	Asn 535	Ser	Leu	Leu	Tyr	Ser 540	Glu	Tyr	Thr	Val
Leu 545	Asn	Glu	Ile	Asn	Asn 550	Leu	Gln	Ile	Ile	Ile 555	Asp	Gly	Lys	Asn	Ile 560
Cys	Asp	Thr	Lys	Leu 565	Lys	Gln	Lys	Ile	Tyr 570	Glu	Glu	Leu	Phe	Lys 575	Lys
Tyr	Lys	Lys	Ile 580	Thr	Gln	Lys	Gln	Ile 585	Ser	Thr	Phe	Ile	Lys 590	His	Glu
Gly	Ile	Cys 595	Asn	Lys	Thr	Asp	Glu 600	Val	Ile	Ile	Leu	Gly 605	Ile	Asp	Lys
Glu	Cys 610	Thr	Ser	Ser	Leu	Lys 615	Ser	Tyr	Ile	Glu	Leu 620	Lys	Asn	Ile	Phe
Gly 625	Lys	Gln	Val	Asp	Glu 630	Ile	Ser	Thr	Lys	Asn 635	Met	Leu	Glu	Glu	Ile 640
Ile	Arg	Trp	Ala	Thr 645	Ile	Tyr	Asp	Glu	Gly 650	Glu	Gly	Lys	Thr	Ile 655	Leu
Lys	Thr	Lys	Ile 660	Lys	Ala	Glu	Tyr	Gly 665	Lys	Tyr	Cys	Ser	Asp 670	Glu	Gln
Ile	Lys	Lys 675	Ile	Leu	Asn	Leu	Lys 680	Phe	Ser	Gly	Trp	Gly 685	Arg	Leu	Ser
Arg	Lys 690	Phe	Leu	Glu	Thr	Val 695	Thr	Ser	Glu	Met	Pro 700	Gly	Phe	Ser	Glu
Pro 705	Val	Asn	Ile	Ile	Thr 710	Ala	Met	Arg	Glu	Thr 715	Gln	Asn	Asn	Leu	Met 720
Glu	Leu	Leu	Ser	Ser 725	Glu	Phe	Lys	Phe	Thr 730	Glu	Asn	Ile	Lys	Lys 735	Ile
Asn	Ser	Gly	Phe 740	Glu	Asp	Val	Glu	Lys 745	Gln	Phe	Ser	Tyr	Asp 750	Gly	Leu
Val	Lys	Pro 755	Leu	Phe	Leu	Ser	Pro 760	Ser	Val	Lys	Lys	Met 765	Leu	Trp	Gln
Thr	Leu 770	Lys	Leu	Val	Lys	Glu 775	Ile	Ser	His	Ile	Thr 780	Gln	Ala	Pro	Pro
Lys 785	Lys	Ile	Phe	Ile	Glu 790	Met	Ala	Lys	Gly	Ala 795	Glu	Leu	Asp	Pro	Val 800
Arg	Thr	Lys	Thr	Arg 805	Leu	Lys	Ile	Leu	Gln 810	Asp	Leu	Tyr	Asn	Asn 815	Cys
Lys	Asn	Asp	Ala 820	Asp	Ala	Phe	Ser	Ser 825	Glu	Ile	Lys	Asp	Leu 830	Ser	Gly
Lys	Ile	Glu 835	Asn	Glu	Asp	Asn	Leu 840	Arg	Leu	Arg	Ser	Asp 845	Lys	Leu	Tyr
Leu	Tyr 850	Tyr	Thr	Gln	Leu	Gly 855	Lys	Cys	Met	Tyr	Cys 860	Gly	Lys	Pro	Ile
Glu 865	Ile	Gly	His	Val	Phe 870	Asp	Thr	Ser	Asn	Tyr 875	Asp	Ile	Asp	His	Ile 880
Tyr	Pro	Gln	Ser	Lys 885	Ile	Lys	Asp	Asp	Ser 890	Ile	Ser	Asn	Arg	Val 895	Leu

Val Cys Ser Ser Cys Asn Lys Asn Lys Glu Asp Lys Tyr Pro Leu Lys
905 910
Ala Glu Ile Gln Ser Lys Gln Arg Gly Phe Trp Asn Phe Leu Gln Arg
915 920 925
Asn Asn Phe Ile Ser Leu Glu Lys Phe Asn Arg Leu Thr Arg Ala Thr
930 935 940
Pro Ile Ser Asp Asp Glu Thr Ala Lys Phe Ile Ala Arg Gln Leu Val
945 950 955 960
Glu Thr Arg Gln Ala Thr Lys Val Ala Ala Arg Val Leu Glu Lys Met
965 970 975
Phe Pro Glu Thr Lys Ile Val Tyr Ser Lys Ala Glu Thr Val Ser Met
980 985 990
Phe Arg Asn Lys Phe Asp Ile Val Lys Cys Arg Glu Ile Asn Asp Phe
995 1000 1005
His His Ala His Asp Ala Tyr Leu Asn Ile Val Val Gly Asn Val
1010 1015 1020
Tyr Asn Thr Lys Phe Thr Asn Asn Leu Trp Asn Phe Ile Lys Glu
1025 1030 1035
Lys Arg Asp Asn Pro Lys Ile Ala Asp Thr Tyr Asn Tyr Tyr Lys
1040 1045 1050
Val Phe Asp Tyr Asp Val Lys Arg Asn Asn Ile Thr Ala Trp Glu
1055 1060 1065
Lys Gly Lys Thr Ile Ile Thr Val Lys Asp Met Leu Lys Arg Asn
1070 1075 1080
Thr Pro Ile Tyr Thr Arg Gln Ala Ala Cys Lys Lys Gly Gly Leu
1085 1090 1095
Phe Asp Gln Thr Ile Met Lys Lys Gly Leu Gly Gln His Pro Leu
1100 1105 1110
Lys Lys Glu Gly Pro Phe Ser Asn Ile Ser Lys Tyr Gly Gly Tyr
1115 1120 1125
Asn Lys Val Ser Ala Ala Tyr Thr Leu Leu Ile Glu Tyr Glu Glu
1130 1135 1140
Lys Gly Asn Lys Ile Arg Ser Leu Glu Thr Ile Pro Leu Tyr Leu
1145 1150 1155
Val Lys Asp Ile Gln Lys Asp Gln Asp Val Leu Lys Ser Tyr Leu
1160 1165 1170
Thr Asp Leu Leu Gly Lys lys Glu Phe Lys Ile Leu Val Pro Lys
1175 1180 1185
Ile Lys Ile Asn Ser Leu Leu Lys Ile Asn Gly Phe Pro Cys His
1190 1195 1200
Ile Thr Gly Lys Thr Asn Asp Ser Phe Leu Leu Arg Pro Ala Val
1205 1210 1215
Gln Phe Cys Cys Ser Asn Asp Glu Val Leu Tyr Phe Lys Lys Ile
1220 1225 1230
Ile Arg Phe Ser Glu Ile Arg Ser Gln Arg Glu Lys Ile Gly Lys
1235 1240 1245
Thr Ile Ser Pro Tyr Glu Asp Leu Ser Phe Arg Ser Tyr Ile Lys
1250 1255 1260
Glu Asn Leu Cys Lys Lys Thr Lys Asn Asp Glu Ile Gly Glu Lys
1265 1270 1275
Glu Phe Tyr Asp Leu Leu Gln Lys Lys Asn Leu Glu Ile Tyr Asp
1280 1285 1290
Met Leu Leu Thr Lys Ile Lys Asp Thr Ile Tyr Lys Lys Asp Pro
1295 1300 1305
Asn Ser Ala Thr Ile Asp Ile Leu Val Lys Gly Lys Glu Lys Phe
1310 1315 1320

Lys Ser Leu Ile Ile Glu Asn Glu Phe Glu Val Ile Leu Glu Ile
1310 1315 1320 1325
Leu Lys Leu Phe Ser Ala Thr Arg Asn Val Ser Asp Leu Gln His
1330 1335 1340 1345
Ile Gly Gly Ser Lys Tyr Ser Gly Val Ala Lys Ile Gly Asn Lys
1350 1355 1360 1365
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Gly Ile Phe Glu Lys Arg Ile Asp Leu Leu Lys Val
1385 1390 1395

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Ala Asn Arg Lys Asp Leu Trp Gly Met Arg Cys Phe Glu Thr Ala Glu
35 40 45
Thr Ala Glu Val Arg Arg Leu His Arg Gly Ala Arg Arg Arg Ile Glu
50 55 60
Arg Arg Lys Lys Arg Ile Lys Leu Leu Gln Glu Leu Phe Ser Gln Glu
65 70 75 80
Ile Ala Lys Thr Asp Glu Gly Phe Phe Gln Arg Met Lys Glu Ser Pro
85 90 95
Phe Tyr Ala Glu Asp Lys Thr Ile Leu Gln Glu Asn Ala Leu Phe Asn
100 105 110
Asp Arg Asp Phe Thr Asp Lys Thr Tyr His Lys Ala Tyr Pro Thr Ile
115 120 125
Asn His Leu Ile Lys Ala Trp Ile Glu Asn Lys Val Lys Pro Asp Pro
130 135 140
Arg Leu Leu Tyr Leu Ala Cys His Asn Ile Ile Lys Lys Arg Gly His
145 150 155 160
Phe Leu Phe Glu Gly Asp Phe Asp Ser Glu Asn Gln Phe Asp Thr Ser
165 170 175
Ile Gln Ala Phe Phe Glu Tyr Leu Arg Glu Asp Met Glu Val Asp Ile
180 185 190
Asp Ala Asp Ser Gln Lys Ile Lys Glu Ile Leu Lys Asp Ser Ser Leu
195 200 205
Lys Asn Ser Glu Lys Gln Ser Arg Leu Asn Lys Ile Leu Gly Leu Lys
210 215 220
Ser Ser Asp Lys Gln Lys Ser Lys Ile Thr Asn Leu Ile Ser Gly Asn
225 230 235 240
Lys Ile Asn Phe Ala Asp Leu Tyr Asp Asn Pro Asp Leu Lys Asp Ala
245 250 255
Glu Lys Asn Ser Ile Ser Phe Ser Lys Asp Asp Phe Asp Ala Leu Ser
260 265 270
Asp Asp Leu Ala Ser Ile Leu Gly Asp Ser Phe Glu Leu Leu Leu Lys
275 280 285
Ala Lys Ala Val Tyr Asn Cys Ser Val Leu Ser Lys Val Ile Gly Asp
290 295 300

Glu Gln Tyr Leu Ser Phe Ala Lys Val Lys Ile Tyr Glu Lys His Lys
305 310 315 320
Thr Asp Leu Thr Lys Leu Lys Asn Val Ile Lys Lys His Phe Pro Lys
325 330 335
Asp Tyr Lys Lys Val Phe Gly Tyr Asn Val Lys Asn Glu Lys Ile Thr Thr
340 345 350
Ile Thr Pro Asp Met
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Ala Asn Arg Lys Asp Leu Trp Gly Met Arg Cys Phe Glu Thr Ala Glu
35 40 45
Thr Ala Glu Val Arg Arg Leu Phe Arg Gly Ala Arg Arg Arg Ile Glu
50 55 60
Arg Arg Lys Lys Arg Ile Lys Leu Leu Gln Glu Leu Phe Ser Gln Glu
65 70 75 80
Ile Ala Lys Thr Asp Glu Gly Phe Phe Gln Arg Met Lys Glu Ser Phe
85 90 95
Phe Tyr Ala Glu Asp Lys Thr Ile Lys Ser Lys Tyr His Lys Ala Tyr
100 105 110
Asp Arg Asp Phe Thr Asp Lys Thr Tyr His Lys Ala Tyr Pro Thr Ile
115 120 125
Asn His Leu Ile Lys Ala Trp Ile Glu Asn Lys Val Lys Pro Asp Pro
130 135 140
Arg Leu Leu Tyr Leu Ala Cys His Asn Ile Ile Lys Lys Arg Gly His
145 150 155 160
Phe Leu Phe Glu Gly Asp Phe Asp Ser Glu Asn Gln Phe Asp Thr Ser
165 170 175
Ile Gln Ala Leu Phe Glu Tyr Leu Arg Glu Asp Met Glu Val Asp Ile
180 185 190
Asp Ala Asp Ser Gln Lys Val Lys Glu Ile Leu Lys Asp Ser Ser Leu
195 200 205
Lys Asn Ser Glu Lys Gln Lys Ser Arg Leu Asn Lys Met Leu Gly Leu Lys
210 215 220
Pro Ser Asp Lys Gln Lys Lys Ala Ile Thr Asn Leu Ile Ser Gly Asn
225 230 235 240
Lys Ile Asn Phe Ala Asp Leu Tyr Asp Asn Pro Asp Leu Lys Asp Ala
245 250 255
Glu Lys Asn Ser Ile Ser Phe Ser Lys Asp Asp Phe Asp Ala Leu Ser
260 265 270
Asp Asp Leu Ala Ser Ile Leu Gly Asp Ser Phe Glu Leu Leu Leu Lys
275 280 285
Ala Lys Ala Val Tyr Asn Cys Ser Val Leu Ser Lys Val Ile Gly Asp
290 295 300
Glu Gln Tyr Leu Ser Phe Ala Lys Val Lys Ile Tyr Glu Lys His Lys
305 310 315 320

Thr	Asp	Leu	Thr	Lys	Leu	Lys	Asn	Val	Ile	Lys	Lys	His	Phe	Pro	Asn
				325					330					335	
Asp	Tyr	Lys	Lys	Val	Phe	Gly	Tyr	Asn	Lys	Asn	Glu	Lys	Asn	Asn	Asn
			340					345					350		
Asn	Tyr	Ser	Ala	Tyr	Val	Gly	Val	Cys	Lys	Thr	Lys	Ser	Lys	Lys	Leu
		355					360					365			
Val	Ile	Asn	Asn	Thr	Val	Asn	Gln	Glu	Asp	Phe	Tyr	Lys	Phe	Leu	Lys
	370					375					380				
Pro	Ile	Leu	Leu	Ala	Lys	Ser	Glu	Ile	Lys	Glu	Val	Asn	Asp	Ile	Leu
385					390					395					400
Thr	Glu	Ile	Glu	Thr	Gly	Thr	Phe	Leu	Pro	Lys	Gln	Ile	Ser	Lys	Ser
				405					410					415	
Asn	Ala	Glu	Ile	Pro	Tyr	Gln	Leu	Arg	Lys	Met	Glu	Leu	Glu	Lys	Ile
			420					425					430		
Leu	Ser	Asn	Ala	Glu	Lys	His	Phe	Ser	Phe	Leu	Lys	Gln	Lys	Asp	Glu
		435					440					445			
Lys	Gly	Leu	Ser	His	Ser	Glu	Lys	Ile	Ile	Met	Leu	Leu	Thr	Phe	Lys
	450					455					460				
Ile	Pro	Tyr	Tyr	Ile	Gly	Pro	Ile	Asn	Asp	Asn	His	Lys	Lys	Ser	Phe
465					470					475					480
Pro	Asp	Arg	Cys	Trp	Val	Ile	Lys	Lys	Glu	Lys	Ser	Pro	Ser	Gly	Lys
				485					490					495	
Thr	Thr	Pro	Trp	Asn	Phe	Phe	Asp	His	Ile	Asp	Lys	Asp	Lys	Thr	Ala
			500					505					510		
Glu	Ala	Phe	Ile	Thr	Ser	Arg	Thr	Asn	Phe	Cys	Thr	Tyr	Leu	Val	Gly
		515					520					525			
Glu	Ser	Val	Leu	Pro	Lys	Asn	Ser	Leu	Leu	Tyr	Ser	Glu	Tyr	Thr	Val
	530					535					540				
Leu	Asn	Glu	Ile	Asn	Asn	Leu	Gln	Ile	Ile	Ile	Asp	Gly	Lys	Asn	Ile
545					550					555					560
Cys	Asp	Ile	Lys	Leu	Lys	Gln	Lys	Ile	Tyr	Glu	Glu	Leu	Phe	Lys	Lys
				565					570					575	
Tyr	Lys	Lys	Ile	Thr	Gln	Lys	Gln	Ile	Ser	Thr	Phe	Ile	Lys	His	Glu
			580					585					590		
Gly	Ile	Cys	Asn	Lys	Thr	Asp	Glu	Val	Ile	Ile	Leu	Gly	Ile	Asp	Lys
		595					600					605			
Glu	Cys	Thr	Ser	Ser	Leu	Lys	Ser	Tyr	Ile	Glu	Leu	Lys	Asn	Ile	Phe
	610					615					620				
Gly	Lys	Gln	Val	Asp	Glu	Ile	Ser	Thr	Lys	Asn	Met	Leu	Glu	Glu	Ile
625					630					635					640
Ile	Arg	Trp	Ala	Thr	Ile	Tyr	Asp	Glu	Gly	Glu	Gly	Lys	Thr	Ile	Leu
				645					650					655	
Lys	Thr	Lys	Ile	Lys	Ala	Glu	Tyr	Gly	Lys	Tyr	Cys	Ser	Asp	Glu	Gln
			660					665					670		
Ile	Lys	Lys	Ile	Leu	Asn	Leu	Lys	Phe	Ser	Gly	Trp	Gly	Arg	Leu	Ser
		675					680					685			
Arg	Lys	Phe	Leu	Glu	Thr	Val	Thr	Ser	Glu	Met	Pro	Gly	Phe	Ser	Glu
	690					695					700				
Pro	Val	Asn	Ile	Ile	Thr	Ala	Met	Arg	Glu	Thr	Gln	Asn	Asn	Leu	Met
705					710					715					720
Glu	Leu	Leu	Ser	Ser	Glu	Phe	Lys	Phe	Thr	Glu	Asn	Ile	Lys	Lys	Ile
				725					730					735	
Asn	Ser	Gly	Phe	Glu	Asp	Val	Glu	Lys	Gln	Phe	Ser	Tyr	Asp	Ser	Leu
			740					745					750		
Val	Lys	Pro	Leu	Phe	Leu	Ser	Pro	Ser	Val	Lys	Lys	Met	Leu	Trp	Gln
		755					760					765			

Thr	Leu	Lys	Leu	Val	Lys	Glu	Ile	Ser	His	Ile	Thr	Gln	Ala	Pro	Pro
	775					780					785				
Lys	Lys	Ile	Phe	Ile	Glu	Met	Ala	Lys	Gly	Ala	Glu	Leu	Asp	Pro	Val
790					795					800					805
Arg	Thr	Lys	Thr	Arg	Leu	Lys	Ile	Leu	Gln	Asp	Leu	Tyr	Asn	Asn	Cys
				810					815					820	
Lys	Asn	Asp	Ala	Asp	Ala	Phe	Ser	Ser	Glu	Ile	Lys	Asp	Leu	Ser	Gly
			825					830					835		
Lys	Ile	Glu	Asn	Glu	Asp	Asn	Leu	Arg	Leu	Arg	Ser	Asp	Lys	Leu	Tyr
		840					845					850			
Leu	Tyr	Tyr	Thr	Gln	Leu	Gly	Lys	Cys	Met	Tyr	Cys	Gly	Lys	Pro	Ile
	855					860					865				
Glu	Ile	Gly	Ala	Val	Phe	Asp	Thr	Ser	Asn	Tyr	Asp	Ile	Asp	His	Ile
870					875					880					885
Tyr	Pro	Gln	Ser	Lys	Ile	Lys	Asp	Asp	Ser	Ile	Ser	Asn	Arg	Val	Leu
				890					895					900	
Val	Cys	Ser	Ser	Cys	Asn	Lys	Asn	Lys	Glu	Asp	Lys	Tyr	Phe	Leu	Lys
			905					910					915		
Ala	Glu	Ile	Gln	Ser	Lys	Gln	Arg	Gly	Phe	Thr	Asn	Phe	Leu	Gln	Arg
		920					925					930			
Asn	Asn	Phe	Ile	Ser	Leu	Glu	Lys	Leu	Asn	Arg	Leu	Thr	Arg	Thr	Ser
	935					940					945				
Pro	Ile	Ser	Asp	Asp	Glu	Thr	Ala	Lys	Phe	Ile	Ala	Arg	Gln	Leu	Val
950					955					960					965
Glu	Thr	Arg	Gln	Ala	Thr	Lys	Val	Ala	Ala	Lys	Val	Leu	Glu	Lys	Met
				970					975					980	
Phe	Pro	Glu	Thr	Lys	Ile	Val	Tyr	Ser	Lys	Ala	Glu	Thr	Val	Ser	Met
			985					990					995		
Phe	Arg	Asn	Lys	Phe	Asp	Ile	Ile	Lys	Cys	Arg	Glu	Ile	Asn	Asp	Phe
		1000					1005								
His	His	Ala	His	Asp	Ala	Tyr	Leu	Asn	Ile	Val	Val	Gly	Asn	Val	
	1010					1015					1020				
Tyr	Asn	Thr	Lys	Phe	Thr	Asn	Asn	Pro	Trp	Asn	Phe	Ile	Lys	Glu	
	1025					1030					1035				
Lys	Arg	Asp	Asn	Pro	Lys	Ile	Ala	Asp	Thr	Tyr	Asn	Tyr	Tyr	Lys	
	1040					1045					1050				
Val	Phe	Asp	Tyr	Asp	Val	Lys	Arg	Asn	Asn	Ile	Thr	Ala	Trp	Glu	
	1055					1060					1065				
Lys	Gly	Lys	Thr	Ile	Ile	Thr	Val	Lys	Asp	Met	Leu	Lys	Arg	Asn	
	1070					1075					1080				
Thr	Pro	Ile	Tyr	Thr	Arg	Gln	Ala	Ala	Cys	Lys	Lys	Gly	Glu	Leu	
	1085					1090					1095				
Phe	Asn	Gln	Thr	Ile	Met	Lys	Lys	Gly	Leu	Gly	Gln	His	Pro	Leu	
	1100					1105					1110				
Lys	Lys	Glu	Gly	Pro	Leu	Ser	Asn	Ile	Ser	Lys	Tyr	Gly	Gly	Tyr	
	1115					1120					1125				
Asn	Lys	Val	Ser	Ala	Ala	Tyr	Tyr	Thr	Leu	Ile	Glu	Tyr	Glu	Glu	
	1130					1135					1140				
Lys	Gly	Ser	Lys	Ile	Arg	Ser	Leu	Glu	Thr	Ile	Pro	Leu	Tyr	Leu	
	1145					1150					1155				
Val	Lys	Asp	Ile	Gln	Lys	Asn	Lys	Asp	Gly	Leu	Lys	Ser	Tyr	Leu	
	1160					1165					1170				
Thr	Asp	Gln	Ile	Gly	Lys	Lys	Glu	Ile	Lys	Ile	Leu	Ile	Pro	Lys	
	1175					1180					1185				
Ile	Lys	Ile	Asn	Ser	Leu	Leu	Lys	Ile	Asn	Gly	Phe	Pro	Cys	His	
	1190					1195					1200				

Ile	Thr	Gly	Lys	Met	Gly	Glu	Ala	Phe	Val	Leu	Arg	Pro	Ala	Val
	1355					1370					1375			
Glu	Phe	Cys	Cys	Ser	Asn	Asp	Glu	Ala	Leu	Tyr	Phe	Lys	Lys	Ile
	1380					1385					1390			
Ile	Arg	Phe	Asn	Glu	Ile	Arg	Lys	Gln	Arg	Glu	Lys	Met	Gly	Lys
	1395					1400					1405			
Thr	Ile	Ser	Pro	Tyr	Glu	Asp	Leu	Ser	Phe	Arg	Ser	Tyr	Ile	Lys
	1410					1415					1420			
Asp	Asn	Leu	Cys	Lys	Lys	Thr	Lys	Ala	Asp	Glu	Ile	Glu	Glu	Lys
	1425					1430					1435			
Glu	Phe	Tyr	Asp	Leu	Leu	Gln	Lys	Lys	Asn	Leu	Glu	Ile	Tyr	Asp
	1440					1445					1450			
Met	Leu	Leu	Thr	Lys	His	Lys	Asp	Thr	Ile	Tyr	Lys	Lys	Arg	Pro
	1455					1460					1465			
Asn	Ser	Ala	Thr	Ile	Asp	Ile	Leu	Val	Lys	Gly	Lys	Glu	Lys	Phe
	1470					1475					1480			
Lys	Ser	Leu	Ile	Ile	Glu	Asn	Gln	Phe	Glu	Val	Ile	Leu	Glu	Ile
	1485					1490					1495			
Leu	Lys	Leu	Phe	Ser	Ala	Thr	Arg	Asn	Val	Ser	Asp	Leu	Gln	His
	1500					1505					1510			
Ile	Gly	Gly	Ser	Lys	Asn	Ala	Gly	Asn	Ala	Arg	Val	Gly	Asn	Lys
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Ile	Ser	Ser	Leu	Asp	Asn	Cys	Ile	Leu	Ile	Tyr	Gln	Ser	Ile	Thr
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Gly	Ile	Phe	Glu	Lys	Arg	Ile	Asp	Leu	Leu	Lys	Ile			
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<400> 803

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			20					25					30		
Leu	Glu	Pro	Ala	Arg	Thr	Lys	Thr	Arg	Leu	Lys	Ile	Leu	Gln	Asp	Leu
		35					40					45			
Tyr	Asn	Asn	Cys	Lys	Asn	Asp	Ala	Asp	Ala	Phe	Ser	Ser	Glu	Ile	Lys
	50					55					60				
Asp	Leu	Ser	Gly	Lys	Ile	Glu	Asn	Glu	Asp	Asn	Leu	Arg	Leu	Arg	Ser
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Asp	Lys	Leu	Tyr	Leu	Tyr	Tyr	Thr	Gln	Leu	Gly	Lys	Cys	Met	Tyr	Cys
				85					90					95	
Gly	Lys	Pro	Ile	Glu	Ile	Gly	His	Val	Phe	Asp	Thr	Ser	Asn	Tyr	Asp
			100					105					110		
Ile	Asp	His	Ile	Tyr	Pro	Gln	Ser	Lys	Ile	Lys	Asp	Asp	Ser	Ile	Ser
		115					120					125			
Asn	Arg	Val	Leu	Val	Cys	Ser	Ser	Cys	Asn	Lys	Asn	Lys	Glu	Asp	Lys
	130					135					140				
Tyr	Pro	Leu	Arg	Ser	Glu	Ile	Gln	Ser	Lys	Gln	Arg	Gly	Phe	Trp	Asn
145					150					155					160
Phe	Leu	Gln	Arg	Asn	Asn	Phe	Ile	Ser	Leu	Glu	Lys	Leu	Asn	Arg	Leu
				165					170					175	

Thr	Arg	Thr	Thr	Pro	Ile	Ser	Asp	Asp	Glu	Thr	Ala	Lys	Phe	Ile	Ala
			190					195					200		
Arg	Gln	Leu	Val	Glu	Thr	Arg	Gln	Ala	Thr	Lys	Val	Ala	Ala	Lys	Val
		205					210					215			
Leu	Glu	Lys	Met	Phe	Pro	Glu	Thr	Lys	Ile	Val	Tyr	Ser	Lys	Ala	Glu
	220					225					230				
Thr	Val	Ser	Met	Phe	Arg	Asn	Lys	Phe	Asp	Ile	Val	Lys	Lys	Arg	Glu
235					240					245					250
Ile	Asn	Asp	Phe	His	His	Ala	His	Asp	Ala	Tyr	Leu	Asn	Ile	Val	Val
				255					260					265	
Gly	Asn	Ile	Tyr	Asn	Thr	Lys	Phe	Thr	Asn	Asn	Pro	Trp	Asn	Phe	Ile
			270					275					280		
Lys	Glu	Lys	Arg	Asp	Asn	Pro	Lys	Ile	Ala	Asp	Thr	Tyr	Asn	Tyr	Tyr
		285					290					295			
Lys	Val	Phe	Asp	Tyr	Asp	Val	Lys	Arg	Asn	Asn	Ile	Thr	Ala	Trp	Glu
	300					305					310				
Lys	Gly	Lys	Thr	Ile	Ile	Thr	Val	Lys	Asp	Met	Leu	Lys	Arg	Asn	Thr
315					320					325					330
Pro	Ile	Tyr	Thr	Arg	Gln	Ala	Ala	Cys	Lys	Lys	Gly	Gly	Leu	Phe	Asp
				335					340					345	
Gln	Thr	Ile	Met	Lys	Lys	Gly	Leu	Gly	Gln	His	Pro	Leu	Lys	Lys	Glu
			350					355					360		
Gly	Pro	Phe	Ser	Asn	Ile	Ser	Lys	Tyr	Gly	Gly	Tyr	Asn	Lys	Val	Ser
		365					370					375			
Ala	Ala	Tyr	Tyr	Thr	Leu	Ile	Glu	Tyr	Glu	Glu	Lys	Glu	Asn	Lys	Ile
	380					385					390				
Arg	Ser	Leu	Glu	Thr	Ile	Pro	Leu	Tyr	Leu	Val	Lys	Asp	Ile	Gln	Lys
395					400					405					410
Ser	Gln	Glu	Lys	Leu	Lys	Ser	Tyr	Leu	Thr	Asp	Leu	Leu	Gly	Lys	Lys
				415					420					425	
Glu	Ile	Lys	Ile	Leu	Val	Pro	Lys	Ile	Lys	Ile	Asn	Ser	Leu	Leu	Lys
			430					435					440		
Ile	Asn	Gly	Phe	Pro	Cys	His	Ile	Thr	Gly	Lys	Thr	Asn	Asp	Ser	Phe
		445					450					455			
Leu	Leu	Arg	Pro	Ala	Val	Gln	Phe	Cys	Cys	Ser	Asn	Asp	Glu	Val	Leu
	460					465					470				
Tyr	Phe	Lys	Lys	Ile	Ile	Arg	Phe	Asn	Glu	Ile	Arg	Ser	Gln	Arg	Glu
475					480					485					490
Lys	Met	Gly	Lys	Thr	Ile	Ser	Pro	Tyr	Glu	Asp	Leu	Ser	Phe	Arg	Ser
				495					500					505	
Tyr	Ile	Lys	Glu	Asn	Leu	Cys	Lys	Lys	Thr	Lys	Asn	Asp	Glu	Ile	Gly
			510					515					520		
Glu	Lys	Glu	Phe	Tyr	Asp	Leu	Leu	Gln	Lys	Lys	Asn	Leu	Glu	Ile	Tyr
		525					530					535			
Asp	Met	Leu	Leu	Thr	Lys	His	Lys	Asp	Thr	Ile	Tyr	Asn	Lys	Arg	Pro
	540					545					550				
Asn	Ser	Thr	Thr	Leu	Gly	Met	Leu	Thr	Lys	Gly	Arg	Tyr	Glu	Phe	Ile
555					560					565					570
Leu	Phe	Cys	Thr	Thr	Arg	Glu	Ala	Ile	Asp	Leu	Gly	Leu	Ile	Lys	Gly
			575					580					585		
Lys	Pro	Ala	Ala	Gly	Val	Ala	Thr	Leu	Gly	Lys	Lys	Ile	Ser	Arg	Leu
		590					595					600			

Asp Asn Cys Ile Leu Ile Tyr Gln Ser Ile Thr Gly Ile Phe Glu Lys
610 615 620
Arg Ile Asp Leu Leu Lys Val
625 630

<210> 804
<211> 631
<212> PRT
<213> Treponema denticola

<400> 804
Met Leu Thr Gln Thr Leu Lys Leu Val Lys Glu Ile Ser His Ile Thr
1 5 10 15
Gln Ala Pro Pro Lys Lys Ile Phe Ile Glu Met Ala Lys Gly Glu Glu
20 25 30
Leu Glu Pro Ala Arg Thr Lys Thr Arg Leu Lys Ile Leu Gln Asp Leu
35 40 45
Tyr Ser Ser Cys Lys Asn Asp Ala Asp Ala Phe Ser Ser Glu Ile Gln
50 55 60
Tyr Leu Ser Gly Lys Ile Glu Asn Glu Asp Asn Leu Arg Leu Arg Ser
65 70 75 80
Asp Lys Leu Tyr Leu Tyr Tyr Thr Gln Leu Gly Lys Cys Met Tyr Cys
85 90 95
Gly Lys Pro Ile Glu Ile Gly His Val Phe Asp Thr Ser Asn Cys Tyr
100 105 110
Ile Asp His Ile Tyr Pro Gln Ser Lys Ile Lys Asp Asp Ser Ile Ser
115 120 125
Asn Arg Val Leu Val Cys Ser Ser Cys Asn Lys Asn Lys Glu Asp Lys
130 135 140
Tyr Pro Leu Lys Ser Glu Ile Gln Ser Lys Gln Arg Gly Phe Trp Asn
145 150 155 160
Phe Leu Gln Arg Asn Asn Phe Ile Ser Leu Glu Lys Leu Asn Arg Leu
165 170 175
Thr Arg Thr Thr Pro Ile Ser Asp Asp Glu Thr Ala Lys Phe Ile Ala
180 185 190
Arg Gln Leu Val Glu Thr Arg Gln Ala Thr Lys Val Ala Ala Lys Val
195 200 205
Leu Glu Lys Met Phe Pro Glu Thr Lys Ile Val Tyr Ser Lys Ala Glu
210 215 220
Thr Val Ser Met Phe Arg Asn Lys Phe Asp Ile Ile Lys Cys Arg Glu
225 230 235 240
Ile Asn Asp Phe His His Ala His Asp Ala Tyr Leu Asn Ile Val Val
245 250 255
Gly Asn Val Tyr Asn Thr Lys Phe Thr Asn Asn Pro Trp Asn Phe Ile
260 265 270
Lys Glu Lys Arg Asp Asn Pro Lys Ile Ala Asp Thr Tyr Asn Tyr Tyr
275 280 285
Lys Val Phe Asp Tyr Asp Val Lys Arg Asn Asn Ile Thr Ala Trp Glu
290 295 300
Lys Gly Lys Thr Ile Ile Thr Val Lys Asp Met Leu Lys Arg Asn Thr
305 310 315 320
Pro Ile Tyr Thr Arg Gln Ala Ala Cys Lys Tyr Gly Glu Leu Phe Asn
325 330 335
Gln Thr Ile Met Lys Lys Gly Leu Gly Gln His Pro Leu Lys Lys Glu
340 345 350

Gly	Pro	Phe	Ser	Asn	Ile	Ser	Lys	Tyr	Gly	Gly	Tyr	Asn	Lys	Val	Ser
		355					360					365			
Ile	Ile	Tyr	Tyr	Thr	Leu	Ile	Glu	Tyr	Glu	Glu	Lys	Val	Asn	Lys	Ile
	370					375					380				
Arg	Ser	Leu	Glu	Thr	Ile	Pro	Leu	Tyr	Leu	Val	Lys	Asp	Ile	Gln	Lys
385					390					395					400
Asp	Gln	Asp	Val	Leu	Lys	Ser	Tyr	Leu	Thr	Asp	Leu	Leu	Gly	Lys	Lys
				405					410					415	
Glu	Ile	Lys	Ile	Leu	Val	Pro	Lys	Ile	Lys	Ile	Asn	Ser	Leu	Leu	Lys
			420					425					430		
Ile	Asn	Gly	Phe	Pro	Cys	His	Ile	Thr	Gly	Lys	Thr	Gly	Asp	Ser	Phe
		435					440					445			
Val	Leu	Arg	Pro	Ala	Val	Gln	Phe	Cys	Cys	Ser	Asn	Asp	Glu	Val	Leu
	450					455					460				
Tyr	Phe	Lys	Lys	Ile	Ile	Arg	Phe	Asn	Glu	Ile	Arg	Ser	Gln	Arg	Glu
465					470					475					480
Lys	Met	Gly	Lys	Thr	Ile	Ser	Pro	Tyr	Glu	Asp	Leu	Ser	Phe	Arg	Ser
				485					490					495	
Tyr	Ile	Lys	Glu	Asn	Leu	Cys	Lys	Lys	Thr	Lys	Ala	Asp	Glu	Ile	Gly
			500					505					510		
Glu	Lys	Glu	Phe	Tyr	Asp	Leu	Leu	Gln	Lys	Lys	Asn	Leu	Glu	Ile	Tyr
		515					520					525			
Asp	Met	Leu	Leu	Thr	Lys	His	Lys	Asp	Thr	Ile	Tyr	Asn	Lys	Arg	Pro
	530					535					540				
Asn	Ser	Thr	Thr	Leu	Gly	Met	Leu	Thr	Lys	Gly	Arg	Tyr	Glu	Phe	Ile
545					550					555					560
Asn	Leu	Lys	Pro	Lys	Asp	Gln	Ile	Ile	Val	Met	Leu	Glu	Ile	Leu	Lys
				565					570					575	
Leu	Phe	Cys	Thr	Thr	Arg	Glu	Ala	Ile	Asp	Leu	Gly	Leu	Ile	Lys	Gly
			580					585					590		
Lys	Pro	Ala	Ala	Gly	Val	Ala	Thr	Leu	Gly	Lys	Lys	Ile	Ser	Asn	Leu
		595					600					605			
Asp	Asn	Cys	Ile	Leu	Ile	Tyr	Gln	Ser	Ile	Thr	Gly	Ile	Phe	Glu	Lys
	610					615					620				
Arg	Ile	Asp	Leu	Leu	Lys	Val									
625					630										

<210> 805
<211> 370
<212> PRT
<213> Treponema denticola

<400> 805

Met	Thr	Glu	Ile	Glu	Thr	Gly	Thr	Phe	Leu	Pro	Lys	Gln	Ile	Ser	Lys
1				5					10					15	
Ser	Asn	Ala	Glu	Ile	Pro	Tyr	Gln	Leu	Arg	Lys	Met	Glu	Leu	Glu	Lys
			20					25					30		
Ile	Leu	Ser	Asn	Ala	Glu	Lys	His	Phe	Ser	Thr	Leu	Lys	Gln	Lys	Asp
			35					40					45		
Glu	Lys	Gly	Leu	Ser	His	Ser	Glu	Lys	Ile	Ile	Met	Leu	Leu	Thr	Phe
	50					55					60				
Lys	Ile	Pro	Tyr	Tyr	Ile	Gly	Pro	Ile	Asn	Asp	Asn	His	Lys	Lys	Ser
65					70					75					80
Phe	Pro	Asp	Arg	Cys	Tyr	Val	Val	Lys	Lys	Glu	Lys	Ser	Pro	Ser	Gly
				85					90					95	

Lys	Thr	Thr	Pro	Trp	Asn	Phe	Phe	Asp	Ile	Ile	Asp	Lys	Glu	Lys	Thr
			100					105					110		
Ala	Glu	Glu	Phe	Ile	Thr	Ser	Arg	Thr	Asn	Phe	Cys	Thr	Tyr	Leu	Val
		115					120					125			
Gly	Glu	Ser	Val	Leu	Pro	Lys	Ser	Ser	Leu	Leu	Tyr	Ser	Glu	Tyr	Thr
	130					135					140				
Val	Leu	Asn	Glu	Ile	Asn	Asn	Leu	Gln	Ile	Ile	Ile	Asp	Gly	Lys	Asn
145					150					155					160
Ile	Cys	Asp	Ile	Lys	Leu	Lys	Gln	Lys	Ile	Tyr	Glu	Glu	Leu	Phe	Lys
				165					170					175	
Lys	Tyr	Lys	Lys	Ile	Thr	Gln	Lys	Gln	Ile	Ser	Thr	Phe	Ile	Lys	Ile
			180					185					190		
Glu	Gly	Ile	Cys	Asn	Lys	Thr	Asp	Glu	Val	Ile	Ile	Leu	Gly	Ile	Asp
		195					200					205			
Lys	Glu	Cys	Thr	Ser	Ser	Leu	Lys	Ser	Tyr	Ile	Glu	Leu	Lys	Asn	Ile
	210					215					220				
Phe	Gly	Lys	Gln	Val	Asp	Glu	Ile	Ser	Thr	Lys	Asn	Met	Leu	Glu	Asp
225					230					235					240
Ile	Ile	Arg	Trp	Ala	Ala	Ile	Tyr	Asp	Glu	Gly	Glu	Gly	Lys	Thr	Ile
				245					250					255	
Leu	Lys	Thr	Lys	Ile	Lys	Ala	Glu	Tyr	Gly	Lys	Tyr	Cys	Ser	Asp	Glu
			260					265					270		
Gln	Ile	Lys	Lys	Ile	Leu	Asn	Leu	Lys	Phe	Ser	Gly	Trp	Gly	Arg	Leu
		275					280					285			
Ser	Arg	Lys	Phe	Leu	Glu	Thr	Val	Thr	Ser	Glu	Met	Pro	Gly	Phe	Ser
	290					295					300				
Glu	Pro	Val	Asn	Ile	Ile	Thr	Ala	Met	Arg	Glu	Thr	Gln	Asn	Asn	Leu
305					310					315					320
Met	Glu	Leu	Leu	Ser	Ser	Glu	Phe	Lys	Phe	Thr	Glu	Asn	Ile	Lys	Lys
				325					330					335	
Ile	Asn	Ser	Gly	Phe	Glu	Asp	Val	Glu	Lys	Gln	Phe	Ser	Tyr	Asp	Gly
			340					345					350		
Leu	Val	Lys	Pro	Leu	Phe	Leu	Ser	Pro	Ser	Val	Lys	Lys	Cys	Cys	Gly
		355					360					365			
Arg	Leu														
	370														

<210> 906
<211> 591
<212> PRT
<213> Treponema phagedenis

<400> 906

Met	Ala	Arg	Gly	Lys	Glu	Ala	Glu	Lys	Gly	Arg	Thr	Ser	Ser	Arg	Tyr
1				5					10					15	
Ala	Ser	Ile	Lys	Ala	Leu	Tyr	Glu	Asn	Cys	Lys	Gln	Asp	Leu	Ala	Asp
			20					25					30		
Tyr	Asp	Ala	Val	Leu	Glu	Gln	Phe	Lys	Ser	Glu	Glu	Pro	Leu	Arg	Leu
		35					40					45			
Arg	Ser	Asp	Lys	Leu	Tyr	Leu	Tyr	Tyr	Thr	Gln	Leu	Gly	Arg	Cys	Met
	50					55					60				
Tyr	Thr	Gly	Arg	Val	Ile	Asp	Ile	Asp	Arg	Leu	Met	Ser	Asp	Asn	Ser
65					70					75					80
Ala	Tyr	Asp	Ile	Asp	His	Ile	Tyr	Pro	Arg	Ser	Lys	Ile	Lys	Asp	Asp
				85					90					95	

Ser Leu Thr Asn Arg Val Leu Val Val Lys Asp Ala Asn Gln Asp Lys
100 105 110
Arg Asp Glu Pro Leu Ser Pro Gln Ile Gln Asp Lys Gln Lys Gly Phe
115 120 125
Trp Asp Phe Leu Lys Ile Asn Asn Phe Ile Ser Ile Glu Lys Tyr Glu
130 135 140
Arg Leu Thr Tyr Arg Gly Phe Ser Ser Leu Asn Arg Leu Leu Thr Ser
145 150 155 160
Ile Ala Arg Gln Leu Val Glu Thr Arg Gln Gly Thr Lys Thr Ala Gly
165 170 175
Gln Ile Leu Glu Gln Leu Tyr Pro Asp Ser Thr Val Val Tyr Cys Lys
180 185 190
Ala Ala Asn Thr Ser Glu Phe Arg Gln Lys Phe Asn Leu Ile Lys Cys
195 200 205
Arg Glu Ile Asn Asp Leu His His Ala His Asp Ala Tyr Leu Asn Ile
210 215 220
Ala Val Gly Asn Val Tyr Tyr Thr Lys Phe Thr Ser Asn Pro Arg Asn
225 230 235 240
Phe Met Lys Leu Lys Glu Pro Tyr Asn Leu Arg Glu Leu Phe Asp Arg
245 250 255
Asp Val Glu Arg Asn Asn Thr Ile Ala Trp Val Lys Asn Lys Thr Ile
260 265 270
Thr Thr Ile Lys Asp Met Leu Lys Arg Asn Thr Pro Leu Tyr Thr Arg
275 280 285
Tyr Ala Tyr Cys Lys Thr Gly Gly Phe Phe Asp Gln Asn Ile Met Lys
290 295 300
Lys Gly Lys Gly Gln Phe Pro Leu Lys Glu Asn Ser Pro Leu Ser Asp
305 310 315 320
Ile Ser Lys Tyr Gly Gly Tyr Asn Lys Val Ser Gly Ala Tyr Phe Ile
325 330 335
Leu Val Gln Lys Lys Glu Lys Asp Ala Val Val Arg Ile Leu Glu Thr
340 345 350
Val Pro Leu Tyr Leu Leu Asn Lys Pro Gly Lys Glu Ser Glu Asn Val
355 360 365
Arg Glu Tyr Leu Ser Thr Ala Leu Gly Thr Lys Asp Phe Lys Ile Leu
370 375 380
Ile Pro Lys Ile Lys Ile Asn Ser Leu Phe Lys Ile Asn Gly Phe Leu
385 390 395 400
Val His Ile Thr Gly Lys Thr Asn Asp Arg Phe Leu Val Arg Ser Ala
405 410 415
Val Gln Phe Phe Cys Asp Asp Asn Leu Thr Leu Phe Phe Lys Arg Ile
420 425 430
Ile Ala Phe Asn Gly Leu Arg Asn Leu Asn Lys Asp Lys Ser Met Thr
435 440 445
Ala Tyr Asp Asp Asn Thr Met Arg Val Tyr Val Arg Gly Asn Leu Phe
450 455 460
Lys Asp Lys Asn Gln Leu Phe Asp Lys Asn Lys Phe Asn Glu Ile Val
465 470 475 480
Lys Gly Lys Asn Ile Ser Val Tyr Lys Asp Met Val Lys Arg Tyr Glu
485 490 495
Thr Ser Ile Leu Lys Phe Asp Pro Asn Thr Ala Val Ile Pro Leu Leu
500 505 510
Lys Ser Gly Glu Asp Lys Phe Ile Asn Leu Pro Ile Glu Glu Gln Phe
515 520 525
Lys Ile Leu Gln Glu Ile Leu Lys Leu Phe Gly Ala Ile Asn Gly Thr
530 535 540

Ala Asn Leu Thr Leu Ile Gly Gly Arg Pro Ser Thr Gly Glu Met Lys
545 550 555 560
Ile Ser Asn Asn Ile Ser Asn Leu Lys Gln Cys Ile Leu Ile His Gln
565 570 575
Ser Pro Thr Gly Val Phe Glu Gln Gln Ile Asp Leu Leu Lys Ile
580 585 590

<210> 61
<211> 1061
<212> PRT
<213> Treponema sp.

<400> 61
Met Ile Met Lys Leu Glu Lys Trp Arg Leu Gly Leu Asp Leu Gly Thr
1 5 10 15
Asn Ser Ile Gly Trp Ser Val Phe Ser Leu Asp Lys Asn Asn Ser Val
20 25 30
Gln Asp Leu Ile Asp Met Gly Val Arg Ile Phe Ser Asp Gly Arg Asp
35 40 45
Pro Lys Thr Lys Glu Pro Leu Ala Val Ala Arg Arg Thr Ala Arg Ser
50 55 60
Gln Arg Lys Leu Ile Tyr Arg Arg Lys Leu Arg Arg Lys Gln Val Phe
65 70 75 80
Lys Phe Leu Gln Glu Gln Gly Leu Phe Pro Lys Thr Lys Glu Glu Cys
85 90 95
Met Thr Leu Lys Ser Leu Asn Pro Tyr Glu Leu Arg Ile Lys Ala Leu
100 105 110
Asp Glu Lys Leu Glu Pro Tyr Glu Leu Gly Arg Ala Leu Phe Asn Leu
115 120 125
Ala Val Arg Arg Gly Phe Lys Ser Asn Arg Lys Asp Gly Ser Arg Glu
130 135 140
Glu Val Ser Glu Lys Lys Ser Pro Asp Glu Ile Lys Thr Gln Ala Asp
145 150 155 160
Met Gln Thr His Leu Glu Lys Ala Ile Lys Glu Asn Gly Cys Arg Thr
165 170 175
Ile Thr Glu Phe Leu Tyr Lys Asn Gln Gly Glu Asn Gly Gly Ile Arg
180 185 190
Phe Ala Pro Gly Arg Met Thr Tyr Tyr Pro Thr Arg Lys Met Tyr Glu
195 200 205
Glu Glu Phe Asn Leu Ile Arg Ser Lys Gln Glu Lys Tyr Tyr Pro Gln
210 215 220
Val Asp Trp Asp Asp Ile Tyr Lys Ala Ile Phe Tyr Gln Arg Pro Leu
225 230 235 240
Lys Pro Gln Gln Arg Gly Tyr Cys Ile Tyr Glu Asn Asp Lys Glu Arg
245 250 255
Thr Phe Lys Ala Met Pro Cys Ser Gln Lys Leu Arg Ile Leu Gln Asp
260 265 270
Ile Gly Asn Leu Ala Tyr Tyr Glu Gly Gly Ser Lys Lys Arg Val Glu
275 280 285
Leu Asn Asp Asn Gln Asp Lys Val Leu Tyr Glu Leu Leu Asn Ser Lys
290 295 300
Asp Lys Val Thr Phe Asp Gln Met Arg Lys Ala Leu Cys Leu Ala Asp
305 310 315 320

Ser Asn Ser Phe Asn Leu Glu Glu Asn Arg Asp Phe Leu Ile Gly Asn
325 330 335
Pro Thr Ala Val Lys Met Arg Ser Lys Asn Arg Phe Gly Lys Leu Trp
340 345 350
Asp Glu Ile Pro Leu Glu Glu Gln Asp Leu Ile Ile Glu Thr Ile Ile
355 360 365
Thr Ala Asp Glu Asp Asp Ala Val Tyr Glu Val Ile Lys Lys Tyr Asp
370 375 380
Leu Thr Gln Glu Glu Gln Arg Asp Phe Ile Val Lys Asn Thr Ile Leu
385 390 395 400
Ser Gly Thr Ser Met Leu Cys Lys Glu Val Ser Glu Lys Leu Val Lys
405 410 415
Arg Leu Glu Glu Ile Ala Asp Leu Lys Tyr His Glu Ala Val Glu Ser
420 425 430
Leu Gly Tyr Lys Phe Ala Asp Gln Thr Val Glu Lys Tyr Asp Leu Leu
435 440 445
Pro Tyr Tyr Gly Lys Val Leu Pro Gly Ser Thr Met Glu Ile Asp Leu
450 455 460
Ser Ala Pro Glu Thr Asn Pro Glu Lys His Tyr Gly Lys Ile Ser Asn
465 470 475 480
Pro Thr Val His Val Ala Leu Asn Gln Thr Arg Val Val Val Asn Ala
485 490 495
Leu Ile Lys Glu Tyr Gly Lys Pro Ser Gln Ile Ala Ile Glu Leu Ser
500 505 510
Arg Asp Leu Lys Asn Asn Val Glu Lys Lys Ala Ile Ala Glu Ile Ala
515 520 525
Gln Asn Gln Arg Ala Lys Glu Lys Ala Asn Ala Ile Glu Arg Tyr Lys
530 535 540
Ala Leu Tyr His Thr Ala Phe Pro Gly Lys Ser Phe Tyr Pro Asn Arg
545 550 555 560
Asn Asp Arg Met Lys Tyr Arg Leu Trp Ser Glu Leu Gly Leu Gly Asn
565 570 575
Lys Cys Ile Tyr Cys Gly Lys Gly Ile Ser Gly Ala Glu Leu Phe Thr
580 585 590
Lys Glu Ile Glu Ile Glu His Ile Leu Pro Phe Ser Arg Thr Leu Leu
595 600 605
Asp Ala Glu Ser Asn Leu Thr Val Ala His Ser Ser Cys Asn Ala Phe
610 615 620
Lys Ala Glu Arg Ser Pro Phe Glu Ala Phe Gly Thr Asn Pro Ser Gly
625 630 635 640
Tyr Ser Trp Gln Glu Ile Ile Gln Arg Ala Asn Gln Leu Lys Asn Thr
645 650 655
Ser Lys Lys Asn Lys Phe Ser Pro Asn Ala Met Asp Ser Phe Glu Lys
660 665 670
Asp Ser Ser Phe Ile Ala Arg Gln Leu Ser Asp Asn Gln Tyr Ile Ala
675 680 685
Lys Ala Ala Leu Arg Tyr Leu Lys Cys Leu Val Glu Asn Pro Ser Asp
690 695 700
Val Trp Thr Thr Asn Gly Ser Met Thr Lys Leu Leu Arg Asp Lys Trp
705 710 715 720
Glu Met Asp Ser Ile Leu Cys Arg Lys Phe Thr Glu Lys Glu Val Ala
725 730 735
Leu Leu Gly Leu Lys Pro Glu Gln Ile Gly Asn Tyr Lys Lys Asn Asp
740 745 750
Phe Asp His Arg His His Ala Ile Asp Ala Val Val Ile Gly Leu Thr
755 760 765

Asp Arg Ser Met Val Glu Lys Leu Ala Thr Lys Asn Ser His Lys Gly
770 775 780
Asn Arg Ile Glu Ile Pro Glu Phe Pro Ile Leu Arg Ser Asp Leu Ile
785 790 795 800
Glu Lys Val Lys Asn Ile Val Val Ser Phe Lys Pro Asp His Gly Ala
805 810 815
Glu Gly Lys Leu Ser Lys Glu Thr Leu Gly Leu Ile Lys Leu His
820 825 830
Gly Lys Glu Thr Phe Val Cys Arg Glu Asn Ile Val Ser Glu Ser Leu Ser Glu
835 840 845
Lys Asn Leu Asp Asp Ile Val Asp Glu Lys Ile Lys Ser Lys Val Lys
850 855 860
Asp Tyr Val Ala Lys His Lys Gly Gln Lys Ile Glu Ala Val Leu Ser
865 870 875 880
Asp Phe Ser Lys Glu Asn Gly Ile Lys Lys Val Arg Cys Val Asn Arg
885 890 895
Val Gln Thr Pro Ile Glu Ile Thr Ser Gly Lys Ile Ser Arg Tyr Leu
900 905 910
Ser Pro Glu Asp Tyr Phe Ala Ala Val Ile Trp Glu Ile Pro Gly Glu
915 920 925
Lys Lys Thr Phe Lys Ala Gln Tyr Ile Arg Arg Asn Glu Val Glu Lys
930 935 940
Asn Ser Lys Gly Leu Asn Val Val Lys Pro Ala Val Leu Glu Asn Gly
945 950 955 960
Lys Pro His Pro Ala Ala Lys Gln Val Cys Leu Leu His Lys Asp Asp
965 970 975
Tyr Leu Glu Phe Ser Asp Lys Gly Lys Met Tyr Phe Cys Arg Ile Ala
980 985 990
Gly Tyr Ala Ala Thr Asn Asn Lys Leu Asp Ile Arg Pro Val Tyr Ala
995 1000 1005
Val Ser Tyr Cys Ala Asp Trp Ile Asn Ser Thr Asn Glu Thr Met
1010 1015 1020
Leu Thr Gly Tyr Trp Lys Pro Thr Pro Thr Gln Asn Trp Val Ser
1025 1030 1035
Val Asn Val Leu Phe Asp Lys Gln Lys Ala Arg Leu Val Thr Val
1040 1045 1050
Ser Pro Ile Gly Arg Val Phe Arg Lys
1055 1060

<210> 808
<211> 281
<212> PRT
<213> Treponema vincentii

<400> 808
Met Lys Thr Leu Gly Leu Asp Ile Gly Thr Asn Ser Ile Gly Trp Gly
1 5 10 15
Ile Val Asp Glu Thr Ala Asn Lys Ile Glu Asp Cys Gly Val Tyr Ile
20 25 30
Phe Pro Glu Gly Val Lys Glu Thr Gly Asn Glu Ser Ser Lys Ala
35 40 45
Ala Glu Arg Thr Ser Phe Arg Leu Ala Arg Arg Leu Lys Phe Arg Arg
50 55 60
Lys Leu Arg Lys Cys Glu Thr Leu Lys Val Leu Ile Lys Asn Lys Met
65 70 75 80

Cys	Pro	Leu	Thr	Met 95	Glu	Glu	Leu	Glu	Lys 9(	Trp	Arg	Lys	Gln	Lys 9E	Ile
Tyr	Pro	Val	Ser 100	Gln	Asp	Phe	Leu	Asn 10E	Trp	Tyr	Arg	Thr	Asp 11(	Glu	Leu
Lys	Asn	Trp 11E	Glu	Pro	Tyr	Phe	Leu 120	Arg	Lys	Lys	Cys	Ala 12E	Glu	Gln	Lys
Ala	Gly 130	Pro	Tyr	Glu	Ile	Gly 13E	Arg	Ala	Leu	Tyr	His 140	Leu	Ala	Gln	Arg
Arg 145	Gly	Phe	Leu	Ser	Asn 150	Arg	Lys	Glu	Ser	Thr 15E	Lys	Ala	Ser	Asp	Gly 160
Lys	Val	Ser	Lys	Ser 16E	Ile	Asp	Glu	Leu	Ser 170	Ser	Leu	Met	Asp	Gly 175	Arg
Thr	Leu	Gly	Gln 180	Tyr	Phe	Tyr	Glu	Leu 18E	Lys	Gln	Ser	Gly	Glu 190	Lys	Val
Arg	Gly	Lys 19E	Tyr	Thr	Ser	Arg	Lys 200	Glu	His	Tyr	Glu	Lys 20E	Glu	Phe	Asn
Lys	Ile 210	Cys	Glu	Val	Gln	Glu 21E	Ile	Ser	Pro	Glu	Leu 220	Lys	Asp	Asp	Leu
Tyr 22E	Arg	Ala	Ile	Phe	Phe 230	Gln	Arg	Lys	Leu	Lys 23E	Ser	Gln	Lys	Phe	Leu 240
Val	Gly	Lys	Cys	Thr 24E	Phe	Glu	Arg	Asn	Lys 250	Pro	Arg	Ala	Pro	Ile 255	Ser
His	Phe	Glu	Phe 260	Glu	Glu	Phe	Arg	Met 26E	Leu	Ser	Phe	Ile	Asn 270	Ser	Ile
Lys	Ile	Ala 27E	Lys	Lys	Leu	Arg	Arg 280	Arg							

<210> 809
<211> 67E
<212> PRT
<213> Unknown

<220>
<213> Description of Unknown:
uncultured bacterium T3_7_42578 sequence

<400> 809

Met 1	Thr	Ala	Glu	Asn 5	Tyr	Ser	Asn	Val	Arg 10	Phe	Ala	Phe	Asp	Ile 15	Gly
Thr	Asn	Ser	Ile 20	Gly	Trp	Ala	Val	Phe 25	Gln	Leu	Asn	Asp	Lys 30	Gln	Glu
Ala	Thr	Ser 35	Ile	Leu	Asn	Ala	Gly 40	Ala	Arg	Ile	Phe	Ser 45	Asp	Gly	Arg
Asp	Pro 50	Lys	Thr	Phe	Glu	Pro 55	Leu	Ala	Val	Arg	Arg 60	Arg	Asn	Val	Arg
Ser 65	Ala	Ser	Arg	Met	Arg 70	Asp	Arg	Tyr	Leu	Arg 75	Arg	Arg	Lys	Arg	Thr 80
Leu	Asp	Lys	Leu	Ile	Gly	Tyr	Gly	Leu	Leu	Pro	Glu	Asp	Lys	Ala	Glu
Arg	Asp	Lys	Ile 100	Leu	Leu	Glu	Thr	Asn 105	Asp	Lys	Pro	Ser	Gly 110	Ser	Thr
Asp	Lys	Lys 115	Thr	Asp	Pro	Tyr	Ser 120	Leu	Arg	Ala	Arg	Ala 125	Leu	Glu	Glu
Lys	Leu 130	Pro	Leu	Ala	Tyr	Val 135	Ala	Arg	Ala	Leu	Phe 140	His	Ile	Gly	Gln

Arg 145	Arg	Gly	Phe	Lys	Ser 150	Asn	Arg	Lys	Ala	Asp 155	Arg	Lys	Ser	Asn	Glu 160
Lys	Gly	Lys	Ile	Ala 165	Ala	Gly	Ile	Glu	Glu 170	Leu	Ser	Gly	Leu	Met 175	His
Gln	Ser	His	Ala 180	Pro	Thr	Leu	Gly	Ala 185	Tyr	Leu	Ala	Lys	Arg 190	Arg	Glu
Glu	Gly	His 195	Val	Val	Arg	Leu	Arg 200	Ala	Ser	Ser	Glu	Ala 205	Leu	Thr	Asn
Lys	Ala 210	Tyr	Ala	Phe	Tyr	Pro 215	Glu	Arg	Ala	Met	Leu 220	Glu	Asp	Glu	Phe
His 225	Lys	Ile	Trp	Gln	Ala 230	Gln	Ala	Glu	Tyr	Tyr 235	Pro	Asp	Val	Leu	Thr 240
Lys	Glu	Arg	Glu	Glu 245	Glu	Leu	Phe	His	Val 250	Met	Phe	Phe	Gln	Arg 255	Pro
Leu	Lys	Glu	Gln 260	Lys	Val	Gly	Leu	Cys 265	Thr	Leu	Val	Glu	Gly 270	Glu	Leu
Arg	Leu	Pro 275	Lys	Ser	Asp	Pro	Leu 280	Phe	Gln	Gln	Phe	Arg 285	Leu	Tyr	Lys
Glu	Ile 290	Asn	Glu	Leu	Ala	Ile 295	Ile	Leu	Pro	Asp	Leu 300	Ser	Gln	Arg	Lys
Leu 305	Thr	Met	Glu	Glu	Arg 310	Asp	Thr	Leu	Ile	Thr 315	Leu	Met	Arg	Pro	Ala 320
Lys	Thr	Lys	Thr	Phe 325	Ala	Ala	Leu	Arg	Lys 330	Ala	Leu	Lys	Ile	Pro 335	Ala
Gly	Gly	Arg	Phe 340	Asn	Lys	Glu	Thr	Glu 345	Asn	Arg	Lys	Gln	Leu 350	Thr	Gly
Asp	Glu	Val 355	Tyr	Ser	Val	Phe	Ser 360	Lys	Pro	Glu	Leu	Phe 365	Gly	Gly	Asp
Trp	Ala 370	Lys	Phe	Ser	Ile	Glu 375	Gln	Gln	Arg	Glu	Ile 380	Ile	Asp	Gln	Leu
Asn 385	Asn	Glu	Glu	Asn	Pro 390	Asp	Lys	Leu	Glu	Glu 395	Trp	Leu	Lys	Asn	Lys 400
Phe	Pro	Lys	Leu	Ser 405	Asp	Glu	Gln	Arg	Ser 410	Glu	Ile	Ile	Asn	Ala 415	Asn
Leu	Pro	Asp	Gly 420	Tyr	Gly	Arg	Phe	Gly 425	Ile	Thr	Ala	Thr	Ser 430	Lys	Ile
Leu	Glu	Gln 435	Leu	Lys	Lys	Asp	Val 440	Ile	Ser	Glu	Ala	Glu 445	Ala	Ala	His
Arg	Cys 450	Gly	Phe	Asp	His	Ser 455	Leu	Ala	Asn	Arg	Asn 460	Trp	Lys	Gly	Leu
Asp 465	Glu	Leu	Pro	Arg	Tyr 470	Gln	Glu	Val	Leu	Glu 475	Arg	His	Ile	Val	Pro 480
Gly	Thr	Gly	Asp	Lys 485	Asn	Asp	Ile	Tyr	Asp 490	Ile	Tyr	Lys	Gly	Arg 495	Leu
Thr	Asn	Pro	Thr 500	Val	His	Ile	Gly	Leu 505	Asn	Gln	Val	Arg	Arg 510	Leu	Thr
Asn	Arg	Leu 515	Ile	Lys	Ala	Tyr	Gly 520	Lys	Pro	Trp	Gln	Ile 525	Val	Val	Glu
Leu	Ala	Arg	Asp	Leu	Pro	Met	Ser	Ser	Glu	Glu	Arg	Lys	Glu	His	Asn

	530					535					540				
Lys 545	Thr	Leu	Asn	Asp	Asn 550	Ile	Lys	Ala	Gly	Phe 555	Glu	Asp	Thr	Gln	Lys 560
Leu	Glu	Arg	Leu	Gly 565	Gln	Lys	Asp	Asn	Ala 570	Asn	Asn	Arg	Leu	Leu 575	Leu
Lys	Leu	Trp	Glu 580	Glu	Leu	Gly	Lys	Asp 585	Pro	Asp	Asn	Arg	Lys 590	Ser	Ile

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

<210>
<211>
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultured bacterium sequence

<400> 811
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Arg Val Ile Tyr His Leu Cys Lys His Arg Gly Phe His Trp Ile Ser
Arg Ala Glu Ala Lys Gln Thr Glu Gly Asp Ser Lys Ser Glu Gly Gly
Lys Val Lys Gln Gly Leu Ala Gly Thr Ala Lys Leu Met Asp Glu Lys
Gly Tyr Arg Ser Ala Lys Ala Leu Ala Ala Glu Phe Pro Glu Ala
Gln Gly Arg Asn Lys Gln Gly Glu Tyr Arg Lys Ala Leu Ser Arg Glu Leu
Leu Ala Lys Glu Leu Ala Leu Leu Phe Ala Arg Gln Arg Val Phe Gly
Asn Arg His Ala Thr Asp Thr Leu Glu Thr Ala Ile Leu Gly Asn Ser
Asp Lys Lys Ser Gly Leu Phe Trp Gln Gln Lys Pro Ala Leu Ala Gly
Ala Asp Leu Leu Lys Met Leu Gly Thr Cys Thr Phe Glu Lys Asn Glu
Tyr Arg Ala Pro Lys Ala Ser Phe Thr Ala Glu Arg His Val Trp Leu
Thr Arg Leu Asn Asn Leu Arg Ile Val Thr Asp Gly Ile Thr Arg Gln
Leu Thr Glu Gln Glu Arg Gln Leu Val Leu Pro Leu Pro Tyr Arg Gln
Ala Gly Asp Leu Thr Tyr Lys Gln Leu Met Ala Leu Thr Lys Ile
Gly Leu Glu Ala Cys Phe Lys Phe Ile Gly Leu Ala Tyr Pro
Thr Glu Ala Gln Lys Ala Gly Lys Thr Lys Asp Pro Glu Ser Ile

Thr	Leu	Val	Lys 250	Ile	Pro	Ala	Trp	Gln 255	Glu	Leu	Arg	Gln	Thr 270	Leu	Asn
Lys	Ala	Ser 275	Leu	Asn	Asp	Glu	Trp 280	Glu	Lys	Leu	Ser	Gly 285	Asp	Ala	Leu
Cys	Gly 290	Gln	Pro	Glu	Ile	Phe 295	Asp	Lys	Ile	Ala	Trp 300	Ile	Leu	Ser	Val
Tyr 305	Lys	Asp	Asp	Asp	Glu 310	Val	Arg	Thr	Glu	Leu 315	Ala	Lys	Leu	Val	Leu 320
Pro	Asn	Pro	Glu	Gly 325	Leu	Thr	Glu	Ala	Leu 330	Leu	Asn	Ile	Arg	Phe 335	Asp
Lys	Phe	His	Ala 340	Leu	Ser	Leu	Lys	Ala 345	Leu	Arg	Ala	Ile	Val 350	Pro	His
Met	Glu	Lys 355	Gly	Leu	Arg	Tyr	Asp 360	Glu	Ala	Cys	Val	Gln 365	Ala	Gly	Tyr
His	His 370	Ser	Gln	Leu	His	Lys 375	Ile	Gly	Glu	Gly	Glu 380	Ile	Lys	Tyr	Leu
Pro 385	Pro	Leu	Tyr	Asp	Gly 390	Arg	Asp	Gly	Asp	Gly 395	Arg	Met	Ile	Phe	Ala 400
Glu	Asp	Ala	Asp	Ile 405	Pro	Arg	Asn	Pro	Val 410	Val	Leu	Arg	Ser	Leu 415	Asn
Gln	Ala	Arg	Lys 420	Val	Val	Asn	Ala	Ile 425	Ile	Arg	Arg	Tyr	Gly 430	Ser	Pro
Ser	Ala	Val 435	His	Ile	Glu	Met	Ala 440	Arg	Asp	Leu	Ser	Arg 445	Pro	Phe	Asp
Glu	Arg 450	Asn	Lys	Ile	Lys	Lys 455	Asp	Gln	Asp	Glu	Tyr 460	Gln	Ala	Arg	Asn
Gln 465	Arg	Asp	Arg	Glu	Gln 470	Phe	Ile	Glu	Leu	Phe 475	Gly	His	Pro	Pro	Lys 480
Gly	Leu	Glu	Phe	Glu 485	Lys	Trp	Arg	Leu	Tyr 490	Arg	Glu	Gln	Asn	Gly 495	Gln
Cys	Ala	Tyr	Ser 500	Gln	Lys	Pro	Leu	Ala 505	Ser	Ser	Gly	Asp	Val 510	Ala	Glu
Ile	Phe	Leu 515	Asp	Gly	Ser	Thr	Glu 520	Ile	Asp	His	Ala	Leu 525	Pro	Tyr	Ser
Arg	Ser 530	Phe	Asp	Asp	Ser	Lys 535	Asn	Asn	Lys	Val	Leu 540	Val	Leu	Thr	Arg
Glu 545	Asn	Arg	Asp	Lys	Gly 550	Asn	Arg	Thr	Pro	Tyr 555	Glu	Tyr	Leu	Gly	Gly 560
Ala	Glu	Asn	Ser	Glu 565	Arg	Trp	Gln	Arg	Phe 570	Phe	Ser	Phe	Val	Glu 575	Ser
Asn	Lys	Ala	Tyr 580	Arg	Leu	Ala	Lys	Arg 585	Thr	Arg	Leu	Leu	Arg 590	Lys	Asp
Phe	Gly	Ala 595	Lys	Glu	Ser	Glu	Glu 600	Phe	Arg	Glu	Arg	Asn 605	Leu	Asn	Asp
Thr	Arg 610	Tyr	Val	Cys	Arg	Phe 615	Phe	Lys	Asn	Tyr	Val 620	Glu	Gln	His	Leu
Lys 625	Leu	Ala	Glu	Gly	Ser 630	Glu	Ala	Lys	Arg	Cys 635	Val	Val	Val	Ser	Gly 640
Gln	Leu	Thr	Asn	Phe 645	Leu	Arg	Thr	Arg	Trp 650	Gly	Leu	Leu	Lys	Ile 655	Arg
Ser	Asp	Ser	Asp 660	Arg	His	His	Ala	Leu 665	Asp	Ala	Ala	Val	Val 670	Ile	Ala
Cys	Ser	His 675	Ser	Met	Val	Gln	Arg 680	Leu	Ser	Asn	Tyr	Ser 685	Arg	Thr	Arg
Glu	Leu 690	Glu	Gln	Val	Arg	Asp 695	Gly	Phe	Val	Asn	Ile 700	Glu	Thr	Gly	Glu

Ile Val Asn Pro Ala Met His Gln Gln Leu Arg Glu His Phe Pro Asp
705 710 715 720
Pro Trp Pro Tyr Phe Arg His Glu Leu Glu Ala Arg Leu Lys Ile Asp
725 730 735
Ser Pro Ala Leu Leu Arg Glu Glu Met Ala Arg Leu Ser Ser Tyr Thr
740 745 750
Glu Glu Glu Leu Ala Ala Leu Lys Pro Leu Phe Val Ser Arg Ala Pro
755 760 765
Gln Arg Arg Asn Gly Gly Ala His Lys Asp Thr Ile Tyr Gly Gln
770 775 780
Pro Glu Lys Leu Lys Lys Asn Gly Ser Val Ser Gln Lys Val Ala Leu
785 790 795 800
Ala Ser Leu Ala Leu Lys Asp Ile Asp Leu Leu Ala Asp Pro His Arg
805 810 815
Asn Ala Lys Leu Tyr Gly Ala Ile Arg Glu Arg Leu Glu Ala Arg His Gly
820 825 830
Gly Lys Gly Asp Lys Ala Phe Pro Ala Thr Asn Pro Leu Arg Lys Pro
835 840 845
Asp Lys Glu Gly Asn Pro Thr Gly Pro Ile Val Arg Thr Val Thr Lys
850 855 860
Val Ile Asp Lys Leu Ser Gly Ile Pro Val Arg Gly Gly Ile Ala Lys
865 870 875 880
Asn Asp Thr Met Leu Arg Val Asp Val Phe Thr Lys Ala Gly Arg Phe
885 890 895
His Leu Val Pro Val Tyr Val His His Arg Val Thr Gly Leu Pro Asn
900 905 910
Gln Ala Ile Thr Arg Gly Lys Asp Glu Asn Gln Trp Ala Ile Ile Asp
915 920 925
Asp Thr Phe Glu Trp Arg Phe Ser Leu Tyr Pro Asn Asp Leu Val Gln
930 935 940
Ile Arg Leu Lys Asp Glu Thr His Leu Gly Tyr Tyr Ala Ser Thr Asp
945 950 955 960
Arg Ser Thr Ser Ser Ile Ser Ile Trp Ala His Asp Arg Asn Gln Ser
965 970 975
Val Gly Lys Asp Gly Leu Ile Arg Ser Ile Gly Val Thr Thr Ala Lys
980 985 990
Asp Ile Glu Lys Phe His Val Asp Thr Leu Gly Asn Val Tyr Pro Ala
995 1000 1005
Pro Pro Glu Lys Arg Arg Gly Leu Ala
1010 1015

<210> 811
<211> 600
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultured bacterium sequence

<400> 811
Val Asn Ala Ile Ile Lys Lys His Gly Ser Leu Ser Ala Val His Ile
1 5 10 15
Glu Met Ala Arg Asp Leu Ser Arg Pro Leu Asp Glu Arg Arg Glu Val
20 25 30

Lys	Lys	Leu 35	Gln	Glu	Glu	Phe	Lys 40	Asp	Arg	Asn	Asp	Lys 45	Ala	Arg	Glu
Ser	Phe 50	Glu	Ala	Asp	His	Gly 55	Tyr	Arg	Pro	Lys	Gly 60	Ile	Val	Phe	Glu
Lys 65	Trp	Met	Leu	Tyr	Arg 70	Glu	Gln	His	Gly	Lys 75	Cys	Ala	Tyr	Ser	Met 80
Glu	Gly	Leu	Asp	Ile 85	Asp	Arg	Val	Leu	Asn 90	Asp	Ala	Asn	Tyr	Ala 95	Gln
Ile	Asp	His	Ala 100	Leu	Pro	Tyr	Ser	Arg 105	Ser	Tyr	Asp	Asp	Ser 110	Lys	Asn
Asn	Lys	Val 115	Leu	Val	Leu	Thr	Arg 120	Glu	Asn	Gln	Asn	Lys 125	Gly	Asn	Arg
Thr	Ala 130	Tyr	Glu	Tyr	Leu	Thr 135	Ser	Phe	Ala	Gly	Gly 140	Glu	Asp	Gly	Asp
Arg 145	Trp	Arg	Asn	Tyr	Ala 150	Ala	Trp	Val	Asn	Ser 155	Asn	Lys	Ser	Tyr	Arg 160
Met	Ala	Lys	Arg	Asn 165	Arg	Leu	Leu	Arg	Lys 170	Asn	Tyr	Gly	Pro	Asp 175	Glu
Ala	Ser	Gly	Phe 180	Lys	Asp	Arg	Asn	Leu 185	Asn	Asp	Thr	Arg	Tyr 190	Ile	Cys
Lys	Phe	Phe 195	Lys	Asn	Tyr	Val	Glu 200	Glu	His	Leu	Gln	Leu 205	Ala	Pro	Arg
Ala	Asp 210	Gly	Asn	Ala	Asn	Lys 215	Arg	Cys	Val	Val	Val 220	Asn	Gly	Gln	Leu
Thr 225	Ala	Phe	Leu	Arg	Ala 230	Arg	Trp	Gly	Leu	Ser 235	Lys	Val	Arg	Ser	Glu 240
Ser	Asp	Arg	His	His 245	Ala	Leu	Asp	Ala	Ala 250	Val	Val	Ala	Ala	Cys 255	Ser
His	Gly	Met	Val 260	Lys	Ala	Leu	Ala	Asp 265	Tyr	Ala	Arg	Asn	Lys 270	Glu	Val
Ala	Tyr	Leu 275	Arg	Glu	Gly	Phe	Pro 280	Asp	Pro	Glu	Thr	Gly 285	Glu	Ile	Ile
Asn	Pro 290	Glu	Ala	His	Ala	Arg 295	Gly	Val	His	His	Phe 300	Pro	Glu	Pro	Trp
Ala 305	His	Phe	Arg	His	Glu 310	Leu	Gln	Val	Arg	Leu 315	Tyr	Ser	Asp	Asp	Leu 320
Gln	Ala	Leu	Arg	Glu 325	Asp	Leu	Gln	Arg	Leu 330	Gly	Thr	Tyr	Ser	Glu 335	Gln
Asp	Leu	Leu	Gly 340	Val	Arg	Thr	Leu	Phe 345	Val	Ser	Arg	Ala	Pro 350	Gln	Arg
Arg	Asn	Asp 355	Gly	Ala	Val	His	Lys 360	Glu	Thr	Ile	Tyr	Ala 365	Gln	Pro	Glu
Ala	Leu 370	Arg	Lys	Gln	Gly	Gly 375	Val	Val	Gln	Lys	Val 380	Pro	Leu	Thr	Ser
Leu 385	Ser	Leu	Lys	Asp	Leu 390	Asp	Asn	Leu	Ala	Asp 395	Pro	His	Arg	Asn	Ala 400
Lys	Leu	Tyr	Thr	Ala 405	Leu	Arg	Ala	Arg	Leu 410	Glu	Ala	His	Gly	Gly 415	Lys
Ala	Asp	Lys	Ala 420	Phe	Gly	Pro	Asp	Gln 425	Pro	Phe	Tyr	Lys	Pro 430	Asp	Lys
Asn	Gly	Asn 435	Pro	Thr	Gly	Pro	Ile 440	Val	Arg	Thr	Ile	Lys 445	Leu	Val	Ile
Asp	Lys 450	Leu	Ser	Gly	Ile	Pro 455	Ile	Arg	Gly	Gly	Val 460	Ala	Lys	Asn	Asp
Thr 465	Met	Leu	Arg	Val	Asp 470	Val	Phe	Thr	Lys	Ala 475	Gly	Lys	Phe	His	Leu 480

Val Pro Val Tyr Val His His Arg Val Thr Gly Leu Pro Asp Arg Ala
465 490 495
Ile Val Ala Phe Lys Asp Glu Val Glu Trp Thr Gln Val Asp Asp Ser
500 505 510
Phe Lys Phe Leu Phe Ser Ile His Pro Asp Asn Leu Ile Arg Ile Gly
515 520 525
Leu Lys Ala Lys Glu Pro Met Ile Gly Tyr Phe Ala Ser Cys His Arg
530 535 540
Gly Thr Gly Ala Phe Asn Val Trp Ser His Asp Arg Asn Thr Ser Val
545 550 555 560
Gly Lys Ser Gly Ser Val Glu Gly Ile Gly Leu Lys Lys Thr Ala Ser
565 570 575
Leu Glu Lys Leu Asn Ile Asp Val Leu Gly Asn Val Tyr Pro Ala Arg
580 585 590
Pro Glu Gln Arg His Gly Leu Ala
595 600

<210> 811
<211> 1011
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultured delta proteobacterium HF0070_07E19 sequence

<400> 812
Met Ser Ser Lys Ala Ile Asp Ser Leu Glu Gln Leu Asp Leu Phe Lys
1 5 10 15
Pro Gln Glu Tyr Thr Leu Gly Leu Asp Leu Gly Ile Lys Ser Ile Gly
20 25 30
Trp Ala Ile Leu Ser Gly Glu Arg Ile Ala Asn Ala Gly Val Tyr Leu
35 40 45
Phe Glu Thr Ala Glu Glu Leu Asn Ser Thr Gly Asn Lys Leu Ile Ser
50 55 60
Lys Ala Ala Glu Arg Gly Arg Lys Arg Arg Ile Arg Arg Met Leu Asp
65 70 75 80
Arg Lys Ala Arg Arg Gly Arg His Ile Arg Tyr Leu Leu Glu Arg Glu
85 90 95
Gly Leu Pro Thr Asp Glu Leu Glu Glu Val Val Val His Gln Ser Asn
100 105 110
Arg Thr Leu Trp Asp Val Arg Ala Glu Ala Val Glu Arg Lys Leu Thr
115 120 125
Lys Gln Glu Leu Ala Ala Val Leu Phe His Leu Val Arg His Arg Gly
130 135 140
Tyr Phe Pro Asn Thr Lys Lys Leu Pro Pro Asp Asp Glu Ser Asp Ser
145 150 155 160
Ala Asp Glu Glu Gln Gly Lys Ile Asn Arg Ala Thr Ser Arg Leu Arg
165 170 175
Glu Glu Leu Lys Ala Per Asp Cys Lys Thr Ile Gly Gln Phe Leu Ala
180 185 190
Gln Asn Arg Asp Arg Gln Arg Asn Arg Glu Gly Asp Tyr Ser Asn Leu
195 200 205
Met Ala Arg Lys Leu Val Phe Glu Glu Ala Leu Gln Ile Leu Ala Phe
210 215 220

Gln Arg Lys Gln Gly Pro Glu Leu Ser Lys Asp Phe Glu Lys Thr Tyr
225 230 235 240
Leu Asp Val Leu Met Gly Gln Arg Ser Gly Arg Ser Pro Lys Leu Gly
245 250 255
Asn Cys Ser Leu Ile Pro Ser Glu Leu Arg Ala Pro Ser Ser Ala Pro
260 265 270
Ser Thr Glu Trp Phe Lys Phe Leu Gln Asn Leu Gly Asn Leu Gln Ile
275 280 285
Ser Asn Ala Tyr Arg Glu Glu Trp Ser Ile Asp Ala Pro Arg Arg Ala
290 295 300
Gln Ile Ile Asp Ala Cys Ser Gln Arg Ser Thr Ser Ser Ser Tyr Trp
305 310 315 320
Ile Arg Arg Asp Phe Gln Ile Pro Asp Glu Tyr Arg Phe Asn Leu Val
325 330 335
Asn Tyr Glu Arg Arg Asp Pro Asp Val Asp Leu Gln Glu Tyr Leu Gln
340 345 350
Gln Gln Glu Arg Lys Thr Leu Ala Asn Phe Arg Asn Trp Lys Gln Leu
355 360 365
Glu Lys Ile Ile Gly Thr Gly His Pro Ile Gln Thr Leu Asp Glu Ala
370 375 380
Arg Leu Ile Thr Leu Asp Lys Asp Asp Glu Lys Leu Ser Asp Gln Ala
385 390 395 400
Leu Ala Asp Leu Leu Pro Glu Ala Asp Lys Ala Ile Thr Gln Leu Cys
405 410 415
Glu Leu Asp Phe Thr Thr Ala Ala Lys Ile Ser Leu Glu Ala Met Tyr
420 425 430
Arg Ile Leu Pro His Met Asn Gln Gly Met Gly Phe Asp Ala Cys Gln
435 440 445
Gln Glu Ser Leu Pro Glu Ile Gly Val Pro Pro Ala Gly Asp Arg Val
450 455 460
Pro Pro Phe Asp Glu Met Tyr Asn Pro Val Val Asn Arg Val Leu Ser
465 470 475 480
Gln Ser Arg Lys Leu Ile Asn Ala Val Ile Asp Glu Tyr Gly Met Pro
485 490 495
Ala Lys Ile Arg Val Glu Leu Ala Arg Asp Leu Gly Lys Gly Arg Glu
500 505 510
Leu Arg Glu Arg Ile Lys Leu Asp Gln Leu Asp Lys Ser Lys Gln Asn
515 520 525
Asp Gln Arg Ala Glu Asp Phe Arg Ala Glu Phe Gln Gln Ala Pro Arg
530 535 540
Gly Asp Gln Ser Leu Arg Tyr Arg Leu Trp Lys Glu Gln Asn Cys Thr
545 550 555 560
Cys Pro Tyr Ser Gly Arg Met Ile Pro Val Asn Ser Val Leu Ser Glu
565 570 575
Asp Thr Gln Ile Asp His Ile Leu Pro Ile Ser Gln Ser Leu Asp Asn
580 585 590
Ser Leu Ser Asn Lys Val Leu Cys Phe Thr Glu Glu Asn Ala Gln Lys
595 600 605
Ser Asn Arg Thr Pro Phe Glu Tyr Leu Asp Ala Ala Asp Phe Gln Arg
610 615 620
Ile Leu Glu Ala Ile Ser Gly Asn Trp Pro Glu Ala Lys Arg Asn Arg
625 630 635 640
Leu Leu Leu His Lys Ser Phe Gly Lys Val Ala Glu Glu Trp Lys Arg
645 650 655
Ala Leu Asn Asp Thr Arg Tyr Leu Ser Lys Trp Ala Gln Phe Asp His
660 665 670

<210> unknown
<211> 1011
<212> PRT
<213> Methanocaldococcus jannaschii

<400> 1
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Lys Asn Glu Leu Ser Pro Ser Thr Phe Lys Thr Phe Glu Lys Asp Pro
20 25 30
Leu Lys Val Asp Gly Phe Thr Asn Glu Val Val Val Leu Pro Lys Phe
35 40 45
Tyr Val Gly Gln Val Ile Asp Met Ile Arg Glu Asp Ala Ile Asn Asp
50 55 60
Pro Glu Ile Lys Asp Val Leu Gly Arg Gly Lys Leu Glu Val Thr Ala
65 70 75 80
Glu Ile Glu Lys Tyr Lys Asp Phe Ala Ile Lys Tyr Phe Gly Lys Gly
85 90 95
Glu Glu Asn Val Arg Asp Glu Ser Phe Tyr Gly Met Ser Val Ala Ile
100 105 110
Arg Lys Asp Glu Ile Val Pro Met Lys Thr Leu Gly Ile Gln Asp Ser
115 120 125
Glu Lys Thr His Lys Leu Tyr Leu Ser Trp Leu Ile Asn Ser Glu Ile
130 135 140
Lys Lys Ile Ala Pro Ile Glu Ile Asp Pro Ile Ser Arg Glu Leu Pro
145 150 155 160
Asp Ile Ala Ile Gly Glu Leu Ala Lys Glu Lys Ala Lys Glu Val Ile
165 170 175
Asp Asp Phe Phe Ile Glu Ile Pro Lys Val Lys Lys Glu Ile Val Asn
180 185 190
Phe Leu Glu Ser Gly Leu Lys Leu Lys Asp Ile Glu Ser Ala Leu Ile
195 200 205
Asp Glu Ala Leu Thr Phe Arg Glu Leu Met Asn Asp Leu Asn Asn Tyr
210 215 220
Arg Gly Trp His Leu Ile Thr Ile Lys Glu Ile Leu Val Lys Glu Met
225 230 235 240
Pro Phe Asn Arg Ser Asn Leu Lys Met Phe Asn Glu Glu Lys Arg Lys
245 250 255
Leu Leu Glu Lys Ile Gln Asp Thr Ser Leu Phe Asn Glu Leu Glu Glu
260 265 270
Lys Tyr Asn Ile Leu Thr Glu Val Glu Gly Lys Phe Leu Asn Leu Tyr
275 280 285
Lys Asp Phe Ile Thr Lys Arg Pro Phe Lys Thr Asp Lys Ile Glu Leu
290 295 300
Asn Phe Asn Lys Leu Asn Glu Glu Ile Thr Lys Pro Ile Glu Met Glu
305 310 315 320
Glu Ile Ile Lys Thr Tyr Ser Glu Leu Leu Asn Ser Ser Ile Ser Tyr
325 330 335
Tyr Glu Phe Lys Met Val Lys Arg Tyr Leu Ile Asp Gln Glu Glu Leu
340 345 350
Asn Val Phe Arg Lys Leu Ile Asp Asp Ile Thr Glu Ile Ala Lys Thr
355 360 365
Ser Glu Glu Ile Phe Asp Glu Phe Glu Asp Asp Phe Lys Asn Lys Thr
370 375 380
Leu Ser Leu Gly Ser Ile Gly Ile Lys Lys Asp Arg Ile Asn Leu Thr
385 390 395 400
Ser Phe Asp Ile Asn Gly Gly Leu Ile Asp Ser Tyr Ile Val Leu Met
405 410 415
Asn Asn Glu Leu Phe Tyr Val Lys Pro Leu Asn Ile Tyr Lys Asp Leu
420 425 430
Val Lys Glu Asn Lys Leu Lys Phe Asp Ile Gln Phe Gln Lys Pro Asn
435 440 445
Glu Glu Pro Leu Leu Lys Thr Leu Ser Ser Thr Ala Val Leu Phe Lys
450 455 460
Glu Asn Lys Ile Tyr Leu Val Gly Ile Met Asn Lys Thr Leu Asn Arg
465 470 475 480
Ile Phe Asn Asn Asp Ile Pro Asn Val Val Ile Lys Leu Asp Lys Val
485 490 495
Glu Asn Thr Lys Arg Asp Asp Val Pro Thr Pro Glu Thr Leu Lys Val
500 505 510
Leu Tyr Glu Ser Leu Asn Phe Asn Glu Lys Glu Pro Lys Asn Ser Phe
515 520 525
Ile Glu Ser Ile Lys Asn Asn Phe Lys Tyr Leu Asn Ser Leu Met Ile
530 535 540
Met Asp Leu Val Pro Ile Lys Asn Leu Ser Leu Ile Asp Asp Ser Ser
545 550 555 560
Val Tyr Glu Phe Val Ser Lys Cys Leu Lys Leu Tyr Glu Lys Leu Lys
565 570 575
Asp Asn Glu Ile Asp Phe Ser Asn Asp Glu Ile Lys Asp Glu Ile Leu
580 585 590
Asn Ser Ile Val Asn Leu Leu Phe Phe Thr Ile Pro Leu Phe Leu Lys
595 600 605
Asp Asp Ile Ile Asp Pro Leu Ile Asn Phe Asp Leu Phe Val Asp Asn
610 615 620
Lys Ile Asp Val Phe Phe Asn Asn Glu Leu Glu Lys Arg Glu Ile Ser
625 630 635 640
Phe Leu Lys Ile Asp Asp Glu Leu Lys Phe Ser Tyr Ile Asn Asn Cys
645 650 655
Leu Asn Pro Val Ser Leu Lys Glu Ile Asn Leu Leu Ile Lys Asp Ala
660 665 670
Asn Leu His Leu Phe Phe Ile Lys Asn Ile Ile Leu Glu Asp Phe Phe
675 680 685
Asn Lys Ser Asp Ile Ser Asp Ile Ser Ser Asp Ile Ile Pro Tyr Arg
690 695 700
Leu Lys Lys Arg Glu Asp Asp Phe Gln Asp Ser Ile Ile Ile Met Lys
705 710 715 720
Gln Leu Asn Asp Phe Arg Gly Asn Gly Lys Asn Asn Glu Leu His Leu
725 730 735
Leu Lys Lys Gly Leu Ser Asn Ile Asn Lys Gly Ile Asp Arg Leu Leu
740 745 750
Lys Val Gly Ser Ile Ser Lys Asp Glu Lys Leu Asn Lys Asp Ile Ile
755 760 765
Asp Ser Ile Lys Asp Phe Leu Gly Phe Met Asn Leu Phe Lys Ser Arg
770 775 780
Leu Asp Ile Glu Asn Lys Asp Asn His Ser Phe Val Leu Ile Asn Asn
785 790 795 800
Ser Ile Ile Pro Ile Ser Asn Phe Asp Leu Leu Asn Asn Glu Leu Ile
805 810 815
Asn Lys Ile Glu Ile Glu Ala Ile Leu Thr Ser Ala Gly Ile Glu Leu
820 825 830
Ser Phe Asp Glu Ile Ala Ser Asp Glu Asp Lys Lys Leu Asp Phe Leu
835 840 845
Asn Ser Ile Met Asp Ala Phe His Trp Cys Ser Phe Met Thr Glu Glu
850 855 860
Leu Leu Asn Lys Asp Asn Ile Asp Phe Asn Ile Lys Leu Thr Ser Asp
865 870 875 880
Ile Leu Lys Lys His Ser Ile Leu Lys Tyr Asn Arg Asn Arg Met Ile
885 890 895
Lys Lys Asp Thr Leu Asp Leu Gln Ile Ile Arg Asp Ser Leu Asn Lys
900 905 910
Leu Gln Asn Phe Ile Lys Ala Glu Glu Ser Phe Ile Gly Ala Phe Leu
915 920 925
Phe Glu Ser Ile Thr Gly Ile Asp Leu Tyr Asn Val Asp Tyr Phe Pro
930 935 940
Leu Leu Glu Lys Ser Gly Ile Asn Ile Asn Asp Asn Lys Asn Lys Lys
945 950 955 960
Pro Asn Leu Asp Ile Thr Leu Phe Lys Asp Leu Leu Leu Phe Lys Glu
965 970 975
Ile Glu Ser Pro Leu Ala Gly Glu Phe Leu Asp Asn Ile Lys Pro Tyr
980 985 990
Asn Val Gly Pro Gly Asn Thr Lys Ser Asn Phe Ala Trp Leu Val Arg
995 1000 1005
Lys Asp Glu Glu Asn Ile Tyr Ile Phe Ser Ile Thr Asn Lys Asp Lys
1010 1015 1020
Lys Phe Ile Asp Ala Ile Phe Ile Pro Asp Val Glu Asp Lys Ser Asp
1025 1030 1035 1040
Lys Val Phe Lys Lys Val Phe Tyr Lys Phe Leu Lys Asp Glu Asn Ile
1045 1050 1055
Asn Asn Leu Ser Leu Ser Phe Lys Lys Leu Lys Asp Asp Tyr Lys Leu
1060 1065 1070
Gly Lys Gln Ile Leu Gln Phe Tyr Lys Lys Ser Ile Lys Asp Ile Leu
1075 1080 1085
Gly Ser Glu Met Leu Asp Ile Ile Glu Asn Leu Ala Asn Ala Glu Leu
1090 1095 1100
Phe Arg Leu Ile Thr Lys Lys Asp Ile Leu Asp Arg Leu Asp Lys Ile
1105 1110 1115 1120
Asn Asn Asp Asp Ile Ser Leu Phe Leu Ile Ser Lys Lys Met Asn Asp
1125 1130 1135
Thr Gly Asn Gly Phe Cys Leu Phe Gln Asp Ala Asn Asn Lys Gly Glu
1140 1145 1150
Ile Ile Phe His Asp Trp Lys Asn Phe Thr Asn Ala Val Ser Asp Ser
1155 1160 1165
Leu Val Lys Leu Ser Lys Glu Phe Ile Ile Thr Asn Tyr Asn Leu Asp
1170 1175 1180
Asn Ser Tyr Ile Asp Asp Leu Phe Lys Asp Gly Lys Leu Tyr Leu Phe
1185 1190 1195 1200
Gln Ile Tyr Asn Lys Asp Phe Ser Lys Tyr Ser Lys Gly Thr Pro Asn
1205 1210 1215
Leu His Thr Met Tyr Phe Lys Leu Leu Phe Asp Glu Asn Asn His Gly
1220 1225 1230
Gln Ile Arg Leu Ser Gly Gly Ala Glu Leu Phe Met Arg Arg Ala Ser
1235 1240 1245
Leu Lys Lys Glu Glu Leu Val Val His Pro Ala Asn Ser Pro Ile Ala
1250 1255 1260
Asn Lys Asn Pro Asp Asn Pro Lys Lys Thr Thr Thr Leu Ser Tyr Asp
1265 1270 1275 1280
Val Tyr Lys Asp Lys Arg Phe Ser Glu Asp Gln Tyr Glu Leu His Ile
1285 1290 1295
Pro Ile Ala Ile Asn Lys Cys Pro Lys Asn Ile Phe Lys Ile Asn Thr
1300 1305 1310
Glu Val Arg Val Leu Leu Lys His Asp Asp Asn Pro Tyr Val Ile Gly
1315 1320 1325
Ile Asp Arg Gly Glu Arg Asn Leu Leu Tyr Ile Val Val Val Asp Gly
1330 1335 1340
Lys Gly Asn Ile Val Glu Gln Tyr Ser Leu Asn Glu Ile Ile Asn Asn
1345 1350 1355 1360
Phe Asn Gly Ile Arg Ile Lys Thr Asp Tyr His Ser Leu Leu Asp Lys
1365 1370 1375
Lys Glu Asn Glu Arg Phe Glu Ala Arg Gln Asn Trp Thr Ser Ile Glu
1380 1385 1390
Asn Ile Lys Glu Leu Lys Ala Gly Tyr Ile Ser Gln Val Val His Lys
1395 1400 1405
Ile Cys Glu Leu Met Glu Lys Tyr Asn Ala Val Val Val Leu Glu Asp
1410 1415 1420
Leu Asn Ser Gly Phe Lys Asn Ser Arg Val Lys Val Glu Lys Gln Val
1425 1430 1435 1440
Tyr Gln Lys Phe Glu Lys Met Leu Ile Asp Lys Leu Asn Tyr Met Val
1445 1450 1455
Asp Lys Lys Ser Asp Pro Cys Ala Pro Gly Gly Val Leu Lys Ala Tyr
1460 1465 1470
Gln Leu Thr Asn Lys Phe Glu Ser Phe Lys Ser Met Ser Thr Gln Asn
1475 1480 1485
Gly Phe Ile Phe Tyr Ile Pro Ala Trp Asn Thr Ser Lys Ile Asp Pro
1490 1495 1500
Val Thr Gly Phe Val Asn Leu Phe Tyr Pro Lys Tyr Glu Asn Val Glu
1505 1510 1515 1520
Lys Ser Lys Glu Phe Phe Asn Lys Phe Asp Ser Ile Arg Tyr Asn Ser
1525 1530 1535
Glu Lys Asn Leu Phe Cys Phe Thr Phe Asp Tyr Asn Asn Phe Ile Thr
1540 1545 1550
Gln Asn Thr Val Met Ser Lys Tyr Ser Val Tyr Ser Tyr Arg Val Arg
1555 1560 1565
Asn Phe Lys Lys Asn Lys Pro Phe Asp Ile Asp Ile Asp Met Thr Lys
1570 1575 1580
Glu Ile Glu Asp Leu Phe Ile Glu Phe Asp Ile Asp Trp Asn Leu Ile
1585 1590 1595 1600
Tyr Ser Ile Lys Asn Ser Tyr Phe Lys Val Gly Leu Gly Lys Gly Tyr
1605 1610 1615
Leu Lys Leu Ile Ala Arg Asp Ser Asp Val Asp Ile Phe Tyr Lys Ile
1620 1625 1630
Ile Lys Asp Arg Ile Asn Asp Ser Asp Asn Leu Lys Leu Glu Lys Ile
1635 1640 1645
Asn Leu Ser Asn Asn Asp Ile Leu Asn Val Ile Glu Lys Leu Phe Lys
1650 1655 1660
Asp Phe Asn Ile Asn Leu Asn Val Lys Ser Ile Lys Lys Val Asn Asn
1665 1670 1675 1680
Val Leu Asp Ser Gly Lys Leu Phe Leu Val Thr Ile Thr Lys Lys Asp
1685 1690 1695
Phe Ser Asn Asp Ser Asn Gly Lys Asn Ile Glu Met Asp Pro Ile Leu
1700 1705 1710
Glu Phe His Arg Ile Tyr Gly Tyr Phe Asn Lys Asn Leu Ser Asp Ile
1715 1720 1725
Ile Ile Lys Ile Pro Lys Ser Lys Ile Leu Lys Pro Asp Lys Asn Arg
1730 1735 1740
Ser Asp Thr Met Phe Ile Lys Lys Phe Leu Tyr Gly Leu Ile Lys Asn
1745 1750 1755 1760
Glu Asn Ser Lys Asn Ile Asp Phe Ser Glu Lys Asp Ile Tyr Asp Glu
1765 1770 1775
Lys Glu Phe Leu Asp Ile Phe Lys Asn Lys Ser Phe Ser Lys Phe Ser
1780 1785 1790
Lys Glu Ile His Leu Asn Glu Leu Asp Leu Ala Asn Ile Phe Ile Ser
1795 1800 1805
Asn Leu Asp Asp Asn Ser Ile Asp Leu Phe Ala Arg Leu Asp Ile Val
1810 1815 1820
Met Asn Ser Leu Ile Asn Gly Phe Thr Leu Phe Asp Asn Lys Glu Lys
1825 1830 1835 1840
Ile Ile Asn Lys Asp Asn Glu Ile Leu Glu Asn Ile Tyr His Lys Leu
1845 1850 1855
Asn Ile Asp Val Lys Lys Arg Asn Tyr Val Ser Lys Asp Lys Asp Gln
1860 1865 1870
Phe Asn Leu Ile Phe Gln Asn Ile Leu Lys Asp Ala Ile Ser Tyr Thr
1875 1880 1885
Asp Gly Glu Arg Leu Asn Leu Ser Phe Leu Ser Ser Lys Gln Asp Arg
1890 1895 1900
Asn Lys Gly Lys Asn Ile Asp Ile Lys Met Leu Val Asn Met Ile Ser
1905 1910 1915 1920
Asn Ile Asp Lys Phe Ile Asn Phe Arg Lys Asn Glu Lys Asn Leu Ile
1925 1930 1935
Asp Asn Asn Ile Leu Ser Phe Asp Val Val Phe Glu Ser Ala Phe Asn
1940 1945 1950
Asn Phe Leu Asp Asp Glu Glu Ile Glu Tyr Leu Phe Asn Leu Lys Asn
1955 1960 1965
Leu Leu Ser Asp Lys Ile Leu Asp Tyr Arg Asn Tyr Ile Ile Gly Lys
1970 1975 1980
Pro Ile Leu Lys Asn Asp Phe Phe Glu Leu Asn Val Ile His Gln Ser
1985 1990 1995 2000
Ile Ser Lys Ser Ile Ile Asp Leu Leu Glu Asn Asp Lys Ile Tyr Leu
2005 2010 2015
Phe Arg Ile Gln Asn Lys Asp Ile Ile Lys Lys Ser Thr Asp Asn Lys
2020 2025 2030
Asn Leu His Thr Ile Tyr Leu Lys Asn Leu Phe Ser Glu Glu Asn Leu
2035 2040 2045
Lys Asp Ile Val Leu Lys Leu Asn Gly Glu Ala Glu Ile Phe Phe Arg
2050 2055 2060
Lys Ala Ser Ile Lys Asn Pro Ile Ile His Lys Lys Gly Ser Ile Leu
2065 2070 2075 2080
Asn Arg Thr Tyr Gln Val Glu Asp Leu Glu Lys Asp Ile Lys Asn Leu
2085 2090 2095
Glu Phe Phe Glu Lys Leu Ser Thr Val Glu Ile Met Asp Lys Gln Asp
2100 2105 2110
Lys Glu Asn Ile Ala Leu Ser Leu Tyr Glu Thr Ile Val Ser Met Leu
2115 2120 2125
Leu Ser Asp Val Val Ser Ser Leu Asp Glu Ser Lys Val Lys Asp Tyr
2130 2135 2140
Phe Ile Asn Leu Lys Gln Lys Ile Ile Glu Leu Asp Asn Ser Lys Asn
2145 2150 2155 2160
Phe Asn Ile Asp Asn Leu Glu Ser Tyr Ile Ser Leu Ile Glu Asn Asp
2165 2170 2175
Leu Ile Lys Lys Leu Lys Asn Tyr Ile Asn Glu Asn Leu Leu Asn Lys
2180 2185 2190
Phe Ile Asn Ile Asp Asn Asp Arg Lys Ile Ser Phe Glu Asn Ile Ser
2195 2200 2205
Asn Ser Glu Ile Ser Lys Ile Ile Phe Asp Tyr Ser Glu Leu Asn Leu
2210 2215 2220
Lys Asp Thr Ile Lys Leu Phe Lys Glu Asn Asn Ile Asn Leu Glu Glu
2225 2230 2235 2240
Lys Asp Ile Phe Ile Leu Lys Asn Leu Tyr Glu Leu Leu Met Lys Asp
2245 2250 2255
Arg Asn Thr Phe Glu Phe Ile Lys Asn Asn Ser Ile Asn Leu Ser Asn
2260 2265 2270
Leu Ser Gly Ser Phe Leu Asp Glu Asn Asn Asn Ile Lys Asp Phe Phe
2275 2280 2285
Asp Ile Lys Leu Phe Leu Lys Glu Glu Lys Asn Asp Lys Gly His Asp
2290 2295 2300
Leu Ile Leu Ser Ser Ala Ile Asn Ser Glu Ile Leu Lys Phe Leu Glu
2305 2310 2315 2320
Ser Asn Asp Ile Asn Ile Phe Ser Lys Asp Ile Asp Leu Ile Asn Asn
2325 2330 2335
Arg Leu Ser Gly Asp Ser Glu Lys Asp Asn Ile Lys Ile Trp Leu Lys
2340 2345 2350
Ser Glu Leu Asp Asn Leu Asn Ile Ile Leu Asp Asp Ile Asn Asn Asn
2355 2360 2365
Phe Thr Tyr Asn Tyr Lys Leu Lys Asp Leu Ser Asn Lys Leu Phe Leu
2370 2375 2380
Gly Tyr Asp Leu Lys Asn Lys Asn Lys Ile Tyr Ala Asp Ile Asn Lys
2385 2390 2395 2400
Leu Val Asn Phe Ile Asn Lys Asn Asn Leu Leu Asp Asn Asn Ile Leu
2405 2410 2415
Tyr Leu Ile Asn Asn Ala Asp Asn Ile Phe Ser Val Leu Asn Ile Asp
2420 2425 2430
Asn Ile Glu Ile Asp Leu Lys Asp Asn Asn Ile Ser Asp Ile Ile Asp
2435 2440 2445
Lys Val Val Asp Phe Ala Asn Asn Leu Asn Ala Trp Tyr Leu Phe Asp
2450 2455 2460
Phe Asp Ile Leu Asn Asp Lys Gly Ile Asp Val Asn Asn Phe Ala Phe
2465 2470 2475 2480
Val Leu Thr Asp Leu Asp Lys Asp Ser Phe Lys Ile Lys Leu Asn Tyr
2485 2490 2495
Phe Ser Leu Asn Asn Tyr Leu Lys Asn Arg Pro Lys Leu Asn Lys Asp
2500 2505 2510
Asn Ile Asp Leu Ser Phe His Asp Ile Ile Asp Asp Leu Ile Ile Leu
2515 2520 2525
Pro Asn Ile Leu Gly Arg Val Asp Tyr Glu Lys Phe Lys Asp Ser Ile
2530 2535 2540
Phe Lys Lys Asn Lys Asp Ile Asn Ile Asn Glu Asp Glu Leu Ile Tyr
2545 2550 2555 2560
Phe Gln Val Ala Lys Asp Asn Glu Leu Lys Asn Ile Ile Leu Asn Leu
2565 2570 2575
Phe Ser Lys Asp Met Leu Pro Asp Ser Ala Asn Leu Lys Phe Asn Lys
2580 2585 2590
Ile Lys Glu Leu Ile Leu Asp Ser Leu Asn Ser Phe Glu Phe Ser Ser
2595 2600 2605
Ile Leu Asn Gly Phe Tyr Ile Ser Ser Val Glu Lys Asp Asn Ile Ile
2610 2615 2620
Gln Ser Phe Ser Lys Val Ile Thr Asp Lys Asn Asp Leu Glu Arg Tyr
2625 2630 2635 2640
Lys Ser Glu Phe Asn Glu Glu Thr Ile Glu Asn Glu Leu Ile Glu Leu
2645 2650 2655
Ile Asn Asn Ile Thr Leu Thr Leu Asp Gln Ile Lys Lys Cys Phe Asn
2660 2665 2670
Ser Phe Met Asn Asn Leu Asp Leu Glu Leu Ile Ser Ile Asn Glu Phe
2675 2680 2685
Val Asp Leu Ser Leu Asp Val Met Lys Glu Ile Asn Arg Ile Gly Asn
2690 2695 2700
Glu Ile Ala Leu Asn Asn Tyr Ala Asn Leu Ile Ser Gln Ile Thr Asp
2705 2710 2715 2720
Ser Ile Ile Asn Ser Leu Glu Phe Gly Phe Leu Asp Ile Ser Ser Lys
2725 2730 2735
Leu Glu Asn Leu Ile Asn Ser Lys Phe Ile Tyr Phe Lys Asp Ile Ile
2740 2745 2750
Leu Asn Asn Arg Leu Asn Asn Ile Ser Thr Leu Phe Ser Asn Asn Ile
2755 2760 2765
Asp Phe Lys Asn Ile Phe Ser Leu Asn Gly Phe Asp Ile Asp Phe Ile
2770 2775 2780
Thr Phe Asn Phe Ser Leu Phe Leu Asn Met Ser Ile Gln Leu Phe Asn
2785 2790 2795 2800
Asp Ile Val Gly Phe Glu Asn Leu Leu Asn Leu Tyr Lys Glu Phe Asn
2805 2810 2815
Glu Ile Asn Ile Asp Leu Ser Ile Tyr His Asp Ile Ser Asp Leu Tyr
2820 2825 2830
Phe Asn Leu Ser Leu Leu Asn Asn Ile Val Asp Asp Phe Trp Ser Leu
2835 2840 2845
Asp Val Phe Phe Leu Ser Asn Val Leu Leu Pro Gly Ser Asn Ile Leu
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Leu Asp Asp Ile Val Asn Ser Phe Ile Lys Asn Asp Leu Asn Leu Ile
2865 2870 2875 2880
Ser Asp Ile Phe Ile Pro Leu Ile Thr Thr Glu Glu Met Asp Asn Ile
2885 2890 2895
Leu Ile Asp Gly Asn Ala Tyr Asn Phe Ile Leu Thr Ser Leu Ser Glu
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Glu Phe Ile Lys Val Glu Asn Asn Asp Ile Leu Asn Gly Lys Leu Ile
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Asp Phe Phe Val Lys Glu Leu Lys Lys Leu Met Asn Ser Ser Ile Ser
2930 2935 2940
Thr Gly Met Leu Val Gly Ile Asp Arg Leu Asp Asn Thr Tyr Val Val
2945 2950 2955 2960
Val Asn Phe Leu Asp Ser Ile Ser Gly Leu Lys Leu Lys Asn Leu Asn
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Lys Ser Tyr Ile Ser Asp Ala Leu Asn Phe Leu Asn Glu Ile Ser Val
2980 2985 2990
Ile Lys Leu Ser Leu Asn Leu Arg Gln Glu Asp Ile Asn Asp Ile Asp
2995 3000 3005
Asp Ser Leu Phe Leu Val Glu Asn Ser Leu Thr Leu Leu Leu Gln Asp
3010 3015 3020
Ile Asn Asp Ser Leu Ser Asp Phe Glu Leu Asn Asp Ile Asn Ile Glu
3025 3030 3035 3040
Phe Ser Leu Glu Leu Asn Tyr Leu Ser Asn Leu Ile Thr Glu Thr Tyr
3045 3050 3055
Phe Phe Asp Ser Ile Asn Asn Pro Glu Asn Asn Val Phe Asp Tyr Arg
3060 3065 3070
Ser Glu Phe Leu Asn Asn Ile Ser Asp Ile Leu Gly Phe Asn Arg Glu
3075 3080 3085
Leu Asn Arg Leu Lys Gln Asn Leu Phe Asn Ile Arg Asn Glu Ser Leu
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Ile Leu Lys Asp Ile Ser Leu Leu Arg Lys Glu Asn Leu Leu Asn Asn
3105 3110 3115 3120
Ile Asp Leu Ile Asn Asn Leu Ile Asn Asn Ser Ile Asn Asn Leu Val
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Pro Leu Phe Ile Thr Asp Glu Ser Asn Tyr Asp Ser Leu Asn Ile Leu
3140 3145 3150
Ser Leu Asp Leu Asp Tyr Ile Val Pro Leu Glu Asn Ile Ser Leu Val
3155 3160 3165
Lys Gln Glu Ile Ile Asp Tyr Phe Asn Asp Asn Ile Asp Leu Val Asn
3170 3175 3180
Asn Leu Ile Ile Leu Thr Ile Asn Ala Leu Ala Gly Ile Pro Lys Asp
3185 3190 3195 3200
Lys Asn Tyr Asp Glu Ile Ile Lys Leu Ile Ser Glu Ser Asp Glu Phe
3205 3210 3215
Ala Ser Ile Leu Ile Pro Thr Ile Lys Lys Glu Leu Leu Ser Leu Ile
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Asn Asp Ser Ile Ile Asn Asn Leu Lys Phe Asp Leu Lys Asn Ile Asn
3235 3240 3245
Leu Ile Asp Leu Ser Arg Gln Leu Lys Asn Ile Ser Asp Asn Ile Asn
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Asp Tyr Ser Lys Asp Ile Thr Glu Ile Leu Asn Asn Ile Ile Asn Asn
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Tyr Lys Asn Ile Leu Asn Leu Asn Leu Glu Ser Leu Asn Phe Asn Lys
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Ile Gln Asp Leu Ile Leu Asp Tyr Arg Asn Asn Ile Ala Asp Asn Glu
3300 3305 3310
Asp Ile Lys Val Phe Asn Ile Leu Ser Ser Leu Thr Ile Lys Ile Asp
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Ile Ile His Asp Gln Asp Phe Ile Asn Leu Tyr Leu Ser Glu Glu Leu
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Ser Lys Val Ser Ser Val Leu Glu Leu Ser Pro Asn Ile Tyr Phe Ile
3345 3350 3355 3360
Asn Asp Lys Lys Ile Asp Leu Ser Asn Asp Glu Ile Lys Ser Ser Leu
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3380 3385 3390
Glu Leu Tyr Leu Ser Ser Asn Glu Leu Lys Thr Leu Ser Leu Ser Leu
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Gly Asn Ile Glu Leu Phe Asn Asp Ile Ser Leu Ser Leu Lys Ile Asp
3410 3415 3420
Leu Ser Asn Leu Ile Leu Asn Ile Ser Asn Ser Leu Leu Gly Arg Ile
3425 3430 3435 3440
Lys Asp Tyr Phe Ser Ser Ile Glu Phe Asp Asn Leu Phe Leu Leu Ser
3445 3450 3455
Asp Ile Val Asn Asp Phe Arg Leu Ser Leu Ile Lys Gln Ile Ile Leu
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Gly Leu Ser Leu Leu Ile Thr Lys Asp Asn Val Glu Leu Asn Asn Ile
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Lys Leu Ser Leu Asn Ile Asp Leu Ser Asn Leu Asn Phe Asn Asn Asp
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Asp Ile Ile Gly Ser Leu Asn Asn Tyr Ile Asn Asp Ile Asn Leu Asn
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Asn Ile Ile Ile Asp Leu Asn Leu Asn Ser Ile Asp Leu Ser Ile Phe
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Phe Asn Asp Ile Asn Leu Ser Asn Ile Asn Asn Ser Ile Asn Asn Ile
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Asn Leu Asn Asn Leu Asn Leu Asn Leu Asn Leu Asn Ser Ile Asn Leu
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Ile Phe Asn Asn Asp Ile Asn Leu Asn Asn Leu Asn Asn Ser Ile Asn
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Asn Ile Asn Leu Asn Asn Leu Asn Leu Asn Leu Asn Leu Asn Ser Ile
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Ser Ile Asn Asn Ile Asn Leu Asn Asn Leu Asn Leu Asn Leu Asn Leu
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Leu Asn Asn Ser Ile Asn Asn Ile Asn Leu Asn Asn Leu Asn Leu Asn
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Asn Leu Asn Leu Asn Leu Asn Ser Ile Asn Leu Asn Ile Phe Asn Asn
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Asp Ile Asn Leu Asn Asn Leu Asn Asn Ser Ile Asn Asn Ile Asn Leu
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Asn Asn Leu Asn Leu Asn Leu Asn Leu Asn Ser Ile Asn Leu Asn Ile
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Phe Asn Asn Asp Ile Asn Leu Asn Asn Leu Asn Asn Ser Ile Asn Asn
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Ile Asn Leu Asn Asn Leu Asn Leu Asn Leu Asn Leu Asn Ser Ile Asn
3970 3975 3980
Leu Asn Ile Phe Asn Asn Asp Ile Asn Leu Asn Asn Leu Asn Asn Ser
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Ile Asn Asn Ile Asn Leu Asn Asn Leu Asn Leu Asn Leu Asn Leu Asn
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Ser Ile Asn Leu Asn Ile Phe Asn Asn Asp Ile Asn Leu Asn Asn Leu
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Asn Leu Asn Ser Ile Asn Leu Asn Ile Phe Asn Asn Asp Ile Asn Leu
4050 4055 4060
Asn Asn Leu Asn Asn Ser Ile Asn Asn Ile Asn Leu Asn Asn Leu Asn
4065 4070 4075 4080
Leu Asn Leu Asn Leu Asn Ser Ile Asn Leu Asn Ile Phe Asn Asn Asp
4085 4090 4095
Ile Asn Leu Asn Asn Leu Asn Asn Ser Ile Asn Asn Ile Asn Leu Asn
4100 4105 4110
Asn Leu Asn Leu Asn Leu Asn Leu Asn Ser Ile Asn Leu Asn Ile Phe
4115 4120 4125
Asn Asn Asp Ile Asn Leu Asn Asn Leu Asn Asn Ser Ile Asn Asn Ile
4130 4135 4140
Asn Leu Asn Asn Leu Asn Leu Asn Leu Asn Leu Asn Ser Ile Asn Leu
4145 4150 4155 4160
Asn Ile Phe Asn Asn Asp Ile Asn Leu Asn Asn Leu Asn Asn Ser Ile
4165 4170 4175
Asn Asn Ile Asn Leu Asn Asn Leu Asn Leu Asn Leu Asn Leu Asn Ser
4180 4185 4190
Ile Asn Leu Asn Ile Phe Asn Asn Asp Ile Asn Leu Asn Asn Leu Asn
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Asn Ser Ile Asn Asn Ile Asn Leu Asn Asn Leu Asn Leu Asn Leu Asn
4210 4215 4220
Leu Asn Ser Ile Asn Leu Asn Ile Phe Asn Asn Asp Ile Asn Leu Asn
4225 4230 4235 4240
Asn Leu Asn Asn Ser Ile Asn Asn Ile Asn Leu Asn Asn Leu Asn Leu
4245 4250 4255
Asn Leu Asn Leu Asn Ser Ile Asn Leu Asn Ile Phe Asn Asn Asp Ile
4260 4265 4270
Asn Leu Asn Asn Leu Asn Asn Ser Ile Asn Asn Ile Asn Leu Asn Asn
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Leu Asn Leu Asn Leu Asn Leu Asn Ser Ile Asn Leu Asn Ile Phe Asn
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Asn Asp Ile Asn Leu Asn Asn Leu Asn Asn Ser Ile Asn Asn Ile Asn
4305 4310 4315 4320
Leu Asn Asn Leu Asn Leu Asn Leu Asn Leu Asn Ser Ile Asn Leu Asn
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Ile Phe Asn Asn Asp Ile Asn Leu Asn Asn Leu Asn Asn Ser Ile Asn
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Asn Leu Asn Ile Phe Asn Asn Asp Ile Asn Leu Asn Asn Leu Asn Asn
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Ser Ile Asn Asn Ile Asn Leu Asn Asn Leu Asn Leu Asn Leu Asn Leu
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Asn Ser Ile Asn Leu Asn Ile Phe Asn Asn Asp Ile Asn Leu Asn Asn
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Leu Asn Asn Ser Ile Asn Asn Ile Asn Leu Asn Asn Leu Asn Leu Asn
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Trp	Ala	Ile 35	Leu	Ser	Gly	Glu	Arg 40	Ile	Ala	Asn	Ala	Gly 45	Val	Tyr	Leu
Phe	Glu 50	Thr	Ala	Glu	Glu	Leu 55	Asn	Ser	Thr	Gly	Asn 60	Lys	Leu	Ile	Ser
Lys 65	Ala	Ala	Glu	Arg	Gly 70	Arg	Lys	Arg	Arg	Ile 75	Arg	Arg	Met	Leu	Asp 80
Arg	Lys	Ala	Arg	Arg	Gly	Arg	His	Ile	Arg	Tyr	Leu	Leu	Glu	Arg	Glu

85 90 95

Gly	Leu	Pro	Thr 100	Asp	Glu	Leu	Glu	Glu 105	Val	Val	Val	His	Gln 110	Ser	Asn
Arg	Thr	Leu 115	Trp	Asp	Val	Arg	Ala 120	Glu	Ala	Val	Glu	Arg 125	Lys	Leu	Thr
Lys	Gln 130	Glu	Leu	Ala	Ala	Val 135	Leu	Phe	His	Leu	Val 140	Arg	His	Arg	Gly
Tyr 145	Phe	Pro	Asn	Thr	Lys 150	Lys	Leu	Pro	Pro	Asp 155	Asp	Glu	Ser	Asp	Ser 160
Ala	Asp	Glu	Glu	Gln 165	Gly	Lys	Ile	Asn	Arg 170	Ala	Thr	Ser	Arg	Leu 175	Arg
Glu	Glu	Leu	Lys 180	Ala	Ser	Asp	Cys	Lys 185	Thr	Ile	Gly	Gln	Phe 190	Leu	Ala
Gln	Asn	Arg 195	Asp	Arg	Gln	Arg	Asn 200	Arg	Glu	Gly	Asp	Tyr 205	Ser	Asn	Leu
Met	Ala 210	Arg	Lys	Leu	Val	Phe 215	Glu	Glu	Ala	Leu	Gln 220	Ile	Leu	Ala	Phe
Gln 225	Arg	Lys	Gln	Gly	His 230	Glu	Leu	Ser	Lys	Asp 235	Phe	Glu	Lys	Thr	Tyr 240
Leu	Asp	Val	Leu	Met 245	Gly	Gln	Arg	Ser	Gly 250	Arg	Ser	Pro	Lys	Leu 255	Gly
Asn	Cys	Ser	Leu 260	Ile	Pro	Ser	Glu	Leu 265	Arg	Ala	Pro	Ser	Ser 270	Ala	Pro
Ser	Thr	Glu 275	Trp	Phe	Lys	Phe	Leu 280	Gln	Asn	Leu	Gly	Asn 285	Leu	Gln	Ile
Ser	Asn 290	Ala	Tyr	Arg	Glu	Glu 295	Trp	Ser	Ile	Asp	Ala 300	Pro	Arg	Arg	Ala
Gln 305	Ile	Ile	Asp	Ala	Cys 310	Ser	Gln	Arg	Ser	Thr 315	Ser	Ser	Tyr	Trp	Gln 320
Ile	Arg	Arg	Asp	Phe 325	Gln	Ile	Pro	Asp	Glu 330	Tyr	Arg	Phe	Asn	Leu 335	Val
Asn	Tyr	Glu	Arg 340	Arg	Asp	Pro	Asp	Val 345	Asp	Leu	Gln	Glu	Tyr 350	Leu	Gln
Gln	Gln	Glu 355	Arg	Lys	Thr	Leu	Ala 360	Asn	Phe	Arg	Asn	Trp 365	Lys	Gln	Leu
Glu	Lys 370	Ile	Ile	Gly	Thr	Gly 375	His	Pro	Ile	Gln	Thr 380	Leu	Asp	Glu	Ala
Ala 385	Arg	Leu	Ile	Thr	Leu 390	Ile	Lys	Asp	Asp	Glu 395	Lys	Leu	Ser	Asp	Gln 400
Leu	Ala	Asp	Leu	Leu 405	Pro	Glu	Ala	Ser	Asp 410	Lys	Ala	Ile	Thr	Gln 415	Leu
Cys	Glu	Leu	Asp 420	Phe	Thr	Thr	Ala	Ala 425	Lys	Ile	Ser	Leu	Glu 430	Ala	Met
Tyr	Arg	Ile 435	Leu	Pro	His	Met	Asn 440	Gln	Gly	Met	Gly	Phe 445	Phe	Asp	Ala

Cys	Gln 450	Gln	Glu	Ser	Leu	Pro 455	Glu	Ile	Gly	Val	Pro 460	Pro	Ala	Gly	Asp
Arg 465	Val	Pro	Pro	Phe	Asp 470	Glu	Met	Tyr	Asn	Pro 475	Val	Val	Asn	Arg	Val 480
Leu	Ser	Gln	Ser	Arg 485	Lys	Leu	Ile	Asn	Ala 490	Val	Ile	Asp	Glu	Tyr 495	Gly
Met	Pro	Ala	Lys 500	Ile	Arg	Val	Glu	Leu 505	Ala	Arg	Asp	Leu	Gly 510	Lys	Gly
Arg	Glu	Leu 515	Arg	Glu	Arg	Ile	Lys 520	Leu	Asp	Gln	Leu	Asp 525	Lys	Ser	Lys
Gln	Asn 530	Asp	Gln	Arg	Ala	Glu 535	Asp	Phe	Arg	Ala	Glu 540	Phe	Gln	Gln	Ala
Pro 545	Arg	Gly	Asp	Gln	Ser 550	Leu	Arg	Tyr	Arg	Leu 555	Trp	Lys	Glu	Gln	Asn 560
Cys	Thr	Cys	Pro	Tyr 565	Ser	Gly	Arg	Met	Ile 570	Pro	Val	Asn	Ser	Val 575	Leu
Ser	Glu	Asp	Thr 580	Gln	Ile	Asp	His	Ile 585	Leu	Pro	Ile	Ser	Gln 590	Ser	Phe
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Gln	Lys 610	Ser	Asn	Arg	Thr	Pro 615	Phe	Glu	Tyr	Leu	Asp 620	Ala	Ala	Asp	Phe
Gln 625	Arg	Leu	Glu	Ala	Ile 630	Ser	Gly	Asn	Trp	Pro 635	Glu	Ala	Lys	Arg	Asn 640
Lys	Leu	Leu	His	Lys 645	Ser	Phe	Gly	Lys	Val 650	Ala	Glu	Glu	Trp	Lys 655	Ser
Arg	Ala	Leu	Asn 660	Asp	Thr	Arg	Tyr	Leu 665	Thr	Ser	Ala	Leu	Ala 670	Asp	His
Leu	Arg	His 675	His	Leu	Pro	Asp	Ser 680	Lys	Ile	Gln	Thr	Val 685	Asn	Gly	Arg
Ile	Thr 690	Gly	Tyr	Leu	Arg	Lys 695	Gln	Trp	Gly	Leu	Glu 700	Lys	Asp	Arg	Asp
Lys 705	His	Thr	His	His	Ala 710	Val	Asp	Ala	Ile	Val 715	Val	Ala	Cys	Thr	Thr 720
Pro	Ala	Ile	Val	Gln 725	Gln	Val	Thr	Leu	Tyr 730	His	Gln	Asp	Ile	Arg 735	Arg
Tyr	Lys	Lys	Leu 740	Gly	Glu	Lys	Arg	Pro 745	Thr	Pro	Trp	Pro	Glu 750	Thr	Pro
Arg	Gln	Asp 755	Val	Leu	Asp	Val	Glu 760	Glu	Glu	Ile	Phe	Ile 765	Thr	Arg	Gln
Pro	Lys 770	Lys	Val	Ser	Gly	Gly 775	Ile	Gln	Thr	Lys	Asp 780	Thr	Leu	Arg	Lys
His 785	Arg	Ser	Lys	Pro	Asp 790	Arg	Gln	Arg	Val	Ala 795	Leu	Thr	Lys	Val	Lys 800
Leu	Ala	Asp	Leu	Glu 805	Arg	Leu	Val	Glu	Lys 810	Asp	Ala	Ser	Asn	Arg 815	Asn
Leu	Tyr	Glu	His 820	Leu	Lys	Gln	Cys	Leu 825	Glu	Glu	Ser	Gly	Asp 830	Gln	Pro
Thr	Lys	Ala	Phe	Lys	Ala	Pro	Phe	Tyr	Met	Pro	Ser	Gly	Pro	Glu	Ala

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Glu 865	Pro	Pro	Tyr	Gln	Leu 870	Thr	Glu	Leu	Ser	Gly 875	Gly	Arg	Arg	Tyr	Asp 880
Ser	Met	Ala	Gln	Gly 885	Arg	Leu	Asp	Ile	Tyr 890	Arg	Tyr	Lys	Pro	Gly 895	Gly

Lys Arg Lys Asp Glu Tyr Arg Val Val Leu Gln Arg Met Ile Asp Leu
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Met Arg Gly Glu Glu Asn Val His Val Phe Gln Lys Gly Val Pro Tyr
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Asp Gln Gly Pro Glu Ile Glu Gln Asn Tyr Thr Phe Leu Phe Ser Leu
930 935 940
Tyr Phe Asp Asp Leu Val Glu Phe Gln Arg Ser Ala Asp Ser Glu Val
945 950 955 960
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35 40 45
Asp Arg Phe Ala Ile Val Asp Gln Cys Lys Val Leu His Asp Ile Ile
50 55 60
Val Ile Ser Ser Ile Ile Lys Pro Gly Gln Ser Leu Ser Glu Ala Lys
65 70 75 80
Ile Glu Ser Tyr Asn Gln His Lys Glu Asp Leu Val Leu Leu Lys Ser
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Val Leu Lys Glu Asp Arg Lys Leu Tyr Asp Asp Met Phe Val Val Asp
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Thr Asp Lys Gly Thr Asn Tyr Val Lys Tyr Thr Lys Gln Gly Val Asn
115 120 125
Gly Asn Thr Ser Ala Thr Gln Glu Glu Phe Tyr Lys Tyr Val Arg Lys
130 135 140
Val Val Ser Val Leu Pro Glu Thr Glu His Thr Arg Arg Ile Val Gln
145 150 155 160
Lys Leu Glu Glu Gly Thr Phe Leu Pro Leu Gln Arg Ile Ser Lys Asn
165 170 175
Gly Val Val Pro Tyr Gln Leu His Glu Leu Val Arg Ile Leu Asp Lys
180 185 190
Ala Thr Val Asn Phe Leu Asn Lys Val Glu Asn Gly Leu Ala Val Ala
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Asp Lys Ile Ile Ser Ile Leu Glu Phe Lys Ile Pro Tyr Tyr Val Gly
210 215 220
Pro Leu Asn Pro Thr His Ser Ile Glu Asn Gly Gly Pro Trp Ala Phe
225 230 235 240

Phe	Ala	Trp	Val	Val 345	Arg	Lys	Glu	Ala	Gly 350	Gln	Val	Leu	Pro	Trp 355	Asn
Phe	Glu	Gln	Lys 360	Val	Asp	Val	Gln	Ala 365	Ser	Ala	Val	Lys	Phe 370	Ile	Glu
Asn	Leu	Thr 375	Asn	Lys	Cys	Thr	Tyr 380	Leu	Ile	Asp	Gln	Asp 385	Val	Leu	Pro
Lys	Tyr 390	Ser	Leu	Leu	Tyr	Ala 395	Glu	Phe	Ser	Leu	Leu 400	Asn	Glu	Leu	Asn
Asn 405	Ile	Arg	Val	Asn	Asp 410	Lys	Pro	Leu	Pro	Ala 415	Asp	Val	Lys	Gln	Ala 420
Phe	Ile	Arg	Asp	His 425	Phe	Ile	Ser	Leu	Gln 430	Asp	Ser	Lys	Thr	Ala 435	Thr
Lys	Lys	Val	Val 440	Ala	Lys	Tyr	Leu	Val 445	Asp	Asn	Asn	Tyr	Val 450	Ser	Gln
Pro	Pro	Ile 455	Ile	Thr	Gly	Met	Asp 460	Gln	Gln	Ile	Ala	Thr 465	Lys	Leu	Thr
Ser	His 470	Arg	Asp	Met	Thr	Arg 475	Ile	Leu	Gly	Glu	His 480	Phe	Asp	His	Ala
Met 485	Ala	Glu	Asp	Ile	Ile 490	Arg	Tyr	Ile	Thr	Ile 495	Phe	Gly	Glu	Ser	Lys 500
Asp	Met	Leu	Arg	Gln 505	Val	Leu	Lys	Asn	Tyr 510	Tyr	Gly	Asp	Arg	Leu 515	Thr
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Arg	Leu	Ser 535	Lys	Lys	Phe	Leu	Ser 540	Asp	Ile	Trp	Gly	Met 545	Lys	Lys	Asn
Asp	Asp 550	Asp	Ala	Glu	Ala	Gly 555	Thr	Ile	Ile	Glu	His 560	Met	Arg	Glu	Gly
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Val	Val	Gln	Glu	Tyr 585	Val	Thr	Asn	Val	Leu 590	Gly	Glu	Lys	Glu	Lys 595	Thr
Ala	Phe	Glu	Met 600	Leu	Glu	Asp	Leu	Ser 605	Leu	Ser	Pro	Met	Val 610	Lys	Arg
Ser	Val	Trp 615	Gln	Thr	Leu	Arg	Ile 620	Leu	Asp	Glu	Ile	Val 625	Ser	Ile	Arg
Lys	Glu 630	Leu	Pro	Lys	Lys	Ile 635	Phe	Val	Glu	Val	Ala 640	Arg	Thr	Asn	Lys
Ala 645	Asp	Lys	Lys	Arg	Thr 650	Gln	Ser	Arg	Lys	Ala 655	Leu	Leu	Glu	Glu	Leu 660
Tyr	Lys	Gln	Ile	Lys 665	Asp	Glu	Asp	Val	His 670	Val	Leu	Gln	Gln	Glu 675	Leu
Glu	Ser	Lys	Glu 680	Asp	Ser	Ala	Leu	Asn 685	Ser	Lys	Lys	Leu	Tyr 690	Leu	Tyr
Phe	Thr	Gln 695	Met	Gly	Arg	Cys	Met 700	Tyr	Ser	Gly	Arg	Arg 705	Ile	Asp	Ile
His	Glu 710	Leu	Phe	Thr	Asp	Lys 715	Tyr	Asp	Ile	Asp	His 720	Ile	Tyr	Pro	Arg
Ser	Leu	Thr	Lys	Asp	Asp	Ser	Ile	His	Asn	Ile	Val	Leu	Val	Glu	Lys
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Gln	Leu	Asn	Ala	Glu	Lys	Thr	Asp	Arg	Phe	Pro	Ile	Leu	Ser	His	Ile
				745					750					755	
Gln	Ser	Lys	Gln	Lys	Gly	Phe	Ile	Lys	Leu	Leu	Trp	Asp	Arg	Gly	Phe
			760					765					770		
Ile	Ser	Glu	Lys	Lys	Tyr	Asp	Arg	Leu	Val	Arg	Thr	Thr	Asp	Leu	Thr
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Asp Glu Glu Leu Asn Gln Phe Ile Asn Arg Gln Met Val Ser Thr Asn
690 695 700
Gln Ser Val Lys Ala Val Thr Thr Leu Leu His Gln Leu Tyr Pro Glu
705 710 715 720
Thr Glu Val Val Phe Ser Lys Ala Glu Asn Val Ser Asp Phe Arg His
725 730 735
Asp Tyr Asp Phe Val Lys Val Arg Ser Ile Asn His His His His Ala
740 745 750
Lys Asp Ala Tyr Leu Asn Ile Val Val Gly Asn Val Tyr His Glu Lys
755 760 765
Phe Thr Lys Asn Phe Leu Ser Phe Ala Lys Gln Lys Gly Thr Arg Arg
770 775 780
Thr Tyr Asn Leu Thr Lys Ile Phe Glu Ile Lys Leu Thr Glu
785 790 795 800
Glu Ser Lys Lys Val Ile Trp Asp Pro Asn Ile His Met Asp Ile Val
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Lys Lys Met Met Lys Ser Asn Asp Val Arg Val Thr Gln Arg Ala Val
820 825 830
Pro Gln Lys Gly Gly Leu Ser Asp Glu Thr Ile Tyr Lys Lys Gly Ile
835 840 845
Ala Lys Arg Gly Val Tyr Leu Ser Lys Leu Lys Ser Ser Asp Glu Arg Val
850 855 860
Arg Asp Val Glu Lys Tyr Gly Gly Arg Thr Ser Ile Thr Ile Ser Glu
865 870 875 880
Tyr Ile Ile Leu Asn Phe Ser Asp Gln Asp Arg Ile Glu
885 890 895
Ile Phe Ser Leu Pro Leu Tyr Ile Ala Gly Lys Lys Asp Ile His Lys
900 905 910
Ala Ile Glu Glu Ala Tyr Leu Ser Thr Cys Lys Lys Pro Ala Ser Val
915 920 925
Val Asp Ile Gln Ile Leu Tyr Arg Gly Leu Tyr Ile Gly Ser Lys Val
930 935 940
Asn Ile Asn Gly Phe Thr Tyr Tyr Met Gly Gly Lys Thr Gly Ser Asn
945 950 955 960
Val Ser Ile Asp Ser Ala Val Asp Val Val Met Asp Ile Thr Ser Ser
965 970 975
Val Tyr Ile Lys Leu Leu Glu Lys Val Ala Ile Lys Lys Ile Glu Asn
980 985 990
Pro Lys Thr Phe Arg Ile Glu Asn Ile Lys Thr Ser Tyr Asn His Lys
995 1000 1005
Glu Val Thr Val Ser Lys Glu Gln Asn Ile Ala Leu Tyr Gln Glu
1010 1015 1020
Leu Leu Lys Lys Leu Asp Thr Pro Leu Phe Ser Lys Met Lys Gly
1025 1030 1035
Asn Lys Leu Glu Glu Phe Arg Thr Val Gly Phe Asp Thr Phe Ile
1040 1045 1050
Ala Leu Ser Leu Glu Glu Gln Ala Ser Val Leu Leu Glu Val Leu
1055 1060 1065
Asn Val Leu Thr Asn Phe Lys Thr Lys Arg Asp Ile Thr Lys Ile
1070 1075 1080
Gly Met Thr Ser Ser Arg Ser Thr Leu Gly Ile Asn Ile Ser Asn
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Lys	Val	Leu	Glu	Arg	Leu	Asn	Pro	Tyr	Gln	Leu	Arg	Ala	Lys	Gly	Leu
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His	Gln	Ala	Leu	Thr	Pro	Gly	Glu	Phe	Ala	Arg	Ala	Leu	Phe	His	Ile
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Asn	Gln	Arg	Arg	Gly	Phe	Gln	Ser	Asn	Arg	Lys	Thr	Asp	Arg	Lys	Asp
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Asn	Glu	Ser	Gly	Ala	Leu	Lys	Gln	Ala	Ile	Ser	Glu	Leu	Arg	Ala	Gln
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Ile	His	Asp	Ser	Gly	Cys	Ala	Thr	Val	Gly	Glu	Trp	Phe	Trp	Lys	Glu
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Arg	Met	Gln	Gln	Lys	Pro	Glu	Gly	Val	His	Arg	Gln	Gly	Val	Arg	Ala
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Phe	Asp	Ala	Leu	Trp	Ala	Val	Gln	Ala	Ala	Leu	Gln	Pro	Gly	Leu	Phe
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Thr	Asp	Ala	Ala	Cys	Lys	Glu	Leu	Arg	Tyr	Thr	Leu	Leu	Phe	Gln	Arg
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Lys	Leu	Arg	Pro	Val	Lys	Pro	Gly	Arg	Cys	Thr	Leu	Leu	Pro	Glu	Glu
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Glu	Arg	Ala	Pro	Leu	Ala	Leu	Pro	Ser	Thr	Gln	Arg	Phe	Arg	Ile	Leu
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Gln	Glu	Val	Asn	His	Leu	Arg	Leu	Leu	Asp	Glu	Ala	Leu	Arg	Glu	Val
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Pro	Leu	Thr	Leu	Ala	Gln	Arg	Asp	Ala	Leu	Val	Ala	Ala	Leu	Glu	Ser
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Gln	Gly	Lys	Leu	Gly	Phe	Ala	Pro	Met	Arg	Lys	Leu	Leu	Lys	Leu	Pro
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Ala	Trp	Ala	Gly	Phe	Asp	Ala	Ala	Leu	Gln	Asp	Glu	Ile	Val	Trp	Gln
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Leu	Val	Ser	Glu	Glu	Gly	Glu	Gly	Arg	Leu	Ile	Ala	Trp	Leu	Gln	Gln
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Gly Glu Val Arg Pro Leu Phe Ala Phe Lys Gln Leu Pro Tyr Tyr Gly
420 425 430
Lys Ala Leu Gln Arg His Val Ala Phe Gly Ser Gly Lys Pro Glu Asp
435 440 445
Pro Glu Glu Lys Arg His Gly Lys Ile Ala Asn Pro Thr Val His Ile
450 455 460
Gly Leu Asn Gln Val Arg Arg Thr Val Asn Ala Leu Ile Arg Arg Tyr
465 470 475 480
Gly Arg Pro Ser Glu Val Val Val Glu Leu Ala Arg Asp Leu Lys Gln
485 490 495
Ser Arg Glu Gln Gln Gln Glu Thr Gln Arg Lys Gln Ala Glu Asn Gln
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Arg Arg Asn Thr Arg Ile Arg Glu Thr Leu Gly Ile Ala Glu Thr Leu
515 520 525
Ser Arg Pro Glu Arg Val Arg Ser Ser Asp Ile Gln Lys Trp Leu Gly
530 535 540
Glu Glu Leu Ser Phe Asp Val Val Asp Arg Cys Pro Tyr Ser Gly Glu
545 550 555 560
Glu Gln Ile Ser Thr Met Leu Leu Ser Pro Lys Val Glu Ile Glu
565 570 575
His Ile Leu Pro Phe Ser Gln Thr Leu Asp Asp Ser Leu Asn Asn Arg
580 585 590
Thr Val Ala Leu Arg Glu Ala Asn Arg Ile Lys Arg Asn Arg Thr Pro
595 600 605
Trp Asp Ala Arg Ala Asp Phe Glu Ala Arg Gly Trp Gly Ser Tyr Glu Gly
610 615 620
Ile Leu His Arg Ala Glu Arg Met Pro Leu Arg Lys Arg Tyr Arg Phe
625 630 635 640
Ala Pro Asp Gly Tyr Gln Arg Trp Leu Gly Glu Asp Lys Asp Phe Leu
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Gly Arg Met Thr Ala Met Leu Arg Ala Lys Phe Gly Leu Asn Asp Val
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Phe Ala Arg Ala Ser Ala Gln Ala Arg Glu Asp Gly Leu Thr Arg Leu
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755 760 765
Arg Ala Val Arg His Ile Trp Val Ser His Lys Pro Asp His Gly Phe
770 775 780
Glu Gly Ala Met Met Glu Glu Thr Ala Tyr Gly Ile Arg Lys Asp Gly
785 790 795 800
Ser Ile Lys Pro Arg Arg Lys Ala Asp Gly Ser Ala Gly Arg Glu Val
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Val Asn Leu Ile Arg Ile Thr Glu Ser Arg Gln Pro Val Arg His Gly
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Val Asp Ser Gln Gly Pro Leu Pro Tyr Lys Gly Tyr Val Gly Gly
835 840 845

Ser	Asn 850	Tyr	Cys	Ile	Glu	Ile 855	Thr	Ala	Asn	Asp	Gln 860	Gly	Lys	Thr	Glu
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Gly	Trp	Gly	Arg	Leu 885	Arg	His	Cys	Ser	His 890	Gly	Gln	Asn	Gly	Arg 895	Pro
Leu	Met	Met	Arg 900	Leu	Met	Ile	Gly	Asp 905	Ala	Val	Arg	Leu	Ala 910	Leu	Asp
Gly	Ser	Glu 915	Lys	Thr	Met	Arg	Val 920	Val	Lys	Ile	Ser	Ala 925	Asn	Gly	Gln
Val	Phe 930	Leu	Val	Ala	Pro	Asn 935	Glu	Ala	Asn	Val	Asp 940	Ala	Arg	Asn	Arg
Asp 945	Lys	Ala	Asp	Pro	Phe 950	Ala	Tyr	Val	Ser	Lys 955	Lys	Ala	Gly	Ser	Phe 960
Gln	Ser	Ala	Lys	Ala 965	Arg	Gln	Val	Ser	Ile 970	Ser	Pro	Ile	Gly	Glu 975	Leu
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 816
guuuucccuu uucaaaagaaa ucucccugggc accuaucuuc uuaggugccc ucccauguuu 60
aaaccugacc aguuaaccgg cuggguaggu uuuu 94

<210> 817
<211> 22
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 817
gagauuuaug aaaagggaaa ac 22

<210> 818
<211> 36
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 818
uaauccaca gccgccaguu ccgcuggcgg cauuuu 36

<210> 819
<211> 18
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 819
aagccaaaaa 10

<210> 820
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 820
tcttcattgc gctta 15

<210> 821
<211> 73
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 821
aacagcauag caaguuaaaa uaaggcuagu ccguuaucaa cuugaaaagu ggcaccgagu 60
cggugcuuuu uuu 73

<210> 822
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 822
gcagcagaag aagccttgct 20

<210> 803
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 803
ttggtatgat aatcgcgcgt ag 22

<210> 814
<211> 112
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> modified_base
<222> (1)..(112)
<223> a, c, u or g

<220>
<221> misc_feature
<222> (107)..(112)
<223> May or may not be present

<400> 814
guuuuagagc uaugcuguuu uguacgcuug cguaacaaua guaggccgaa aaggccgagu 60
ucggcaccgc cgccuucgcg gcggcgguuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu 120
uuaaaa 125

<210> 825
<211> 123
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> modified_base
<222> (12)..(111)
<223> a, c, u or g

<220>
<221> misc_feature
<222> (107)..(111)
<223> May or may not be present

<400> 825
guuuagagcu gnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn ncagcaaguu 120
aaa 123

<210> 826
<211> 114
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<221>
<221> modified_base
<222> (13)..(112)
<223> a, c, u or g

<221>
<221> misc_feature
<222> (10)..(112)
<223> May or may not be present

<400> 826
guuuuagagc ugnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nncagcgagu 120
uaaa 124

<210> 827
<211> 128
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> modified_base
<222> (14)..(113)
<223> a, c, u or g

<220>
<221> misc_feature
<222> (17)..(113)
<223> May or may not be present

<400> 827
guucuuguac ucunnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnagaagcu 120
acaaagau 128

<110> 826
<111> 122
<112> RNA
<113> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> modified_base
<222> (1)..(1)
<223> a, c, u or g

<220>
<221> misc_feature
<222> (1)..(111)
<223> May or may not be present

<400> 826
guguguagcuc gnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 50
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au 122

<210> 827
<211> 42
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 827
guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc cg 42

<210> 828
<211> 7
<212> PRT
<213> Simian virus 40

<400> 828
Pro Lys Lys Lys Arg Lys Val
1 5

<210> 829
<211> 16
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Nucleoplasmin bipartite NLS sequence

<400> 831
Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys
1 5 10 15

<210> 832
<211> 9
<212> PRT
<213> Homo sapiens

<400> 832
Pro Ala Ala Lys Arg Val Lys Leu Asp
1 5

<210> 833
<211> 11
<212> PRT
<213> Homo sapiens

<400> 833
Arg Glu Arg Arg Asn Glu Leu Lys Arg Ser Pro
1 5 10

<210> 834
<211> 38
<212> PRT
<213> Homo sapiens

<400> 834
Asn Gln Ser Ser Asn Phe Gly Pro Met Lys Gly Gly Asn Phe Gly Gly
1 5 10 15
Arg Ser Ser Gly Pro Tyr Gly Gly Gly Gly Gln Tyr Phe Ala Lys Pro
20 25 30
Arg Asn Gln Gly Gly Tyr
35

<210> 835
<211> 42
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
IBB domain from importin-alpha sequence

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Any naturally occurring amino acid

<400> 835
Arg Met Arg Ile Xaa Phe Lys Asn Lys Gly Lys Asp Thr Ala Glu Leu
1 5 10 15

Arg Arg Arg Arg Val Glu Val Ser Val Glu Leu Arg Lys Ala Lys Lys
20 25 30
Asp Glu Gln Ile Leu Lys Arg Arg Asn Val
35 40

<210> 836
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Myoma T protein sequence

<400> 836
Val Ser Arg Lys Arg Pro Arg Pro
1 5

<210> 837
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Myoma T protein sequence

<400> 837
Pro Pro Lys Lys Ala Arg Glu Asp
1 5

<210> 838
<211> 8
<212> PRT
<213> Homo sapiens

<400> 838
Pro Gln Pro Lys Lys Lys Pro Leu
1 5

<210> 839
<211> 12
<212> PRT
<213> Mus musculus

<400> 839
Ser Ala Leu Ile Lys Lys Lys Lys Lys Met Ala Pro
1 5 10

<210> 840
<211> 5

<210> PRT
<213> Influenza virus

<400> 840
Asp Arg Leu Arg Arg
1 5

<210> 841
<211>
<212> PRT
<213> Influenza virus

<400> 841
Arg Lys Gln Lys Lys Arg Lys
1 5

<210> 842
<211> 11
<212> PRT
<213> Hepatitus delta virus

<400> 842
Arg Lys Leu Lys Lys Lys Ile Lys Lys Leu
1 5 10

<210> 843
<211> 10
<212> PRT
<213> Mus musculus

<400> 843
Arg Glu Lys Lys Lys Phe Leu Lys Arg Arg
1 5 10

<210> 844
<211> 20
<212> PRT
<213> Homo sapiens

<400> 844
Lys Arg Lys Gly Asp Glu Val Asp Gly Val Asp Glu Val Ala Lys Lys
1 5 10 15
Lys Ser Lys Lys
20

<210> 845
<211> 17
<212> PRT
<213> Homo sapiens

<400> 845
Arg Lys Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys
1 5 10 15
Lys

<210> 846
<211> 1428
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 846
Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
1 5 10 15
Tyr Lys Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
20 25 30
Gly Ile His Gly Val Pro Ala Ala Asp Lys Lys Tyr Ser Ile Gly Leu
35 40 45
Asp Ile Gly Thr Asn Ser Val Gly Trp Ala Val Ile Thr Asp Glu Tyr
50 55 60
Lys Val Pro Ser Lys Lys Phe Lys Val Leu Gly Asn Thr Asp Arg His
65 70 75 80
Ser Ile Lys Lys Asn Leu Ile Gly Ala Leu Leu Phe Asp Ser Gly Glu
85 90 95
Thr Ala Glu Ala Thr Arg Leu Lys Arg Thr Ala Arg Arg Arg Tyr Thr
100 105 110
Arg Arg Lys Asn Arg Ile Cys Tyr Leu Gln Glu Ile Phe Ser Asn Glu
115 120 125
Met Ala Lys Val Asp Asp Ser Phe Phe His Arg Leu Glu Glu Ser Phe
130 135 140
Leu Val Glu Glu Asp Lys Lys His Glu Arg His Pro Ile Phe Gly Asn
145 150 155 160
Ile Val Asp Glu Val Ala Tyr His Glu Lys Tyr Pro Thr Ile Tyr His
165 170 175
Leu Arg Lys Lys Leu Val Asp Ser Thr Asp Lys Ala Asp Leu Arg Leu
180 185 190
Ile Tyr Leu Ala Leu Ala His Met Ile Lys Phe Arg Gly His Phe Leu
195 200 205
Ile Glu Gly Asp Leu Asn Pro Asp Asn Ser Asp Val Asp Lys Leu Phe
210 215 220
Ile Gln Leu Val Gln Thr Tyr Asn Gln Leu Phe Glu Glu Asn Pro Ile
225 230 235 240
Asn Ala Ser Gly Val Asp Ala Lys Ala Ile Leu Ser Ala Arg Leu Ser
245 250 255
Lys Ser Arg Arg Leu Glu Asn Leu Ile Ala Gln Leu Pro Gly Glu Lys
260 265 270
Lys Asn Gly Leu Phe Gly Asn Leu Ile Ala Leu Ser Leu Gly Leu Thr
275 280 285
Pro Asn Phe Lys Ser Asn Phe Asp Leu Ala Glu Asp Ala Lys Leu Gln
290 295 300
Leu Ser Lys Asp Thr Tyr Asp Asp Asp Leu Asp Asn Leu Leu Ala Gln
305 310 315 320

Ile	Gly	Asp	Gln	Tyr 325	Ala	Asp	Leu	Phe	Leu 330	Ala	Ala	Lys	Asn	Leu 335	Ser
Asp	Ala	Ile	Leu 340	Leu	Ser	Asp	Ile	Leu 345	Arg	Val	Asn	Thr	Glu 350	Ile	Thr
Lys	Ala	Pro 355	Leu	Ser	Ala	Ser	Met 360	Ile	Lys	Arg	Tyr	Asp 365	Glu	His	His
Gln	Asp 370	Leu	Thr	Leu	Leu	Lys 375	Ala	Leu	Val	Arg	Gln 380	Gln	Leu	Pro	Glu
Lys 385	Tyr	Lys	Glu	Ile	Phe 390	Phe	Asp	Gln	Ser	Lys 395	Asn	Gly	Tyr	Ala	Gly 400
Tyr	Ile	Asp	Gly	Gly 405	Ala	Ser	Gln	Glu	Glu 410	Phe	Tyr	Lys	Phe	Ile 415	Lys
Pro	Ile	Leu	Glu 420	Lys	Met	Asp	Gly	Thr 425	Glu	Glu	Leu	Leu	Val 430	Lys	Leu
Asn	Arg	Glu 435	Asp	Leu	Leu	Arg	Lys 440	Gln	Arg	Thr	Phe	Asp 445	Asn	Gly	Ser
Ile	Pro 450	His	Gln	Ile	His	Leu 455	Gly	Glu	Leu	His	Ala 460	Ile	Leu	Arg	Arg
Gln 465	Glu	Asp	Phe	Tyr	Pro 470	Phe	Leu	Lys	Asp	Asn 475	Arg	Glu	Lys	Ile	Glu 480
Lys	Ile	Leu	Thr	Phe 485	Arg	Ile	Pro	Tyr	Tyr 490	Val	Gly	Pro	Leu	Ala 495	Arg
Gly	Asn	Ser	Arg 500	Phe	Ala	Trp	Met	Thr 505	Arg	Lys	Ser	Glu	Glu 510	Thr	Ile
Thr	Pro	Trp 515	Asn	Phe	Glu	Glu	Val 520	Val	Asp	Lys	Gly	Ala 525	Ser	Ala	Gln
Ser	Phe 530	Ile	Glu	Arg	Met	Thr 535	Asn	Phe	Asp	Lys	Asn 540	Leu	Pro	Asn	Glu
Lys 545	Val	Leu	Pro	Lys	His 550	Ser	Leu	Leu	Tyr	Glu 555	Tyr	Phe	Thr	Val	Tyr 560
Asn	Glu	Leu	Thr	Lys 565	Val	Lys	Tyr	Val	Thr 570	Glu	Gly	Met	Arg	Lys 575	Pro
Ala	Phe	Leu	Ser 580	Gly	Glu	Gln	Lys	Lys 585	Ala	Ile	Val	Asp	Leu 590	Leu	Phe
Lys	Thr	Asn 595	Arg	Lys	Val	Thr	Val 600	Lys	Gln	Leu	Lys	Glu 605	Asp	Tyr	Phe
Lys	Lys 610	Ile	Glu	Cys	Phe	Asp 615	Ser	Val	Glu	Ile	Ser 620	Gly	Val	Glu	Asp
Arg 625	Phe	Asn	Ala	Ser	Leu 630	Gly	Thr	Tyr	His	Asp 635	Leu	Leu	Lys	Ile	Ile 640
Lys	Asp	Lys	Asp	Phe 645	Leu	Asp	Asn	Glu	Glu 650	Asn	Glu	Asp	Ile	Leu 655	Glu
Asp	Ile	Val	Leu 660	Thr	Leu	Thr	Leu	Phe 665	Glu	Asp	Arg	Glu	Met 670	Ile	Glu
Glu	Arg	Leu 675	Lys	Thr	Tyr	Ala	His 680	Leu	Phe	Asp	Asp	Lys 685	Val	Met	Lys
Gln	Leu 690	Lys	Arg	Arg	Arg	Tyr 695	Thr	Gly	Trp	Gly	Arg 700	Leu	Ser	Arg	Lys
Leu	Ile	Asn	Gly	Ile	Arg	Asp	Lys	Gln	Ser	Gly	Lys	Thr	Ile	Leu	Asp
Phe	Leu	Lys	Ser	Asp	Gly	Phe	Ala	Asn	Arg	Asn	Phe	Met	Gln	Leu	Ile
His	Asp	Asp	Ser	Leu	Thr	Phe	Lys	Glu	Asp	Ile	Gln	Lys	Ala	Gln	Val
Ser	Gly	Gln	Gly	Asp	Ser	Leu	His	Glu	His	Ile	Ala	Asn	Leu	Ala	Gly

Ser Pro Ala Ile Lys Lys Gly Ile Leu Gln Thr Val Lys Val Val Asp
770 775 780
Glu Leu Val Lys Val Met Gly Arg His Lys Pro Glu Asn Ile Val Ile
785 790 795 800
Glu Met Ala Arg Glu Asn Gln Thr Thr Gln Lys Gly Gln Lys Asn Ser
805 810 815
Arg Glu Arg Met Lys Arg Ile Glu Glu Gly Ile Lys Glu Leu Gly Ser
820 825 830
Gln Ile Leu Lys Glu His Pro Val Glu Asn Thr Gln Leu Gln Asn Glu
835 840 845
Lys Leu Tyr Leu Tyr Tyr Leu Gln Asn Gly Arg Asp Met Tyr Val Asp
850 855 860
Gln Glu Leu Asp Ile Asn Arg Leu Ser Asp Tyr Asp Val Asp His Ile
865 870 875 880
Val Pro Gln Ser Phe Leu Lys Asp Asp Ser Ile Asp Asn Lys Val Leu
885 890 895
Thr Arg Ser Asp Lys Asn Arg Gly Lys Ser Asp Asn Val Pro Ser Glu
900 905 910
Glu Val Val Lys Lys Met Lys Asn Tyr Trp Arg Gln Leu Leu Asn Ala
915 920 925
Lys Leu Ile Thr Gln Arg Lys Phe Asp Asn Leu Thr Lys Ala Glu Arg
930 935 940
Gly Gly Leu Ser Glu Leu Asp Lys Ala Gly Phe Ile Lys Arg Gln Leu
945 950 955 960
Val Glu Thr Arg Gln Ile Thr Lys His Val Ala Gln Ile Leu Asp Ser
965 970 975
Arg Met Asn Thr Lys Tyr Asp Glu Asn Asp Lys Leu Ile Arg Glu Val
980 985 990
Lys Val Ile Thr Leu Lys Ser Lys Leu Val Ser Asp Phe Arg Lys Asp
995 1000 1005
Phe Gln Phe Tyr Lys Val Arg Glu Ile Asn Asn Tyr His His Ala
1010 1015 1020
His Asp Ala Tyr Leu Asn Ala Val Val Gly Thr Ala Leu Ile Lys
1025 1030 1035
Lys Tyr Pro Lys Leu Glu Ser Glu Phe Val Tyr Gly Asp Tyr Lys
1040 1045 1050
Val Tyr Asp Val Arg Lys Met Ile Ala Lys Ser Glu Gln Glu Ile
1055 1060 1065
Gly Lys Ala Thr Ala Lys Tyr Phe Phe Tyr Ser Asn Ile Met Asn
1070 1075 1080
Phe Phe Lys Thr Glu Ile Thr Leu Ala Asn Gly Glu Ile Arg Lys
1085 1090 1095
Arg Pro Leu Ile Glu Thr Asn Gly Glu Thr Gly Glu Ile Val Trp
1100 1105 1110
Asp Lys Gly Arg Asp Phe Ala Thr Val Arg Lys Val Leu Ser Met
1115 1120 1125
Pro Gln Val Asn Ile Val Lys Lys Thr Glu Val Gln Thr Gly Gly
1130 1135 1140
Phe Ser Lys Glu Ser Ile Leu Pro Lys Arg Asn Ser Asp Lys Leu
1145 1150 1155
Ile Ala Arg Lys Lys Asp Trp Asp Pro Lys Lys Tyr Gly Gly Phe
1160 1165 1170
Asp Ser Pro Thr Val Ala Tyr Ser Val Leu Val Val Ala Lys Val
1175 1180 1185
Glu Lys Gly Lys Ser Lys Lys Leu Lys Ser Val Lys Glu Leu Leu
1190 1195 1200

Gly	Ile	Thr	Ile	Met	Glu	Arg	Ser	Ser	Phe	Glu	Lys	Asn	Pro	Ile
	1295					1310					1315			
Asp	Phe	Leu	Glu	Ala	Lys	Gly	Tyr	Lys	Glu	Val	Lys	Lys	Asp	Leu
	1320					1325					1330			
Ile	Ile	Lys	Leu	Pro	Lys	Tyr	Ser	Leu	Phe	Glu	Leu	Glu	Asn	Gly
	1335					1340					1345			
Arg	Lys	Arg	Met	Leu	Ala	Ser	Ala	Gly	Glu	Leu	Gln	Lys	Gly	Asn
	1350					1355					1360			
Glu	Leu	Ala	Leu	Pro	Ser	Lys	Tyr	Val	Asn	Phe	Leu	Tyr	Leu	Ala
	1365					1370					1375			
Ser	His	Tyr	Glu	Lys	Leu	Lys	Gly	Ser	Pro	Glu	Asp	Asn	Glu	Gln
	1380					1385					1390			
Lys	Gln	Leu	Phe	Val	Glu	Gln	His	Lys	His	Tyr	Leu	Asp	Glu	Ile
	1395					1400					1405			
Ile	Glu	Gln	Ile	Ser	Glu	Phe	Ser	Lys	Arg	Val	Ile	Leu	Ala	Asp
	1410					1415					1420			
Ala	Asn	Leu	Asp	Lys	Val	Leu	Ser	Ala	Tyr	Asn	Lys	His	Arg	Asp
	1425					1430					1435			
Lys	Pro	Ile	Arg	Glu	Gln	Ala	Glu	Asn	Ile	Ile	His	Leu	Phe	Thr
	1440					1445					1450			
Leu	Thr	Asn	Leu	Gly	Ala	Pro	Ala	Ala	Phe	Lys	Tyr	Phe	Asp	Thr
	1455					1460					1465			
Thr	Ile	Asp	Arg	Lys	Arg	Tyr	Thr	Ser	Thr	Lys	Glu	Val	Leu	Asp
	1470					1475					1480			
Ala	Thr	Leu	Ile	His	Gln	Ser	Ile	Thr	Gly	Leu	Tyr	Glu	Thr	Arg
	1485					1490					1495			
Ile	Asp	Leu	Ser	Gln	Leu	Gly	Gly	Asp	Lys	Arg	Pro	Ala	Ala	Thr
	1500					1505					1510			
Lys	Lys	Ala	Gly	Gln	Ala	Lys	Lys	Lys	Lys					
	1515					1520								

<210> 847
<211> 4677
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 847

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cgctccgatg ccgctccagg gtgagcgctg tttaaaatagc caggccccg attgcaaaga 180
cattatagcg agctaccaaa gccatattca aacacctaga tcactaccac ttctacacag 240
gccactcgag cttgtgatcg cactccgcta aggggcgcc tcttcctctt cgtttcagtc 300
acaacccgca aacatgtatc catcgatgt tccagattac gcttcgcccg agaaaaagcg 360
caaggtcgaa gcgtccgacg agaagtacac catcggcctg gacatcggca ccaactctgt 420
ggcctgggcc gtgatcaccg acgagtacaa ggtgccctcc aagaaattca aggtgctggg 480
caacaccgac cggcacagca tcaagaagaa cctgatcgga gccctgctgt tcgacagcgg 540
cgaaacagcc gaggccacgc ggctgaagcg aacggccaga agaagatacc ctcgacggaa 600
gaatcggatc tgctatctgc aagagatctt cagcaacgag atggccaagg tggacgacag 660
cttcttccac agactggaag agtccttcct ggtggaagag gataagaagc acgagcgcca 720
ccccatcttc ggcaacatcg tggacgaggt ggcctaccac gagaagtacc ccaccatcta 780
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cagccgcgag agaatgaaga gaatcgaaga gggcatcaaa gagctgggca gccagatcct 2760
gaaagaacac cccgtggaaa acacccagct gcagaacgag aagctgtacc tgtactacct 2820
gcagaatggg cgggatatgt acgtggacca ggaactggac atcaaccggc tgtccgacta 2880
cgatgtggac catatcgtgc ctcagagctt tctgaaggac gactccatcg acaacaaggt 2940
gctgaccaga agcgacaaga accgggggaa gagcgacaac gtgccctccg aagaggtcgt 3000
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Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
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Lys Arg Thr Ala Arg Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
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Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
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Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
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Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
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Met Ile Lys Phe Arg Gly His Xaa Leu Ile Glu Gly Asp Leu Asn Pro
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Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
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Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
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Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
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Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
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Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
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Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
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Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
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Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
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Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
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His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
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740 745 750

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755 760 765
Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780
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930 935 940
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1115 1120 1125
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1175 1180 1185

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Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
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Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
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Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
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Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
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His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
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Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
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Asn	Gln	Leu 190	Phe	Glu	Glu	Asn	Pro 200	Ile	Asn	Ala	Ser	Gly 205	Val	Asp	Ala
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Ala	Leu	Val	Arg 340	Gln	Gln	Leu	Pro	Glu 345	Lys	Tyr	Lys	Glu	Ile 350	Phe	Phe
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Pro	Tyr 450	Tyr	Val	Gly	Pro	Leu 455	Ala	Arg	Gly	Asn	Ser 460	Arg	Phe	Ala	Trp
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Lys 545	Lys	Ala	Ile	Val	Asp 550	Leu	Leu	Phe	Lys	Thr 555	Asn	Arg	Lys	Val	Thr 560
Val	Lys	Gln	Leu	Lys 565	Glu	Asp	Tyr	Phe	Lys 570	Lys	Ile	Glu	Cys	Phe 575	Asp
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Thr	Tyr	His 595	Asp	Leu	Leu	Lys	Ile 600	Ile	Lys	Asp	Lys	Asp 605	Phe	Leu	Asp
Asn	Glu 610	Glu	Asn	Glu	Asp	Ile 615	Leu	Glu	Asp	Ile	Val 620	Leu	Thr	Leu	Thr
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Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
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Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
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785 790 795 800
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Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys
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Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn
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Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
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Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Ser
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His	Glu 130	Lys	Tyr	Pro	Thr	Ile 135	Tyr	His	Leu	Arg	Lys 140	Lys	Leu	Val	Asp
Ser 145	Thr	Asp	Lys	Ala	Asp 150	Leu	Arg	Leu	Ile	Tyr 155	Leu	Ala	Leu	Ala	His 160
Met	Ile	Lys	Phe	Arg 165	Gly	His	Phe	Leu	Ile 170	Glu	Gly	Asp	Leu	Asn 175	Pro
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Lys	Ala 210	Ile	Leu	Ser	Ala	Arg 215	Leu	Ser	Lys	Ser	Arg 220	Arg	Leu	Glu	Asn
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Asp	Asp	Leu 275	Asp	Asn	Leu	Leu	Ala 280	Gln	Ile	Gly	Asp	Gln 285	Tyr	Ala	Asp
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Ile 305	Leu	Arg	Val	Asn	Thr 310	Glu	Ile	Thr	Lys	Ala 315	Pro	Leu	Ser	Ala	Ser 320
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Ala	Leu	Val	Arg 340	Gln	Gln	Leu	Pro	Glu 345	Lys	Tyr	Lys	Glu	Ile 350	Phe	Phe
Asp	Gln	Ser 355	Lys	Asn	Gly	Tyr	Ala 360	Gly	Tyr	Ile	Asp	Gly 365	Gly	Ala	Ser
Gln	Glu 370	Glu	Phe	Tyr	Lys	Phe 375	Ile	Lys	Pro	Ile	Leu 380	Glu	Lys	Met	Asp
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Pro	Tyr 450	Tyr	Val	Gly	Pro	Leu 455	Ala	Arg	Gly	Asn	Ser 460	Arg	Phe	Ala	Trp
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Val	Val	Asp	Lys	Gly	Ala	Ser	Ala	Gln	Ser	Phe	Ile	Glu	Arg	Met	Thr
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Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
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Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545 550 555 560
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
565 570 575
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
580 585 590
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
595 600 605
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
610 615 620
Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640
His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
645 650 655
Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670
Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700
Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720
His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735
Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750
Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765
Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780
Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800
Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815
Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830
Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
835 840 845
Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860
Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880
Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910
Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925
Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945 950 955 960
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975

Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990

Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005

Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
1010 1015 1020

Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
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Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
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Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
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Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080

Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
1085 1090 1095

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

Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
1115 1120 1125

Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
1130 1135 1140

Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
1145 1150 1155

Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
1160 1165 1170

Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
1175 1180 1185

Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
1190 1195 1200

Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly
1205 1210 1215

Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
1220 1225 1230

Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser
1235 1240 1245

Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys
1250 1255 1260

His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys
1265 1270 1275

Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala
1280 1285 1290

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

Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala
1310 1315 1320

Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser
1325 1330 1335

Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr
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Gly Leu Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp
1355 1360 1365

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<C12> PRT
<113> Streptococcus pyogenes

<400> 881

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			20					25					30		
Lys	Val	Leu	Gly	Asn	Thr	Asp	Arg	His	Ser	Ile	Lys	Lys	Asn	Leu	Ile
		35					40					45			
Gly	Ala	Leu	Leu	Phe	Asp	Ser	Gly	Glu	Thr	Ala	Glu	Ala	Thr	Arg	Leu
	50					55					60				
Lys	Arg	Thr	Ala	Arg	Arg	Arg	Tyr	Thr	Arg	Arg	Lys	Asn	Arg	Ile	Cys
65					70					75					80
Tyr	Leu	Gln	Glu	Ile	Phe	Ser	Asn	Glu	Met	Ala	Lys	Val	Asp	Asp	Ser
				85					90					95	
Phe	Phe	His	Arg	Leu	Glu	Glu	Ser	Phe	Leu	Val	Glu	Glu	Asp	Lys	Lys
			100					105					110		
His	Glu	Arg	His	Pro	Ile	Phe	Gly	Asn	Ile	Val	Asp	Glu	Val	Ala	Tyr
		115					120					125			
His	Glu	Lys	Tyr	Pro	Thr	Ile	Tyr	His	Leu	Arg	Lys	Lys	Leu	Val	Asp
	130					135					140				
Ser	Thr	Asp	Lys	Ala	Asp	Leu	Arg	Leu	Ile	Tyr	Leu	Ala	Leu	Ala	His
145					150					155					160
Met	Ile	Lys	Phe	Arg	Gly	His	Phe	Leu	Ile	Glu	Gly	Asp	Leu	Asn	Pro
				165					170					175	
Asp	Asn	Ser	Asp	Val	Asp	Lys	Leu	Phe	Ile	Gln	Leu	Val	Gln	Thr	Tyr
			180					185					190		
Asn	Gln	Leu	Phe	Glu	Glu	Asn	Pro	Ile	Asn	Ala	Ser	Gly	Val	Asp	Ala
		195					200					205			
Lys	Ala	Ile	Leu	Ser	Ala	Arg	Leu	Ser	Lys	Ser	Arg	Arg	Leu	Glu	Asn
	210					215					220				
Leu	Ile	Ala	Gln	Leu	Pro	Gly	Glu	Lys	Lys	Asn	Gly	Leu	Phe	Gly	Asn
225					230					235					240
Leu	Ile	Ala	Leu	Ser	Leu	Gly	Leu	Thr	Pro	Asn	Phe	Lys	Ser	Asn	Phe
				245					250					255	
Asp	Leu	Ala	Glu	Asp	Ala	Lys	Leu	Gln	Leu	Ser	Lys	Asp	Thr	Tyr	Asp
			260					265					270		
Asp	Asp	Leu	Asp	Asn	Leu	Leu	Ala	Gln	Ile	Gly	Asp	Gln	Tyr	Ala	Asp
		275					280					285			
Leu	Phe	Leu	Ala	Ala	Lys	Asn	Leu	Ser	Asp	Ala	Ile	Leu	Leu	Ser	Asp
	290					295					300				
Ile	Leu	Arg	Val	Asn	Thr	Glu	Ile	Thr	Lys	Ala	Pro	Leu	Ser	Ala	Ser
305					310					315					320
Met	Ile	Lys	Arg	Tyr	Asp	Glu	His	His	Gln	Asp	Leu	Thr	Leu	Leu	Lys
				325					330					335	
Ala	Leu	Val	Arg	Gln	Gln	Leu	Pro	Glu	Lys	Tyr	Lys	Glu	Ile	Phe	Phe
			340					345					350		
Asp	Gln	Ser	Lys	Asn	Gly	Tyr	Ala	Gly	Tyr	Ile	Asp	Gly	Gly	Ala	Ser
		355					360					365			
Gln	Glu	Glu	Phe	Tyr	Lys	Phe	Ile	Lys	Pro	Ile	Leu	Glu	Lys	Met	Asp
	370					375					380				
Gly	Thr	Glu	Glu	Leu	Leu	Val	Lys	Leu	Asn	Arg	Glu	Asp	Leu	Leu	Arg
385					390					395					400
Lys	Gln	Arg	Thr	Phe	Asp	Asn	Gly	Ser	Ile	Pro	His	Gln	Ile	His	Leu
				405					410					415	

Gly	Glu	Leu	His 420	Ala	Ile	Leu	Arg	Arg 425	Gln	Glu	Asp	Phe	Tyr 430	Pro	Phe
Leu	Lys	Asp 435	Asn	Arg	Glu	Lys	Ile 440	Glu	Lys	Ile	Leu	Thr 445	Phe	Arg	Ile
Pro	Tyr 450	Tyr	Val	Gly	Pro	Leu 455	Ala	Arg	Gly	Asn	Ser 460	Arg	Phe	Ala	Trp
Met 465	Thr	Arg	Lys	Ser	Glu 470	Glu	Thr	Ile	Thr	Pro 475	Trp	Asn	Phe	Glu	Glu 480
Val	Val	Asp	Lys	Gly 485	Ala	Ser	Ala	Gln	Ser 490	Phe	Ile	Glu	Arg	Met 495	Thr
Asn	Phe	Asp	Lys 500	Asn	Leu	Pro	Asn	Glu 505	Lys	Val	Leu	Pro	Lys 510	His	Ser
Leu	Leu	Tyr 515	Glu	Tyr	Phe	Thr	Val 520	Tyr	Asn	Glu	Leu	Thr 525	Lys	Val	Lys
Tyr	Val 530	Thr	Glu	Gly	Met	Arg 535	Lys	Pro	Ala	Phe	Leu 540	Ser	Gly	Glu	Gln
Lys 545	Lys	Ala	Ile	Val	Asp 550	Leu	Leu	Phe	Lys	Thr 555	Asn	Arg	Lys	Val	Thr 560
Val	Lys	Gln	Leu	Lys 565	Glu	Asp	Tyr	Phe	Lys 570	Lys	Ile	Glu	Cys	Phe 575	Asp
Ser	Val	Glu	Ile 580	Ser	Gly	Val	Glu	Asp 585	Arg	Phe	Asn	Ala	Ser 590	Leu	Gly
Thr	Tyr	His 595	Asp	Leu	Leu	Lys	Ile 600	Ile	Lys	Asp	Lys	Asp 605	Phe	Leu	Asp
Asn	Glu 610	Glu	Asn	Glu	Asp	Ile 615	Leu	Glu	Asp	Ile	Val 620	Leu	Thr	Leu	Thr
Leu 625	Phe	Glu	Asp	Arg	Glu 630	Met	Ile	Glu	Glu	Arg 635	Leu	Lys	Thr	Tyr	Ala 640
His	Leu	Phe	Asp	Asp 645	Lys	Val	Met	Lys	Gln 650	Leu	Lys	Arg	Arg	Arg 655	Tyr
Thr	Gly	Trp	Gly 660	Arg	Leu	Ser	Arg	Lys 665	Leu	Ile	Asn	Gly	Ile 670	Arg	Asp
Lys	Gln	Ser 675	Gly	Lys	Thr	Ile	Leu 680	Asp	Phe	Leu	Lys	Ser 685	Asp	Gly	Phe
Ala	Asn 690	Arg	Asn	Phe	Met	Gln 695	Leu	Ile	His	Asp	Asp 700	Ser	Leu	Thr	Phe
Lys 705	Glu	Asp	Ile	Gln	Lys 710	Ala	Gln	Val	Ser	Gly 715	Gln	Gly	Asp	Ser	Leu 720
His	Glu	His	Ile	Ala 725	Asn	Leu	Ala	Gly	Ser 730	Pro	Ala	Ile	Lys	Lys 735	Gly
Ile	Leu	Gln	Thr 740	Val	Lys	Val	Val	Asp 745	Glu	Leu	Val	Lys	Val 750	Met	Gly
Arg	His	Lys 755	Pro	Glu	Asn	Ile	Val 760	Ile	Glu	Met	Ala	Arg 765	Glu	Asn	Gln
Thr	Thr 770	Gln	Lys	Gly	Gln	Lys 775	Asn	Ser	Arg	Glu	Arg 780	Met	Lys	Arg	Ile
Glu 785	Glu	Gly	Ile	Lys	Glu 790	Leu	Gly	Ser	Gln	Ile 795	Leu	Lys	Glu	His	Pro 800
Val	Glu	Asn	Thr	Gln 805	Leu	Gln	Asn	Glu	Lys 810	Leu	Tyr	Leu	Tyr	Tyr 815	Leu
Gln	Asn	Gly	Arg 820	Asp	Met	Tyr	Val	Asp 825	Gln	Glu	Leu	Asp	Ile 830	Asn	Arg
Leu	Ser	Asp 835	Tyr	Asp	Val	Asp	His 840	Ile	Val	Pro	Gln	Ser 845	Phe	Leu	Lys
Asp	Asp 850	Ser	Ile	Asp	Asn	Lys 855	Val	Leu	Thr	Arg	Ser 860	Asp	Lys	Asn	Arg

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
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Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
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Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925
Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945 950 955 960
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975
Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990
Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005
Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
1010 1015 1021
Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
1025 1030 1035
Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
1040 1045 1050
Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
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Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080
Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
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Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
1100 1105 1110
Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
1115 1120 1125
Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
1130 1135 1140
Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
1145 1150 1155
Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
1160 1165 1170
Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
1175 1180 1185
Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
1190 1195 1200
Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly
1205 1210 1215
Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
1220 1225 1230
Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser
1235 1240 1245
Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys
1250 1255 1260
His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys
1265 1270 1275
Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala
1280 1285 1290

Tyr	Asn	Lys	His	Arg	Asp	Lys	Pro	Ile	Arg	Glu	Gln	Ala	Glu	Asn
	1295					1300					1305			
Ile	Ile	His	Leu	Phe	Thr	Leu	Thr	Asn	Leu	Gly	Ala	Pro	Ala	Ala
	1310					1315					1320			
Phe	Lys	Tyr	Phe	Asp	Thr	Thr	Ile	Asp	Arg	Lys	Arg	Tyr	Thr	Ser
	1325					1330					1335			
Thr	Lys	Glu	Val	Leu	Asp	Ala	Thr	Leu	Ile	His	Gln	Ser	Ile	Thr
	1340					1345					1350			
Gly	Leu	Tyr	Glu	Thr	Arg	Ile	Asp	Leu	Ser	Gln	Leu	Gly	Gly	Asp
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<212> PRT
<213> Streptococcus pyogenes

<400> 551

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			20					25					30		
Lys	Val	Leu	Gly	Asn	Thr	Asp	Arg	His	Ser	Ile	Lys	Lys	Asn	Leu	Ile
		35					40					45			
Gly	Ala	Leu	Leu	Phe	Asp	Ser	Gly	Glu	Thr	Ala	Glu	Ala	Thr	Arg	Leu
	50					55					60				
Lys	Arg	Thr	Ala	Arg	Arg	Arg	Tyr	Thr	Arg	Arg	Lys	Asn	Arg	Ile	Cys
65					70					75					80
Tyr	Leu	Gln	Glu	Ile	Phe	Ser	Asn	Glu	Met	Ala	Lys	Val	Asp	Asp	Ser
				85					90					95	
Phe	Phe	His	Arg	Leu	Glu	Glu	Ser	Phe	Leu	Val	Glu	Glu	Asp	Lys	Lys
			100					105					110		
His	Glu	Arg	His	Pro	Ile	Phe	Gly	Asn	Ile	Val	Asp	Glu	Val	Ala	Tyr
		115					120					125			
His	Glu	Lys	Tyr	Pro	Thr	Ile	Tyr	His	Leu	Arg	Lys	Lys	Leu	Val	Asp
	130					135					140				
Ser	Thr	Asp	Lys	Ala	Asp	Leu	Arg	Leu	Ile	Tyr	Leu	Ala	Leu	Ala	His
145					150					155					160
Met	Ile	Lys	Phe	Arg	Gly	His	Phe	Leu	Ile	Glu	Gly	Asp	Leu	Asn	Pro
				165					170					175	
Asp	Asn	Ser	Asp	Val	Asp	Lys	Leu	Phe	Ile	Gln	Leu	Val	Gln	Thr	Tyr
			180					185					190		
Asn	Gln	Leu	Phe	Glu	Glu	Asn	Pro	Ile	Asn	Ala	Ser	Gly	Val	Asp	Ala
		195					200					205			
Lys	Ala	Ile	Leu	Ser	Ala	Arg	Leu	Ser	Lys	Ser	Arg	Arg	Leu	Glu	Asn
	210					215					220				
Leu	Ile	Ala	Gln	Leu	Pro	Gly	Glu	Lys	Lys	Asn	Gly	Leu	Phe	Gly	Asn
225					230					235					240
Leu	Ile	Ala	Leu	Ser	Leu	Gly	Leu	Thr	Pro	Asn	Phe	Lys	Ser	Asn	Phe
									250					255	
Asp	Leu	Ala	Glu	Asp	Ala	Lys	Leu	Gln	Leu	Ser	Lys	Asp	Thr	Tyr	Asp
			260					265					270		
Asp	Asp	Leu	Asp	Asn	Leu	Leu	Ala	Gln	Ile	Gly	Asp	Gln	Tyr	Ala	Asp
		275					280					285			
Leu	Phe	Leu	Ala	Ala	Lys	Asn	Leu	Ser	Asp	Ala	Ile	Leu	Leu	Ser	Asp
	290					295					300				

Ile 305	Leu	Arg	Val	Asn	Thr 310	Glu	Ile	Thr	Lys	Ala 315	Pro	Leu	Ser	Ala	Ser 320
Met	Ile	Lys	Arg	Tyr 325	Asp	Glu	His	His	Gln 330	Asp	Leu	Thr	Leu	Leu 335	Lys
Ala	Leu	Val	Arg 340	Gln	Gln	Leu	Pro	Glu 345	Lys	Tyr	Lys	Glu	Ile 350	Phe	Phe
Asp	Gln	Ser 355	Lys	Asn	Gly	Tyr	Ala 360	Gly	Tyr	Ile	Asp	Gly 365	Gly	Ala	Ser
Gln	Glu 370	Glu	Phe	Tyr	Lys	Phe 375	Ile	Lys	Pro	Ile	Leu 380	Glu	Lys	Met	Asp
Gly 385	Thr	Glu	Glu	Leu	Leu 390	Val	Lys	Leu	Asn	Arg 395	Glu	Asp	Leu	Leu	Arg 400
Lys	Gln	Arg	Thr	Phe 405	Asp	Asn	Gly	Ser	Ile 410	Pro	His	Gln	Ile	His 415	Leu
Gly	Glu	Leu	His 420	Ala	Ile	Leu	Arg	Arg 425	Gln	Glu	Asp	Phe	Tyr 430	Pro	Phe
Leu	Lys	Asp 435	Asn	Arg	Glu	Lys	Ile 440	Glu	Lys	Ile	Leu	Thr 445	Phe	Arg	Ile
Pro	Tyr 450	Tyr	Val	Gly	Pro	Leu 455	Ala	Arg	Gly	Asn	Ser 460	Arg	Phe	Ala	Trp
Met 465	Thr	Arg	Lys	Ser	Glu 470	Glu	Thr	Ile	Thr	Pro 475	Trp	Asn	Phe	Glu	Glu 480
Val	Val	Asp	Lys	Gly 485	Ala	Ser	Ala	Gln	Ser 490	Phe	Ile	Glu	Arg	Met 495	Thr
Asn	Phe	Asp	Lys 500	Asn	Leu	Pro	Asn	Glu 505	Lys	Val	Leu	Pro	Lys 510	His	Ser
Leu	Leu	Tyr 515	Glu	Tyr	Phe	Thr	Val 520	Tyr	Asn	Glu	Leu	Thr 525	Lys	Val	Lys
Tyr	Val 530	Thr	Glu	Gly	Met	Arg 535	Lys	Pro	Ala	Phe	Leu 540	Ser	Gly	Glu	Gln
Lys 545	Lys	Ala	Ile	Val	Asp 550	Leu	Leu	Phe	Lys	Thr 555	Asn	Arg	Lys	Val	Thr 560
Val	Lys	Gln	Leu	Lys 565	Glu	Asp	Tyr	Phe	Lys 570	Lys	Ile	Glu	Cys	Phe 575	Asp
Ser	Val	Glu	Ile 580	Ser	Gly	Val	Glu	Asp 585	Arg	Phe	Asn	Ala	Ser 590	Leu	Gly
Thr	Tyr	His 595	Asp	Leu	Leu	Lys	Ile 600	Ile	Lys	Asp	Lys	Asp 605	Phe	Leu	Asp
Asn	Glu 610	Glu	Asn	Glu	Asp	Ile 615	Leu	Glu	Asp	Ile	Val 620	Leu	Thr	Leu	Thr
Leu 625	Phe	Glu	Asp	Arg	Glu 630	Met	Ile	Glu	Glu	Arg 635	Leu	Lys	Thr	Tyr	Ala 640
His	Leu	Phe	Asp	Asp 645	Lys	Val	Met	Lys	Gln 650	Leu	Lys	Arg	Arg	Arg 655	Tyr
Thr	Gly	Trp	Gly 660	Arg	Leu	Ser	Arg	Lys 665	Leu	Ile	Asn	Gly	Ile 670	Arg	Asp
Lys	Gln	Ser 675	Gly	Lys	Thr	Ile	Leu 680	Asp	Phe	Leu	Lys	Ser 685	Asp	Gly	Phe
Ala	Asn	Arg	Asn	Phe	Met	Gln	Leu	Ile	His	Asp	Asp	Ser	Leu	Thr	Phe

690					695					700					
Lys 705	Glu	Asp	Ile	Gln	Lys 710	His	Gln	Val	Ser	Gly 715	Gln	Gly	Asp	Ser	Leu 720
His	Glu	His	Ile	Ala 725	Asn	Leu	Ala	Gly	Ser 730	Pro	Ala	Ile	Lys	Lys 735	Gly
Ile	Leu	Gln	Thr 740	Val	Lys	Val	Val	Asp 745	Glu	Leu	Val	Lys	Val 750	Met	Gly

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765
Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780
Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800
Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815
Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830
Leu Ser Asp Tyr Asp Val Asp Ala Ile Val Pro Gln Ser Phe Leu Lys
835 840 845
Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860
Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880
Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910
Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925
Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945 950 955 960
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975
Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990
Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005
Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
1010 1015 1020
Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
1025 1030 1035
Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
1040 1045 1050
Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
1055 1060 1065
Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080
Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
1085 1090 1095
Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
1100 1105 1110
Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
1115 1120 1125
Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
1130 1135 1140
Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
1145 1150 1155
Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
1160 1165 1170
Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
1175 1180 1185

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

<210> 853
<211> 1368
<212> PRT
<213> Streptococcus pyogenes

<400> 853

Met	Asp	Lys	Lys	Tyr	Ser	Ile	Gly	Leu	Asp	Ile	Gly	Thr	Asn	Ser	Val
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Gly	Trp	Ala	Val	Ile	Thr	Asp	Glu	Tyr	Lys	Val	Pro	Ser	Lys	Lys	Phe
			20					25					30		
Lys	Val	Leu	Gly	Asn	Thr	Asp	Arg	His	Ser	Ile	Lys	Lys	Asn	Leu	Ile
		35					40					45			
Gly	Ala	Leu	Leu	Phe	Asp	Ser	Gly	Glu	Thr	Ala	Glu	Ala	Thr	Arg	Leu
	50					55					60				
Lys	Arg	Thr	Ala	Arg	Arg	Arg	Tyr	Thr	Arg	Arg	Lys	Asn	Arg	Ile	Cys
65					70					75					80
Tyr	Leu	Gln	Glu	Ile	Phe	Ser	Asn	Glu	Met	Ala	Lys	Val	Asp	Asp	Ser
				85					90					95	
Phe	Phe	His	Arg	Leu	Glu	Glu	Ser	Phe	Leu	Val	Glu	Glu	Asp	Lys	Lys
			100					105					110		
His	Glu	Arg	His	Pro	Ile	Phe	Gly	Asn	Ile	Val	Asp	Glu	Val	Ala	Tyr
		115					120					125			
His	Glu	Lys	Tyr	Pro	Thr	Ile	Tyr	His	Leu	Arg	Lys	Lys	Leu	Val	Asp
	130					135					140				
Ser	Thr	Asp	Lys	Ala	Asp	Leu	Arg	Leu	Ile	Tyr	Leu	Ala	Leu	Ala	His
145					150					155					160
Met	Ile	Lys	Phe	Arg	Gly	His	Phe	Leu	Ile	Glu	Gly	Asp	Leu	Asn	Pro
				165					170					175	
Asp	Asn	Ser	Asp	Val	Asp	Lys	Leu	Phe	Ile	Gln	Leu	Val	Gln	Thr	Tyr
			180					185					190		

Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
195 200 205
Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
210 215 220
Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225 230 235 240
Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
245 250 255
Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260 265 270
Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
275 280 285
Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
290 295 300
Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305 310 315 320
Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335
Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350
Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365
Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380
Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385 390 395 400
Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
405 410 415
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
420 425 430
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
450 455 460
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465 470 475 480
Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
485 490 495
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
500 505 510
Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
515 520 525
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
530 535 540
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545 550 555 560
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
565 570 575
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
580 585 590
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
595 600 605
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
610 615 620
Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640

His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
635 640 645 650 655

Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670

Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685

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

Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720

His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735

Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765

Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780

Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800

Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815

Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830

Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
835 840 845

Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880

Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895

Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910

Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Pro Pro Arg Gln Ile Thr
915 920 925

Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940

Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945 950 955 960

Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975

Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990

Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005

Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
1010 1015 1020

Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
1025 1030 1035

Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
1040 1045 1050

Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
1055 1060 1065

Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080

Arg	Lys 1085	Val	Leu	Ser	Met	Pro 1090	Gln	Val	Asn	Ile	Val 1095	Lys	Lys	Thr
Glu	Val 1100	Gln	Thr	Gly	Gly	Phe 1105	Ser	Lys	Glu	Ser	Ile 1110	Leu	Pro	Lys
Arg	Asn 1115	Ser	Asp	Lys	Leu	Ile 1120	Ala	Arg	Lys	Lys	Asp 1125	Trp	Asp	Pro
Lys	Lys 1130	Tyr	Gly	Gly	Phe	Asp 1135	Ser	Pro	Thr	Val	Ala 1140	Tyr	Ser	Val
Leu	Val 1145	Val	Ala	Lys	Val	Glu 1150	Lys	Gly	Lys	Ser	Lys 1155	Lys	Leu	Lys
Ser	Val 1160	Lys	Glu	Leu	Leu	Gly 1165	Ile	Thr	Ile	Met	Glu 1170	Arg	Ser	Ser
Phe	Glu 1175	Lys	Asn	Pro	Ile	Asp 1180	Phe	Leu	Glu	Ala	Lys 1185	Gly	Tyr	Lys
Glu	Val 1190	Lys	Lys	Asp	Leu	Ile 1195	Ile	Lys	Leu	Pro	Lys 1200	Tyr	Ser	Leu
Phe	Glu 1205	Leu	Glu	Asn	Gly	Arg 1210	Lys	Arg	Met	Leu	Ala 1215	Ser	Ala	Gly
Glu	Leu 1220	Gln	Lys	Gly	Asn	Glu 1225	Leu	Ala	Leu	Pro	Ser 1230	Lys	Tyr	Val
Asn	Phe 1235	Leu	Tyr	Leu	Ala	Ser 1240	His	Tyr	Glu	Lys	Leu 1245	Lys	Gly	Ser
Pro	Glu 1250	Asp	Asn	Glu	Gln	Lys 1255	Gln	Leu	Phe	Val	Glu 1260	Gln	His	Lys
His	Tyr 1265	Leu	Asp	Glu	Ile	Ile 1270	Glu	Gln	Ile	Ser	Glu 1275	Phe	Ser	Lys
Arg	Val 1280	Ile	Leu	Ala	Asp	Ala 1285	Asn	Leu	Asp	Lys	Val 1290	Leu	Ser	Ala
Tyr	Asn 1295	Lys	His	Arg	Asp	Lys 1300	Pro	Ile	Arg	Glu	Gln 1305	Ala	Glu	Asn
Ile	Ile 1310	His	Leu	Phe	Thr	Leu 1315	Thr	Asn	Leu	Gly	Ala 1320	Pro	Ala	Ala
Phe	Lys 1325	Tyr	Phe	Asp	Thr	Thr 1330	Ile	Asp	Arg	Lys	Arg 1335	Tyr	Thr	Ser
Thr	Lys 1340	Glu	Val	Leu	Asp	Ala 1345	Thr	Leu	Ile	His	Gln 1350	Ser	Ile	Thr
Gly	Leu 1355	Tyr	Glu	Thr	Arg	Ile 1360	Asp	Leu	Ser	Gln	Leu 1365	Gly	Gly	Asp

<210> 854
<211> 1131
<212> PRT
<213> Acidovorax ebreus

<400> 854

Met	Ala	Gln	His	Val	Phe	Gly	Leu	Asp	Ile	Gly	Ile	Ala	Ser	Val	Gly
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Trp	Ala	Ile	Leu	Gly	Glu	Gln	Arg	Ile	Ile	Asp	Leu	Gly	Val	Arg	Cys
			20					25					30	
Phe	Asp	Lys	Ala	Glu	Thr	Ala	Lys	Glu	Gly	Asp	Pro	Leu	Asn	Leu	Thr
		35					40					45			
Arg	Arg	Gln	Ala	Arg	Leu	Leu	Arg	Arg	Arg	Arg	Leu	Tyr	Arg	Arg	Ala	Trp
	50					55						60				
Arg	Leu	Thr	Gln	Leu	Ser	Arg	Leu	Leu	Lys	Arg	Lys	Gly	Leu	Ile	Ala
65					70					75					80

Asp	Ala	Lys	Leu	Phe 85	Ala	Lys	Ala	Pro	Ser 90	Tyr	Gly	Asp	Ser	Ala 95	Trp
Glu	Leu	Arg	Arg 100	Gln	Gly	Leu	Asp	Arg 105	Leu	Leu	Thr	Pro	Leu 110	Glu	Trp
Ala	Arg	Val 115	Ile	Tyr	His	Gln	Cys 120	Lys	His	Arg	Gly	Phe 125	His	Trp	Thr
Ser	Lys 130	Ala	Glu	Glu	Ala	Lys 135	Ala	Asp	Ser	Asp	Ala 140	Glu	Gly	Gly	Arg
Val 145	Lys	Gln	Gly	Leu	Ala 150	His	Thr	Lys	Ala	Leu 155	Met	Gln	Ala	Lys	Asn 160
Tyr	Arg	Ser	Ala	Ala 165	Glu	Met	Val	Leu	Ala 170	Glu	Phe	Pro	Asp	Ala 175	Gln
Arg	Asn	Lys	Arg 180	Gly	Gln	Tyr	Asp	Lys 185	Ala	Leu	Ser	Arg	Val 190	Leu	Leu
Gly	Glu	Glu 195	Leu	Ala	Leu	Leu	Phe 200	Ala	Thr	Gln	Arg	Arg 205	Leu	Gly	Asn
Pro	His 210	Ala	Ser	Asp	Phe	Phe 215	Glu	Lys	Leu	Ile	Leu 220	Gly	Asp	Gly	Asp
Arg 225	Lys	Ser	Gly	Leu	Phe 230	Trp	Gln	Gln	Lys	Pro 235	Ala	Leu	Ser	Gly	Ala 240
Asp	Leu	Leu	Lys	Met 245	Leu	Gly	Lys	Cys	Thr 250	Phe	Glu	Lys	Gly	Glu 255	Tyr
Arg	Ala	Pro	Lys 260	Ala	Ser	Phe	Ser	Val 265	Glu	Arg	His	Val	Trp 270	Leu	Thr
Arg	Leu	Asn 275	Asn	Leu	Arg	Ile	Val 280	Val	Asp	Gly	Arg	Ser 285	Arg	Pro	Leu
Asn	Glu 290	Ala	Glu	Arg	Gln	Ala 295	Ala	Leu	Leu	Leu	Pro 300	Tyr	Gln	Thr	Glu
Thr 305	Ser	Lys	Tyr	Lys	Thr 310	Leu	Lys	Asn	Ala	Phe 315	Ile	Lys	Ala	Gly	Leu 320
Trp	Gly	Asp	Gly	Val 325	Arg	Phe	Gly	Gly	Leu 330	Ala	Tyr	Pro	Ser	Gln 335	Ala
Gln	Ile	Asp	Ala 340	Glu	Lys	Thr	Lys	Asp 345	Pro	Glu	Asp	Gln	Phe 350	Leu	Val
Lys	Leu	Pro 355	Ala	Trp	His	Glu	Leu 360	Arg	Lys	Ala	Phe	Lys 365	Ala	Ala	Gly
His	Glu 370	Ala	Leu	Trp	Gln	Gln 375	Ile	Ser	Thr	Pro	Ala 380	Leu	Asp	Gly	Asp
Pro 385	Thr	Leu	Leu	Asp	Gln 390	Ile	Ala	Thr	Val	Leu 395	Ser	Val	Tyr	Lys	Asp 400
Gly	Ala	Glu	Val	Val 405	Gln	Gln	Leu	Arg	Gln 410	Leu	Ala	Leu	Pro	Glu 415	Pro
Ala	Ala	Ser	Ile 420	Ala	Val	Leu	Glu	Lys 425	Ile	Ser	Phe	Asp	Lys 430	Phe	Ser
Ser	Leu	Ser 435	Leu	Lys	Ala	Leu	Arg 440	Arg	Ile	Val	Pro	Leu 445	Met	Gln	Ser
Gly	Leu 450	Arg	Tyr	Asp	Glu	Ala 455	Val	Ala	Gln	Ile	Pro 460	Glu	Tyr	Gly	His
His 465	Ser	Gln	Arg	Ile	Glu 470	Pro	Gly	Ala	Ala	Lys 475	His	Leu	Tyr	Leu	Pro 480
Pro	Phe	Tyr	Glu	Ala 485	Gln	Arg	Lys	Tyr	Ala 490	Gly	Lys	Gly	Asp	His 495	Ile
Gly	Ser	Met	Gln 500	Phe	Arg	Asp	Asn	Ala 505	Asp	Ile	Pro	Arg	Asn 510	Pro	Val
Val	Leu	Arg 515	Ala	Leu	Asn	Gln	Ala 520	Arg	Lys	Val	Val	Asn 525	Ala	Leu	Ile

Arg	Glu 530	Tyr	Gly	Ser	Pro	Ile 535	Ala	Val	Asn	Ile	Glu 540	Met	Ala	Arg	Asp
Leu 545	Ser	Arg	Pro	Leu	Asp 550	Glu	Arg	Asn	Lys	Val 555	Lys	Arg	Ala	Gln	Glu 560
Glu	Phe	Arg	Asp	Arg 565	Lys	Asp	Arg	Ala	Arg 570	Ser	Glu	Phe	Glu	Arg 575	Asp
Phe	Gly	Tyr	Lys 580	Pro	Lys	Ala	Ala	Ala 585	Phe	Glu	Lys	Tyr	Met 590	Leu	Tyr
Arg	Glu	Gln 595	Leu	Gly	Gln	Cys	Ala 600	Tyr	Ser	Gln	Gln	Pro 605	Leu	Asp	Ile
Gln	Arg 610	Val	Leu	Asp	Asp	His 615	Asn	Tyr	Ala	Gln	Val 620	Asp	His	Ala	Leu
Arg 625	Tyr	Ser	Arg	Ser	Tyr 630	Asp	Asp	Ser	Lys	Asn 635	Asn	Lys	Val	Leu	Val 640
Leu	Thr	His	Glu	Asn 645	Gln	Asn	Lys	Gly	Asn 650	Arg	Thr	Ala	Phe	Glu 655	Tyr
Leu	Thr	Ser	Phe 660	Pro	Asp	Gly	Glu	Asp 665	Gly	Glu	Arg	Trp	Arg 670	Thr	Phe
Val	Ala	Trp 675	Val	Gln	Gly	Asn	Lys 680	Ala	Tyr	Arg	Met	Ala 685	Lys	Arg	Asn
Arg	Leu 690	Leu	Arg	Lys	Asn	Tyr 695	Gly	Val	Asp	Glu	Ser 700	Lys	Gly	Phe	Ile
Asp 705	Arg	Asn	Leu	Asn	Asp 710	Thr	Arg	Tyr	Ile	Cys 715	Lys	Phe	Phe	Lys	Asn 720
Tyr	Val	Glu	Glu	His 725	Leu	Gln	Leu	Ala	Ala 730	Arg	Ala	Asp	Gly	Asp 735	Thr
Ala	Arg	Arg	Cys 740	Val	Val	Val	Asn	Gly 745	Gln	Leu	Thr	Ala	Phe 750	Leu	Arg
Ala	Arg	Trp 755	Gly	Leu	Thr	Lys	Val 760	Arg	Gly	Asp	Ser	Asp 765	Arg	His	His
Ala	Leu 770	Asp	Ala	Ala	Val	Val 775	Ala	Ala	Cys	Thr	His 780	Gly	Met	Val	Lys
Ala 785	Leu	Ala	Asp	Tyr	Ser 790	Arg	Arg	Lys	Glu	Ile 795	Ser	Phe	Leu	Gln	Glu 800
Gly	Phe	Pro	Asp	Pro 805	Glu	Thr	Gly	Glu	Ile 810	Leu	Asn	Pro	Ala	Ala 815	Phe
Asp	Arg	Ala	Arg 820	Gln	His	Phe	Pro	Glu 825	Pro	Trp	Thr	His	Phe 830	Ala	His
Glu	Leu	Lys 835	Ala	Arg	Leu	Phe	Thr 840	Asp	Asp	Leu	Ala	Ala 845	Leu	Arg	Glu
Asp	Met 850	Gln	Arg	Leu	Gly	Ser 855	Tyr	Thr	Thr	Glu	Asp 860	Leu	Gly	Arg	Leu
Arg 865	Thr	Leu	Phe	Val	Ser 870	Arg	Ala	Pro	Gln	Arg 875	Arg	Ser	Gly	Gly	Ala 880
Val	His	Lys	Glu	Thr 885	Ile	Tyr	Ala	Gln	Pro 890	Glu	Ser	Leu	Lys	Gln 895	Gln
Gly	Gly	Val	Ile 900	Glu	Lys	Ile	Leu	Leu 905	Thr	Ser	Leu	Lys	Leu 910	Gln	Asp
Phe	Asp	Lys 915	Leu	Leu	Asn	Pro	Glu 920	Ser	Asn	Asp	His	Phe 925	Val	Glu	Pro
His	Arg 930	Asn	Glu	Arg	Leu	Tyr 935	Ala	Ala	Ile	Arg	Gln 940	Arg	Leu	Glu	Gln
Phe 945	Gly	Gly	Arg	Ala	Asp 950	Lys	Ala	Phe	Gly	Pro 955	Asp	Asn	Leu	Phe	His 960
Lys	Pro	Asp	Lys	Asn 965	Asn	Gln	Pro	Thr	Gly 970	Pro	Val	Val	Arg	Ser 975	Ile

Lys Leu Val Arg Gly Lys Gln Thr Gly Ile Pro Ile Arg Gly Gly Leu
980 985 990

Ala Lys Asn Asp Ser Met Leu Arg Val Asp Ile Phe Thr Lys Ala Gly
995 1000 1005

Lys Phe His Leu Val Pro Val Tyr Val His His Arg Val Thr Gly
1010 1015 1020

Leu Pro Asn Arg Ala Ile Val Ala Phe Lys Asp Glu Asp Glu Trp
1025 1030 1035

Thr Leu Ile Asp Glu Ser Phe Ala Phe Leu Phe Ser Val Tyr Pro
1040 1045 1050

Asn Asp Tyr Val Lys Val Thr Leu Lys Lys Glu Gln Gln Ser Gly
1055 1060 1065

Tyr Tyr Ser Gly Ala Asp Arg Ser Thr Gly Ala Met Asn Leu Trp
1070 1075 1080

Ala His Asp Arg Ala Ala Ser Val Gly Lys Asp Gly Leu Ile Arg
1085 1090 1095

Gly Ile Gly Val Lys Thr Ala Leu Ser Val Glu Lys Tyr Gln Leu
1100 1105 1110

Asp Val Leu Gly Arg Ile Tyr Leu Ala Pro Pro Glu Thr Arg Ser
1115 1120 1125

Gly Leu Ala
1130

<210> 855
<211> 1126
<212> PRT
<213> Unknown.

<220>
<223> Description of Unknown:
Acid mine drainage bacteria Ga0052161_JGI Cas9 sequence

<400> 855

Met Ala Asp Ser Leu Ser Arg Pro Trp Arg Leu Ala Leu Asp Val Gly
1 5 10 15

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

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

Gly Val Asn Leu Phe Asp Ser Gly Val Glu Asp Gly Ile Pro Lys Asn
50 55 60

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

Lys Val Arg Lys Arg Asn Leu Arg Asp Val Leu Val Ala Ala Asp Cys
85 90 95

Leu Pro Cys Asp Ser Ala Thr Ser Gln Arg Ser Leu Leu Lys Gly Glu
100 105 110

Pro Arg Ser Ala Ser Ile Ala Leu Arg Asp Gln Met Val Pro Ile Asp
115 120 125

Gly Asp Gly Ser Val Ala Ile Pro Ala Val Trp Ala Trp Arg Trp Lys
130 135 140

Ala Leu Arg Lys Phe Gly Ile Gln Leu Thr His His Glu Leu Gly Val Ile
145 150 155 160

Leu Met Ala Leu Ala Arg Gly Gln Gly Phe Ser Glu Glu Ser
165 170 175

Asp Ser Arg Thr Val Ala Pro Leu Val Ser Glu Leu Gln Glu Lys Ile
180 185 190
Ser Arg Ala Gly Cys Thr Ala Phe Gly Asp Tyr Ala Ala Glu Ile Leu
195 200
Ala Lys Ser Pro Gly Ala Thr Ile Arg Ala Ser Asn Ala Glu Pro Asn
210 215 220
Phe Val Ser Arg Gln Met Val Leu Gly Glu Phe Arg Ala Ile Arg Asn
225 230 235 240
Ala Gln Thr Arg Leu Leu Ser Pro Lys Arg Ser Trp Asp Glu Ile Glu Asn
245 250 255
Ile Ile Phe Asp Gln Ala Pro Leu Ala Pro Pro Arg Pro Gly Asn Cys
260 265 270
Pro Leu Val Lys Glu Asp Val Arg Leu Glu Arg Ala His Pro Leu Ala
275 280 285
Glu Arg Leu Val Lys Ile Val Gln Thr Leu Arg Asn Val Arg Leu Phe Asp
290 295 300
Ala Asp Gly Ala Val Pro Glu Asp Arg Pro Thr Glu Leu Thr Pro Asp
305 310 315 320
Glu Ile Arg Lys Ala Glu Lys Phe Leu Ser Thr Arg Lys Ser Ala Thr
325 330 335
Ala Ile Ser Leu Phe Lys Ser Leu Arg Ser Asn
340 345 350
Tyr His Gly Ser Arg Ala Glu Ala Thr Asp Leu Pro Gly Asn Glu
355 360 365
Thr Asn Val Ala Ala Ala Arg Glu Asp Ala Phe Gly Ala Ala Trp Ala
370 375 380
Ala Phe Glu Pro Ser Lys Gln Arg Asp Ile Val Glu Leu Ala Leu Ser
385 390 395 400
Ile Arg Gly Gly Arg Thr Ala Asp Glu Ile Arg Ala Ala Ala Asp Thr
405 410 415
Trp Gly Ile Ser Ile Asp Ala Ala Arg Phe Ile Asp Met Leu Pro
420 425 430
Lys Gly Arg Ala Ala Tyr Gly Leu Thr Ala Thr Asn Arg Leu Leu Ala
435 440 445
Val Met Leu Glu Glu Gly Leu Ser Leu Phe Asp Ala Arg Asp Arg Glu
450 455 460
Tyr Pro Gln Ala Ala Gln Ser Arg Lys Phe Cys Ser Leu Pro Tyr Tyr
465 470 475 480
Ala Ile Ala Leu Pro Asp His Val Phe Asp Gly Asp Pro Arg Ala Asp
485 490 495
Glu Thr Ala Thr Asp Glu Gln Arg Tyr Gly His Val Arg Asn Pro Ile
500 505 510
Val His Val Ala Leu Asn Gln Ile Arg Gly Leu Val Asn Ala Leu Val
515 520 525
Ala Glu Phe Gly Ala Pro Val Glu Ile Thr Val Glu Leu Ala Arg Glu
530 535 540
Ile Ser Leu Ser Asp Asp Glu Lys Lys Lys Leu Leu Lys Ser Gln Lys
545 550 555 560
Glu Arg Ala Glu Met Arg Glu Thr Ala Ala Ala Thr Ile Arg Glu Cys
565 570 575
Gly Tyr Lys Pro Ser Arg Asp Leu Ile Asp Arg Tyr Val Leu Tyr Cys
580 585 590
Gly Gln Asp Arg Arg Leu Val Gln Gly Glu Phe Ala Glu Ile Lys Cys
595 600 605
Val Tyr Ser Gly Lys Pro Ile Glu Ser Phe Lys Arg Leu Phe Ser Asn
610 615 620

Asp Ile Glu Ile Asp His Ile Val Pro Arg Gln Arg Ser His Asp Asp
625 630 635 640
Ser Leu Ala Asn Lys Val Leu Ala Tyr Arg Gly Ala Asn Arg Asn Lys
645 650 655
Leu Asn Arg Thr Pro Phe Glu Phe Trp Gly His Thr Glu His Ser Trp Ala
660 665 670
Glu Ile Trp Glu Arg Ala Glu Phe Ala Phe Arg Lys Asn Pro Lys Lys
675 680 685
Leu Ala Arg Phe Arg Glu Thr Ala Ala Gln Glu Phe Thr Gly Asp Phe
690 695 700
Ala Ser Arg His Leu Asn Asp Thr Arg Tyr Ile Ser Lys Met Thr Arg
705 710 715 720
Leu Tyr Leu Glu Arg Leu Lys Gly Thr Glu Cys Val Tyr Ala Thr Arg
725 730 735
Gly Ser Ile Thr Gly Arg Leu Arg Lys Leu
740 745
Leu Pro Val Pro Ala Ala Val Gln Ser Leu Ile Asp Ile Ser Arg Ala
750 755 760
Ser Ser Arg Asp Val Pro Ile Glu Leu Lys Arg His Arg His Arg His
765 770 775
His Ala Ile Asp Ala Ala Leu Ile Gly Leu Val Asp His His Thr Leu
780 785 790 795
Gln Tyr Tyr Phe Glu Lys Thr Glu Ser Gln Thr Asp Lys Arg Phe Pro
800 805 810
Leu Pro Trp Pro Thr Phe Lys Glu Leu Ala Glu Arg Leu Gln Gly
815 820 825
Leu Val Val Arg Arg Arg Pro Glu His Lys Arg Gly Phe Arg Tyr Gln
830 835 840
Gly Gln Leu Val Glu Asp Ser Arg Tyr Arg Leu Arg Gly Arg Gln Asn Glu
845 850 855
Lys Asn Val Leu Ser Ser Arg Thr Ser Leu Ile Gly Leu Val Ile Asp
860 865 870 875
Lys Phe Gly Asn Leu Ile Pro Gly Thr Arg Ser Ala Gly Ile Gln Phe
880 885 890
Ser Cys Lys Glu Ala Phe Glu Ser Ser Ile Met Arg Ile Asp Pro Thr
895 900 905 910
Gly Arg Leu Ile Thr Leu Leu Asn Trp Glu Thr Leu Gln Ala Ile Arg
915 920 925
Asn Ser Tyr Leu Thr Ser Arg Pro Gly Asp Gly Asp Ser Gly Pro Leu
930 935 940
Glu Arg Lys Lys Ala Glu Arg Glu Ala Thr Ala Phe Ala Trp Lys Ser
945 950 955 960
Leu Cys Ser Arg Ala Ala Thr Thr Ala Gly Gly Ile Ser Ser Val Arg
965 970 975
Lys Lys Ile Val Leu Glu Asp Pro Val Ile Val Gly Pro Glu Lys Ser
980 985 990
Ala Val Lys Ser Ala Gly Tyr Ala Phe Ala Tyr Val Ile Lys Arg Asn
995 1000 1005
Val Pro Asn Thr Arg Tyr Gln Leu Phe Pro Val Ala Met Lys Asp
1010 1015 1020
His Glu Thr Asp Gln Gly Pro Pro Leu Lys Pro Gly Glu Val Val
1025 1030 1035
Val Cys Lys Leu His Lys Gly Asp Met Leu Ser Leu Leu Leu Glu
1040 1045 1050
Ser Asn Ser Leu Ser Ser Pro Val Tyr Cys Thr Val Gln Gly Phe
1055 1060 1065

Lys Ser Ser Gly Val Leu Thr Leu Thr Thr Gln Tyr Asn Ala Ala
1070 1075 1080
Arg Asn Gly Gly Arg Ala Val Asn Thr Val Pro Glu Ile Glu Ser
1085 1090 1095
Ser Asp Gly Arg Asn Ala Val Asn Lys Val Phe Gly Thr Trp Arg
1100 1105 1110
Ala Arg Ile Val Arg Pro Thr Val Leu Gly Arg Leu Pro
1115 1120 1125

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<111> Unknown

<120>
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Tranium mine bacteria FW106_JGI Cas9 sequence

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Gln Gln Ala Ala Ala Pro Met Val Phe Gly Phe Asp Ile Gly Ile Ala
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Ser Val Gly Trp Thr Val Leu Gly Pro Thr Arg Ile Ile Asp Leu Gly
35 40 45
Val Arg Ala Phe Asp Lys Ala Glu Thr Ala Lys Glu Gly Glu Pro Leu
50 55 60
Asn Leu Ala Arg Arg Thr Ala Arg Leu Met Arg Arg Arg Leu Arg Arg
65 70 75 80
Arg Ala Trp Arg Leu Thr Lys Leu Ala Arg Leu Leu Lys Arg His Gly
85 90 95
Val Ile Asp Glu Val Ala Leu Phe Met Pro Glu His Pro Tyr Pro His
100 105 110
Ser Leu Trp Lys Leu Arg Val Glu Ala Leu Asp Arg Pro Leu Ala Ala
115 120 125
Glu Glu Trp Ala Arg Val Ile Tyr His Leu Cys Lys His Arg Gly Phe
130 135 140
His Trp Ile Ser Arg Ala Glu Glu Lys Lys Ala Glu Ala Asp Ser Lys
145 150 155 160
Gly Glu Gly Gly Lys Val Lys Gln Gly Leu Ala Gly Thr Lys Arg Leu
165 170 175
Met Glu Asp Lys Gly Tyr Arg Ser Ala Ala Glu Met Val Leu Ala Glu
180 185 190
Phe Pro Asp Ala Gln Arg Asn Lys Gln Gly Asp Tyr Thr Lys Ser Leu
195 200 205
Ser Arg Val Leu Leu Gly Asp Glu Leu Ser Leu Leu Phe Thr Arg Gln
210 215 220
Arg Glu Leu Gly Asn Gln His Ala Thr Pro Glu Leu Gln Leu Ser Val
225 230 235 240
Leu Gly Thr Gly Asp His Lys Ser Gly Leu Phe Trp Ala Gln Lys Pro
245 250 255
Ala Leu Ala Gly Asp Ala Leu Leu Gly Met Leu Gly Lys Cys Thr Phe
260 265 270
Glu Lys Ser Glu Tyr Arg Ala Pro Lys Ala Ser Phe Thr Ala Glu Arg
275 280 285

His	Val	Trp	Leu	Thr	Arg	Leu	Asn	Asn	Leu	Arg	Val	Val	Ala	Asp	Gly
	290					295					300				
Arg	Val	Arg	Pro	Leu	Asn	Glu	Gln	Glu	Arg	Gln	Ile	Ala	Leu	Arg	Leu
305					310					315					320
Pro	Tyr	Gln	Gln	Ala	Ser	Asp	Leu	Thr	Tyr	Lys	Gln	Leu	Arg	Ala	Ala
				325					330					335	
Leu	Val	Lys	Ala	Gly	Val	Leu	Pro	Asp	Ser	Phe	Arg	Phe	Thr	Gly	Leu
			340					345					350		
Ala	Tyr	Pro	Asn	Ala	Thr	Gln	Gln	Ser	Asp	Ser	Lys	Ile	Lys	Asp	Pro
		355					360					365			
Glu	Ala	Ala	Pro	Leu	Ile	Arg	Ile	Pro	Ala	Tyr	Gln	Glu	Ile	Arg	Leu
	370					375					380				
Thr	Leu	Lys	Lys	Ala	Gly	Leu	Glu	Thr	Glu	Trp	Glu	Gly	Met	Ala	Ser
385					390					395					400
Leu	Ala	Ile	Asp	Gly	Lys	Pro	Glu	Leu	Leu	Asp	Gln	Ile	Ala	Trp	Val
				405					410					415	
Leu	Thr	Val	Phe	Lys	Glu	Asp	Asp	Glu	Val	Arg	Ala	Glu	Leu	Arg	Lys
			420					425					430		
Leu	Asn	Leu	Pro	Gln	Ala	Asp	Lys	Met	Val	Glu	Ala	Leu	Leu	Asp	Ile
		435					440					445			
Arg	Phe	Asp	Lys	Phe	His	Ala	Leu	Ser	Leu	Lys	Ala	Leu	Arg	Asn	Ile
	450					455					460				
Val	Pro	His	Met	Glu	Leu	Gly	Leu	Arg	Tyr	Asp	Glu	Ala	Cys	Glu	Lys
465					470					475					480
Ala	Gly	Tyr	His	His	Ser	Gln	Leu	Phe	Thr	Val	Gly	Ala	Gly	Thr	His
				485					490					495	
Arg	Tyr	Leu	Pro	Pro	Phe	Tyr	Ser	Lys	Arg	Asp	Ala	Ser	Gly	Arg	Met
			500					505					510		
Ile	Phe	Asp	Gln	Glu	Leu	Asp	Ile	Pro	Arg	Asn	Pro	Val	Val	Leu	Arg
		515					520					525			
Ala	Leu	Asn	Gln	Ala	Arg	Lys	Val	Ile	Asn	Ala	Leu	Ile	Arg	His	Tyr
	530					535					540				
Gly	Pro	Pro	Ser	Glu	Val	Arg	Ile	Glu	Leu	Ala	Arg	Asp	Leu	Ser	Arg
545					550					555					560
Pro	Phe	Asp	Glu	Arg	Lys	Lys	Ile	Gln	Thr	Ala	Gln	Asp	Glu	Tyr	Arg
				565					570					575	
Glu	Arg	Asn	Glu	Lys	Glu	Lys	Ile	Arg	Phe	Leu	Glu	Glu	Phe	Ser	Leu
			580					585					590		
Ser	Gly	Thr	Ala	Lys	Gly	Arg	Asp	Phe	Glu	Lys	Trp	Gln	Leu	Tyr	Arg
		595					600					605			
Glu	Gln	Gln	Gly	Lys	Cys	Ala	Tyr	Ser	Leu	Glu	Ala	Leu	Asp	Leu	His
	610					615					620				
Arg	Leu	Phe	Glu	Val	Gly	Tyr	Val	Glu	Ile	Asp	His	Ala	Leu	Pro	Tyr
625					630					635					640
Ser	Arg	Ser	Tyr	Asp	Asp	Ser	Lys	Asn	Asn	Lys	Val	Leu	Val	Leu	Ala
				645					650					655	
Lys	Glu	Asn	Arg	Asn	Lys	Gly	Asn	Gln	Thr	Pro	Tyr	Glu	Tyr	Leu	Asp
			660					665					670		
Gly	Met	Glu	Asn	Thr	Glu	Arg	Trp	Arg	Ala	Phe	Ala	Ser	Phe	Val	Glu
		675					680					685			
Ser	Asn	Lys	Thr	Tyr	Arg	Val	Ala	Lys	Arg	Ser	Arg	Leu	Leu	Arg	Lys
	690					695					700				
Glu	Phe	Gly	Ala	Lys	Glu	Ser	Ser	Glu	Phe	Lys	Glu	Arg	Asn	Leu	Asn
705					710					715					720
Asp	Thr	Arg	Tyr	Ile	Cys	Lys	Phe	Phe	Lys	Asn	Tyr	Val	Glu	Arg	Tyr
				725					730					735	

Leu Gln Leu Ala Glu Asn Ser Glu Ala Lys Arg Cys Val Val Val Ser
750 755 760 765

Gly Gln Leu Thr Ser Phe Leu Arg Ala Arg Trp Gly Leu Ile Lys Val
770 775 780

Arg Glu Asp Ser Asp Arg His His Ala Leu Asp Ala Ala Val Val Ala
785 790 795 800

Ala Cys Ser His Gly Met Val Lys Arg Leu Ser Asp Tyr Ala Arg Arg
805 810 815

Arg Glu Leu Glu Lys Val Ser Glu Gly Phe Val Asp Met Glu Thr Gly
820 825 830

Glu Ile Val Asn Pro Ala Met Phe Arg Gln Leu Glu Gln His Phe Pro
835 840 845

Glu Pro Trp Pro Asn Phe Arg His Glu Leu Glu Ala Arg Arg Lys Ile
850 855 860

Asp Asp Pro Ala Ser Leu Arg Ser Glu Ile Glu Arg Leu Gly Thr Tyr
865 870 875 880

Ser Ser Asp Val Leu Gln Ile Leu Lys Pro Leu Phe Val Ser Arg Ala
885 890 895

Val Gln Arg Arg Asn Arg Gly Ala Ala His Glu Lys Glu Thr Ile Tyr
900 905 910

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

Leu Ala Ser Leu Thr Leu Lys Asp Ile Asp Lys Leu Ile Asn Pro His
930 935 940

Arg Asn Glu Lys Leu Tyr Ala Ala Ile Arg Ser Arg Leu Glu Ala His
945 950 955 960

Gly Gly Lys Gly Asp Lys Ala Phe Pro Ser Asn Asn Pro Leu Arg Lys
965 970 975

Pro Asp Arg Glu Gly Asn Ala Thr Gly Pro Ile Val Arg Thr Val Thr
980 985 990

Met Val Ile Asp Lys Leu Ser Gly Ile Pro Val Arg Gly Gly Val Ala
995 1000 1005

Lys Asn Asp Ser Met Leu Arg Val Asp Val Phe Thr Lys Ala Gly Lys
1010 1015 1020

Phe His Leu Val Pro Val Tyr Val His His Ser Val Ala Lys Thr
1025 1030 1035

Leu Pro Asp Arg Ala Ile Val Gln Ala Lys Asp Glu Asp Glu Trp
1040 1045 1050

Thr Leu Ile Asp Asn Ser Phe Asp Phe Cys Phe Ser Leu Tyr Pro
1055 1060 1065

Asn Asp Leu Ile Lys Ile Ser Gln Lys Gly Lys Pro Pro Leu Ile
1070 1075 1080

Gly Tyr Tyr Gly Ser Cys Asn Arg Asn Thr Gly Ala Ile Asn Leu
1085 1090 1095

Trp Ala His Asp Arg Ser Asn Ala Ile Gly Lys Asn Gly Leu Ile
1100 1105 1110

Glu Ser Val Gly Val Lys Val Ala Leu Asn Leu Glu Lys Phe His
1115 1120 1125

Val Asp Val Leu Gly Asn Ile Phe Pro Ala Pro Lys Glu Glu Arg
1130 1135 1140

Arg Gly Leu Ala
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<210> PRT
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<400> 85

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			20					25					30		
Glu	Gln	Gly	Phe	Ile	Glu	Glu	Asp	Lys	Ala	Arg	Asn	Asp	His	Tyr	Lys
		35					40					45			
Glu	Leu	Lys	Pro	Ile	Ile	Asp	Arg	Ile	Tyr	Lys	Thr	Tyr	Ala	Asp	Gln
	50					55					60				
Cys	Leu	Gln	Leu	Val	Gln	Leu	Asp	Trp	Glu	Asn	Leu	Ser	Ala	Ala	Ile
65					70					75					80
Asp	Ser	Tyr	Arg	Lys	Glu	Lys	Thr	Glu	Glu	Thr	Arg	Asn	Ala	Leu	Ile
				85					90					95	
Glu	Glu	Gln	Ala	Thr	Tyr	Arg	Asn	Ala	Ile	His	Asp	Tyr	Phe	Ile	Gly
			100					105					110		
Arg	Thr	Asp	Asn	Leu	Thr	Asp	Ala	Ile	Asn	Lys	Arg	His	Ala	Glu	Ile
		115					120					125			
Tyr	Lys	Gly	Leu	Phe	Lys	Ala	Glu	Leu	Phe	Asn	Gly	Lys	Val	Leu	Lys
	130					135					140				
Gln	Leu	Gly	Thr	Val	Thr	Thr	Thr	Glu	His	Glu	Asn	Ala	Leu	Leu	Arg
145					150					155					160
Ser	Phe	Asp	Lys	Phe	Thr	Thr	Tyr	Phe	Ser	Gly	Phe	Tyr	Glu	Asn	Arg
				165					170					175	
Lys	Asn	Val	Phe	Ser	Ala	Glu	Asp	Ile	Ser	Thr	Ala	Ile	Pro	His	Arg
			180					185					190		
Ile	Val	Gln	Asp	Asn	Phe	Pro	Lys	Phe	Lys	Glu	Asn	Cys	His	Ile	Phe
		195					200					205			
Thr	Arg	Leu	Ile	Thr	Ala	Val	Pro	Ser	Leu	Arg	Glu	His	Phe	Glu	Asn
	210					215					220				
Val	Lys	Lys	Ala	Ile	Gly	Ile	Phe	Val	Ser	Thr	Ser	Ile	Glu	Glu	Val
225					230					235					240
Phe	Ser	Phe	Pro	Phe	Tyr	Asn	Gln	Leu	Leu	Thr	Gln	Thr	Gln	Ile	Asp
				245					250					255	
Leu	Tyr	Asn	Gln	Leu	Leu	Gly	Gly	Ile	Ser	Arg	Glu	Ala	Gly	Thr	Glu
			260					265					270		
Lys	Ile	Lys	Gly	Leu	Asn	Glu	Val	Leu	Asn	Leu	Ala	Ile	Gln	Lys	Asn
		275					280					285			
Asp	Glu	Thr	Ala	His	Ile	Ile	Ala	Ser	Leu	Pro	His	Arg	Phe	Ile	Pro
	290					295					300				
Leu	Phe	Lys	Gln	Ile	Leu	Ser	Asp	Arg	Asn	Thr	Leu	Ser	Phe	Ile	Leu
305					310					315					320
Glu	Glu	Phe	Lys	Ser	Asp	Glu	Glu	Val	Ile	Gln	Ser	Phe	Cys	Lys	Tyr
				325					330					335	
Lys	Thr	Leu	Leu	Arg	Asn	Glu	Asn	Val	Leu	Glu	Thr	Ala	Glu	Ala	Leu
			340					345					350		
Phe	Asn	Glu	Leu	Asn	Ser	Ile	Asp	Leu	Thr	His	Ile	Phe	Ile	Ser	His
		355					360					365			
Lys	Lys	Leu	Glu	Thr	Ile	Ser	Ser	Ala	Leu	Cys	Asp	His	Trp	Asp	Thr
	370					375					380				
Leu	Arg	Asn	Ala	Leu	Tyr	Glu	Arg	Arg	Ile	Ser	Glu	Leu	Thr	Gly	Lys
385					390					395					400
Ile	Thr	Lys	Ser	Ala	Lys	Glu	Lys	Val	Gln	Arg	Ser	Leu	Lys	His	Glu
				405					410					415	

Asp	Ile	Asn	Leu 420	Gln	Glu	Ile	Ile	Ser 425	Ala	Ala	Gly	Lys	Glu 430	Leu	Ser
Glu	Ala	Phe 435	Lys	Gln	Lys	Thr	Ser 440	Glu	Ile	Leu	Ser	His 445	Ala	His	Ala
Ala	Leu 450	Asp	Gln	Pro	Leu	Pro 455	Thr	Thr	Leu	Lys	Lys 460	Gln	Glu	Glu	Lys
Glu 465	Ile	Leu	Lys	Ser	Gln 470	Leu	Asp	Ser	Leu	Leu 475	Gly	Leu	Tyr	His	Leu 480
Leu	Asp	Trp	Phe	Ala 485	Val	Asp	Glu	Ser	Asn 490	Glu	Val	Asp	Pro	Glu 495	Phe
Ser	Ala	Arg	Leu 500	Thr	Gly	Ile	Lys	Leu 505	Glu	Met	Glu	Pro	Ser 510	Leu	Ser
Phe	Tyr	Asn 515	Lys	Ala	Arg	Asn	Tyr 520	Ala	Thr	Lys	Lys	Pro 525	Tyr	Ser	Val
Glu	Lys 530	Phe	Lys	Leu	Asn	Phe 535	Gln	Met	Pro	Thr	Leu 540	Ala	Ser	Gly	Trp
Asp 545	Val	Asn	Lys	Glu	Lys 550	Asn	Asn	Gly	Ala	Ile 555	Leu	Phe	Val	Lys	Asn 560
Gly	Leu	Tyr	Tyr	Leu 565	Gly	Ile	Met	Pro	Lys 570	Gln	Lys	Gly	Arg	Tyr 575	Lys
Ala	Leu	Ser	Phe 580	Glu	Pro	Thr	Glu	Lys 585	Thr	Ser	Glu	Gly	Phe 590	Asp	Lys
Met	Tyr	Tyr 595	Asp	Tyr	Phe	Pro	Asp 600	Ala	Ala	Lys	Met	Ile 605	Pro	Lys	Cys
Ser	Thr 610	Gln	Leu	Lys	Ala	Val 615	Thr	Ala	His	Phe	Gln 620	Thr	His	Thr	Thr
Pro 625	Ile	Leu	Leu	Ser	Asn 630	Asn	Phe	Ile	Glu	Pro 635	Leu	Glu	Ile	Thr	Lys 640
Glu	Ile	Tyr	Asp	Leu 645	Asn	Asn	Pro	Glu	Lys 650	Glu	Pro	Lys	Lys	Phe 655	Gln
Thr	Ala	Tyr	Ala 660	Lys	Lys	Thr	Gly	Asp 665	Gln	Lys	Gly	Tyr	Arg 670	Glu	Ala
Leu	Cys	Lys 675	Trp	Ile	Asp	Phe	Thr 680	Arg	Asp	Phe	Leu	Ser 685	Lys	Tyr	Thr
Lys	Thr 690	Thr	Ser	Ile	Asp	Leu 695	Ser	Ser	Leu	Arg	Pro 700	Ser	Ser	Gln	Tyr
Lys 705	Asp	Leu	Gly	Glu	Tyr 710	Tyr	Ala	Glu	Leu	Asn 715	Pro	Leu	Leu	Tyr	His 720
Ile	Ser	Phe	Gln	Arg 725	Ile	Ala	Glu	Lys	Glu 730	Ile	Met	Asp	Ala	Val 735	Glu
Thr	Gly	Lys	Leu 740	Tyr	Leu	Phe	Gln	Ile 745	Tyr	Asn	Lys	Asp	Phe 750	Ala	Lys
Gly	His	His 755	Gly	Lys	Pro	Asn	Leu 760	His	Thr	Leu	Tyr	Trp 765	Thr	Gly	Leu
Phe	Ser 770	Pro	Glu	Asn	Leu	Ala 775	Lys	Thr	Ser	Ile	Lys 780	Leu	Asn	Gly	Gln
Ala 785	Glu	Leu	Phe	Tyr	Arg 790	Pro	Lys	Ser	Arg	Met 795	Lys	Arg	Met	Ala	His 800
Arg	Leu	Gly	Glu	Lys	Met	Leu	Asn	Lys	Lys	Leu	Lys	Asp	Gln	Lys	Thr
				805					810					815	
Pro	Ile	Pro	Asp	Thr	Leu	Tyr	Gln	Glu	Leu	Tyr	Asp	Tyr	Val	Asn	His
			820					825					830		
Arg	Leu	Ser	His	Asp	Leu	Ser	Asp	Glu	Ala	Arg	Ala	Leu	Leu	Pro	Asn
		835					840					845			
Val	Ile	Thr	Lys	Glu	Val	Ser	His	Glu	Ile	Ile	Lys	Asp	Arg	Arg	Phe
	850					855					860				

Thr Ser Asp Lys Phe Phe Phe His Val Pro Ile Thr Leu Asn Tyr Gln
865 870 875 880

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

Lys Glu His Pro Glu Thr Pro Ile Ile Gly Ile Asp Arg Gly Glu Arg
900 905 910

Asn Leu Ile Tyr Ile Thr Val Ile Asp Ser Thr Gly Lys Ile Leu Glu
915 920 925

Gln Arg Ser Leu Asn Thr Ile Gln Gln Phe Asp Tyr Gln Lys Lys Leu
930 935 940

Asp Asn Arg Glu Lys Glu Arg Val Ala Ala Arg Gln Ala Trp Ser Val
945 950 955 960

Val Gly Thr Ile Lys Asp Leu Lys Gln Gly Tyr Leu Ser Gln Val Ile
965 970 975

His Glu Ile Val Asp Leu Met Ile His Tyr Gln Ala Val Val Val Leu
980 985 990

Glu Asn Leu Asn Phe Gly Phe Lys Ser Lys Arg Thr Gly Ile Ala Glu
995 1000 1005

Lys Ala Val Tyr Gln Gln Phe Glu Lys Met Leu Ile Asp Lys Leu
1010 1015 1020

Asn Cys Leu Val Leu Lys Asp Tyr Pro Ala Glu Lys Val Gly Gly
1025 1030 1035

Val Leu Asn Pro Tyr Gln Leu Thr Asp Gln Phe Thr Ser Phe Ala
1040 1045 1050

Lys Met Gly Thr Gln Ser Gly Phe Leu Phe Tyr Val Pro Ala Pro
1055 1060 1065

Tyr Thr Ser Lys Ile Asp Pro Leu Thr Gly Phe Val Asp Pro Phe
1070 1075 1080

Val Trp Lys Thr Ile Lys Asn His Glu Ser Arg Lys His Phe Leu
1085 1090 1095

Glu Gly Phe Asp Phe Leu His Tyr Asp Val Lys Thr Gly Asp Phe
1100 1105 1110

Ile Leu His Phe Lys Met Asn Arg Asn Leu Ser Phe Gln Arg Gly
1115 1120 1125

Leu Pro Gly Phe Met Pro Ala Trp Asp Ile Val Phe Glu Lys Asn
1130 1135 1140

Glu Thr Gln Phe Asp Ala Lys Gly Thr Pro Phe Ile Ala Gly Lys
1145 1150 1155

Arg Ile Val Pro Val Ile Glu Asn His Arg Phe Thr Gly Arg Tyr
1160 1165 1170

Arg Asp Leu Tyr Pro Ala Asn Glu Leu Ile Ala Leu Leu Glu Glu
1175 1180 1185

Lys Gly Ile Val Phe Arg Asp Gly Ser Asn Ile Leu Pro Lys Leu
1190 1195 1200

Leu Glu Asn Asp Asp Ser His Ala Ile Asp Thr Met Val Ala Leu
1205 1210 1215

Ile Arg Ser Val Leu Gln Met Arg Asn Ser Asn Ala Ala Thr Gly
1220 1225 1230

Glu Asp Tyr Ile Asn Ser Pro Val Arg Asp Leu Asn Gly Val Cys
1235 1240 1245

Phe Asp Ser Arg Phe Gln Asn Pro Glu Trp Pro Met Asp Ala Asp
1250 1255 1260

Ala Asn Gly Ala Tyr His Ile Ala Leu Lys Gly Gln Leu Leu Leu
1265 1270 1275

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Asn His Leu Lys Glu Ser Lys Asp Leu Lys Leu Gln Asn Gly Ile
    1180                1185                1190
Ser Asn Gln Asp Trp Leu Ala Tyr Ile Gln Glu Leu Arg Asn
    1195                1200                1205
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<211> 1126
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<213> Unknown

<220>
<223> Description of Unknown:
Lachnospiraceae bacterium

<400> 858

Met	Ser	Lys	Leu	Glu	Lys	Phe	Thr	Asn	Cys	Tyr	Ser	Leu	Ser	Lys	Thr
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			20					25					30		
Asn	Lys	Arg	Leu	Leu	Val	Glu	Asp	Glu	Lys	Arg	Ala	Glu	Asp	Tyr	Lys
		35					40					45			
Gly	Val	Lys	Lys	Leu	Leu	Asp	Arg	Tyr	Tyr	Leu	Ser	Phe	Ile	Asn	Asp
	50					55					60				
Val	Leu	His	Ser	Ile	Lys	Leu	Lys	Asn	Leu	Asn	Asn	Tyr	Ile	Ser	Leu
65					70					75					80
Phe	Arg	Lys	Lys	Thr	Arg	Thr	Glu	Lys	Glu	Asn	Lys	Glu	Leu	Glu	Asn
				85					90					95	
Leu	Glu	Ile	Asn	Leu	Arg	Lys	Glu	Ile	Ala	Lys	Ala	Phe	Lys	Gly	Asn
			100					105					110		
Glu	Gly	Tyr	Lys	Ser	Leu	Phe	Lys	Lys	Asp	Ile	Ile	Glu	Thr	Ile	Leu
		115					120					125			
Pro	Glu	Phe	Leu	Asp	Asp	Lys	Asp	Glu	Ile	Ala	Leu	Val	Asn	Ser	Phe
	130					135					140				
Asn	Gly	Phe	Thr	Thr	Ala	Phe	Thr	Gly	Phe	Phe	Asp	Asn	Arg	Glu	Asn
145					150					155					160
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Phe	Asn	Phe	Val	Leu	Thr	Gln	Glu	Gly	Ile	Asp	Val	Tyr	Asn	Ala	Ile
225					230					235					240
Ile	Gly	Gly	Phe	Val	Thr	Glu	Ser	Gly	Glu	Lys	Ile	Lys	Gly	Leu	Asn
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Phe	Lys	Pro	Leu	Tyr	Lys	Gln	Val	Leu	Ser	Asp	Arg	Glu	Ser	Leu	Ser
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Leu	Glu	Lys	Leu	Phe	Lys	Asn	Phe	Asp	Glu	Tyr	Ser	Ser	Ala	Gly	Ile
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Gly	Glu	Trp	Asn	Val	Ile	Arg	Asp	Lys	Trp	Asn	Ala	Glu	Tyr	Asp	Asp
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Ile	Ile	Leu	Lys	Lys	Lys	Ala	Val	Val	Thr	Glu	Lys	Tyr	Glu	Asp	Asp
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Glu	Glu	Tyr	Ala	Asp	Ala	Asp	Leu	Ser	Val	Val	Glu	Lys	Leu	Lys	Glu
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Ile	Ile	Ile	Gln	Lys	Val	Asp	Glu	Ile	Tyr	Lys	Val	Tyr	Gly	Ser	Ser
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Glu	Lys	Leu	Phe	Asp	Ala	Asp	Phe	Val	Leu	Glu	Lys	Ser	Leu	Lys	Lys
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Gln	Lys	Pro	Tyr	Ser	Lys	Asp	Lys	Phe	Lys	Leu	Tyr	Phe	Gln	Asn	Pro
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Thr	Met	Tyr	Phe	Lys	Leu	Leu	Phe	Asp	Glu	Asn	Asn	His	Gly	Gln	Ile
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Asn Pro Asp Asn Pro Lys Lys Thr Thr Thr Leu Ser Tyr Asp Val Tyr
Lys Asp Lys Arg Phe Ser Glu Asp Glu Tyr Glu Leu His Ile Pro Ile
Ala Ile Asn Lys Cys Pro Lys Asn Ile Phe Lys Ile Asn Thr Glu Val
Arg Val Leu Leu Lys His Asp Asp Asn Pro Tyr Val Ile Gly Ile Asp
Arg Gly Glu Arg Asn Leu Leu Tyr Ile Val Val Val Asp Gly Lys Gly
Asn Ile Val Glu Ile Lys Thr Asp Tyr Ile Ser Leu Leu Asp Lys Glu
Lys Glu Arg Phe Glu Ala Arg Gln Asn Trp Thr Ser Val Glu Asn Ile
Lys Glu Leu Lys Ala Gly Tyr Ile Ser Gln Val Val Ile Lys Ile Cys
Glu Leu Val Glu Lys Tyr Asp Ala Val Ile Ala Leu Glu Asp Leu Asn
Ser Gly Phe Lys Asn Ser Arg Val Lys Val Glu Lys Gln Val Tyr Gln
Lys Phe Glu Lys Met Leu Ile Asp Lys Leu Asn Tyr Met Val Asp Lys
Lys Ser Asn Pro Cys Ala Thr Gly Gly Ala Leu Lys Gly Tyr Gln Ile
Thr Asn Lys Phe Glu Ser Phe Lys Ser Met Ser Thr Gln Asn Gly Phe
Ile Phe Tyr Ile Pro Ala Trp Leu Thr Ser Lys Ile Asp Pro Ser Thr
Gly Phe Val Asn Leu Leu Lys Thr Lys Tyr Thr Ser Ile Ala Asp
Ser Lys Lys Phe Ile Ser Ser Phe Asp Arg Ile Met Tyr Val Pro
Glu Glu Asp Leu Phe Glu Phe Ala Leu Asp Tyr Lys Asn Phe Ser
Arg Thr Asp Ala Asn Tyr Ile Lys Lys Trp Lys Leu Tyr Ser Tyr
Gly Asn Arg Ile Arg Ile Phe Arg Asn Pro Lys Lys Asn Asn Val
Phe Asp Trp Glu Glu Val Cys Leu Thr Ser Ala Tyr Lys Glu Leu
Phe Asn Lys Tyr Gly Ile Asn Tyr Gln Gln Gly Asp Ile Arg Ala
Leu Leu Cys Glu Gln Ser Asp Lys Ala Phe Tyr Ser Ser Phe Met
Ala Leu Met Ser Leu Met Leu Gln Met Arg Asn Ser Ile Thr Gly
Arg Thr Asp Val Asp Phe Leu Ile Ser Pro Val Lys Asn Ser Asp
Gly Ile Phe Tyr Asp Ser Arg Asn Tyr Glu Ala Gln Glu Asn Ala
Ile Leu Pro Lys Asn Ala Asp Ala Asn Gly Ala Tyr Asn Ile Ala
Arg Lys Val Leu Trp Ala Ile Gly Gln Phe Lys Lys Ala Glu Asp

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<400> 889

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Asn	Ile	Lys 35	Lys	Asn	Gly	Leu	Ile 40	Arg	Arg	Asp	Glu	Gln 45	Arg	Leu	Asp
Asp	Tyr 50	Glu	Lys	Leu	Lys	Lys 55	Val	Ile	Asp	Glu	Tyr 60	His	Glu	Asp	Phe
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Lys	Thr	Met	Arg 100	Asp	Thr	Leu	Ala	Lys 105	Ala	Phe	Ser	Glu	Asp 110	Glu	Arg
Tyr	Lys	Ser 115	Ile	Phe	Lys	Lys	Glu 120	Leu	Val	Lys	Lys	Asp 125	Ile	Pro	Val
Trp	Cys 130	Pro	Ala	Tyr	Lys	Ser 135	Leu	Cys	Lys	Lys	Phe 140	Asp	Asn	Phe	Thr
Thr 145	Ser	Leu	Val	Pro	Phe 150	His	Glu	Asn	Arg	Lys 155	Asn	Leu	Tyr	Thr	Ser 160
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Pro	Lys	Phe	Ile 180	Gln	Asn	Ile	Glu	Ala 185	Leu	Cys	Glu	Leu	Gln 190	Lys	Lys
Met	Gly	Ala 195	Asp	Leu	Tyr	Leu	Glu 200	Met	Met	Glu	Asn	Leu 205	Arg	Asn	Val
Trp	Pro 210	Ser	Phe	Val	Lys	Thr 215	Pro	Asp	Asp	Leu	Cys 220	Asn	Leu	Lys	Thr
Tyr 225	Asn	His	Leu	Met	Val 230	Gln	Ser	Ser	Ile	Ser 235	Glu	Tyr	Asn	Arg	Phe 240
Val	Gly	Gly	Tyr	Ser 245	Thr	Glu	Asp	Gly	Thr 250	Lys	His	Gln	Gly	Ile 255	Asn
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Gly	Leu	Val 275	Phe	Leu	His	Lys	Gln 280	Ile	Leu	Ala	Lys	Val 285	Asp	Ser	Ser
Ser	Phe 290	Ile	Ser	Asp	Thr	Leu 295	Glu	Asn	Asp	Asp	Gln 300	Val	Phe	Cys	Val
Leu 305	Arg	Gln	Phe	Arg	Lys 310	Leu	Phe	Trp	Asn	Thr 315	Val	Ser	Ser	Lys	Glu 320
Asp	Asp	Ala	Ala	Ser 325	Leu	Lys	Asp	Leu	Phe 330	Cys	Gly	Leu	Ser	Ile 335	Tyr
Asp	Pro	Glu	Ala 340	Ile	Tyr	Val	Ser	Asp 345	Ala	His	Leu	Ala	Thr 350	Ile	Ser

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

Ala Glu Leu Asp Asp Leu Leu Ala His Tyr Ser Glu Glu Ser Leu Pro
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Ala Gly Phe Ser Leu Leu Ser Tyr Phe Thr Ser Leu Gly Gly Gln Lys
420 425 430

Tyr Leu Val Ser Asp Val Glu Gly Ser Asn
435 440

Ile Trp Asp Glu Val Leu Ile Ala Phe Arg Asp Leu Gln Val Ile Leu
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Asp Lys Asp Phe Thr Glu Lys Lys Leu Gly Lys Asp Glu Glu Ala Val
465 470 475 480

Ser Val Ile Lys Lys Ala Leu Asp Ser Ala Leu Arg Leu Arg Lys Phe
485 490 495

Phe Asp Leu Leu Ser Gly Thr Gly Ala Glu Ile Arg Arg Asp Ser Ser
500 505 510

Phe Tyr Ala Leu Tyr Thr Asp Arg Met Asp Lys Leu Lys Gly Leu Leu
515 520 525

Lys Met Tyr Asn Lys Val Arg Asn Tyr Leu Thr Lys Lys Pro Tyr Ser
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Ile Glu Lys Phe Lys Leu His Phe Asp Asn Pro Ser Leu Leu Ser Gly
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Trp Asp Lys Asn Lys Glu Leu Asn Asn Leu Ser Val Ile Phe Arg Gln
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Asn Gly Tyr Tyr Tyr Leu Gly Ile Met Pro Lys Gly Lys Asn Leu
580 585 590

Phe Lys Thr Leu Pro Lys Leu Gly Ala Glu Glu Met Phe Tyr Glu Lys
595 600 605

Met Glu Tyr Lys Gln Ile Ala Glu Pro Met Leu Met Leu Pro Lys Val
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Phe Phe Pro Lys Lys Thr Lys Pro Ala Phe Ala Pro Asp Gln Ser Val
625 630 635 640

Val Asp Ile Tyr Asn Lys Lys Thr Phe Lys Thr Gly Gln Lys Gly Phe
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Asn Lys Lys Asp Leu Tyr Arg Leu Ile Asp Phe Tyr Lys Glu Ala Leu
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Thr Val His Glu Trp Lys Leu Phe Asn Phe Ser Phe Ser Pro Thr Glu
675 680 685

Gln Tyr Arg Asn Ile Gly Glu Phe Phe Asp Glu Val Arg Glu Gln Ala
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Tyr Lys Val Ser Met Val Asn Val Pro Ala Ser Tyr Ile Asp Glu Ala
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Val Glu Asn Gly Lys Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe
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Ser Pro Tyr Ser Lys Gly Ile Pro Asn Leu His Thr Leu Tyr Trp Lys
740 745 750

Ala Leu Phe Ser Glu Gln Asn Gln Ser Arg Val Tyr Lys Leu Cys Gly
755 760 765

Gly Gly Glu Leu Phe Tyr Arg Lys Ala Ser Leu His Met Gln Asp Thr
770 775 780

Thr Val His Pro Lys Gly Ile Ser Ile His Lys Lys Asn Leu Asn Lys
785 790 795 800

Lys Gly Glu Thr Ser Leu Phe Asn Tyr Asp Leu Val Lys Asp Lys Arg
805 810 815

Phe Thr Glu Asp Lys Phe Phe Phe His Val Pro Ile Ser Ile Asn Tyr
820 825 830

Lys Asn Lys Lys Ile Thr Asn Val Asn Gln Met Val Arg Asp Tyr Ile
835 840 845

Ala Gln Asn Asp Asp Leu Gln Ile Ile Ile Gly Ile Asp Arg Gly Glu Arg
850 855 860

Asn Leu Leu Tyr Ile Ser Arg Ile Asp Thr Arg Gly Asn Leu Leu Glu
865 870 875 880

Gln Phe Ser Leu Asn Val Ile Glu Ser Asp Lys Gly Asp Leu Arg Thr
885 890 895

Asp Tyr Gln Lys Ile Leu Gly Asp Arg Glu Gln Glu Arg Leu Arg Arg
900 905 910

Arg Gln Glu Trp Lys Ser Ile Glu Ser Ile Lys Asp Leu Lys Asp Gly
915 920 925

Tyr Met Ser Gln Val Val His Glu Ile Cys Asn Met Val Val Glu His
930 935 940

Lys Ala Ile Val Val Leu Glu Asn Leu Asn Leu Ser Phe Met Lys Gly
945 950 955 960

Arg Lys Lys Val Glu Lys Ser Val Tyr Glu Lys Phe Glu Arg Met Leu
965 970 975

Val Asp Lys Leu Asn Tyr Leu Val Val Asp Lys Lys Asn Leu Ser Asn
980 985 990

Glu Pro Gly Gly Leu Tyr Ala Ala Tyr Gln Leu Thr Asn Pro Leu Phe
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Ser Phe Glu Glu Leu His Arg Tyr Pro Gln Ser Gly Ile Leu Phe
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Phe Val Asp Pro Trp Asn Thr Ser Leu Thr Asp Pro Ser Thr Gly
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Phe Val Asn Leu Leu Gly Arg Ile Asn Tyr Thr Asn Val Gly Asp
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Ala Arg Lys Phe Phe Asp Arg Phe Asn Ala Ile Arg Tyr Asp Gly
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Lys Gly Asn Ile Leu Phe Asp Leu Asp Leu Ser Arg Phe Asp Val
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Arg Val Glu Thr Gln Arg Lys Leu Trp Thr Leu Thr Thr Phe Gly
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Ser Arg Ile Ala Lys Ser Lys Lys Ser Gly Lys Trp Met Val Glu
1100 1105 1110

Arg Ile Glu Asn Leu Ser Leu Cys Phe Leu Glu Leu Phe Glu Gln
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Phe Asn Ile Gly Tyr Arg Val Glu Lys Asp Leu Lys Lys Ala Ile
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Leu Ser Gln Asp Arg Lys Glu Phe Tyr Val Arg Leu Ile Tyr Leu
1145 1150 1155

Phe Asn Leu Met Met Gln Ile Arg Asn Ser Asp Gly Glu Glu Asp
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Tyr Ile Leu Ser Pro Ala Leu Asn Glu Lys Asn Leu Gln Phe Asp
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Ser Arg Leu Ile Glu Ala Lys Asp Leu Pro Val Asp Ala Asp Ala
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Asn Gly Ala Tyr Asn Val Ala Arg Lys Gly Leu Met Val Val Gln
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Leu	Leu	Lys	Gln	Tyr	Phe	Asp	Cys	Tyr	Asn	Glu	Leu	Lys	Ala	Phe	Lys
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Asn	Lys	Cys	Thr	Ser	Ile	Gln	Arg	Ala	Met	Arg	Glu	Ala	Ile	Ser	Gln
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Ala	Phe	Leu	Lys	Ser	Pro	Gln	Lys	Lys	Leu	Leu	Ala	Ile	Lys	Asn	Leu
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Phe	Thr	Ser	Tyr	Phe	Ser	Gly	Phe	Glu	Thr	Asn	Arg	Glu	Asn	Phe	Tyr
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Ser	Asp	Glu	Glu	Lys	Ser	Thr	Ser	Ile	Ala	Tyr	Arg	Leu	Val	His	Asp
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Phe	Asn	Asn	Thr	Leu	Thr	Gln	Lys	Gly	Ile	Asp	Asn	Tyr	Asn	Ala	Val
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Pro	Leu	Ala	Thr	Leu	Leu	Ser	Ser	Leu	Asp	Lys	Tyr	Asn	Leu	Asn	Gly
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Tyr	Arg	Asn	Phe	Ser	Ile	Asp	Glu	Ala	Ile	Asp	Ala	Asn	Ala	Glu	Leu
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Gln	Thr	Phe	Asn	Asn	Tyr	Glu	Leu	Ile	Ala	Asn	Ala	Leu	Arg	Ala	Lys
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Cys	Phe	Asn	Lys	Pro	Lys	Leu	Met	Thr	Gly	Trp	Val	Asp	Ser	Lys	Thr
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Glu	Gly	Glu	Asn	Ser	Tyr	Lys	Glu	Asp	Lys	Lys	Arg	Leu	Asn	Lys	Val
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Ile	Ile	Ala	Tyr	Ile	Glu	Gln	Ile	Lys	Gln	Thr	Asn	Ile	Lys	Lys	Ser
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Ile	Ile	Glu	Ser	Ile	Ser	Lys	Tyr	Pro	Asn	Ile	Ser	Asp	Asp	Asp	Lys
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Val	Thr	Pro	Ser	Ser	Leu	Leu	Glu	Lys	Ile	Lys	Lys	Val	Ser	Ile	Asp
705					710					715					720
Ser	Tyr	Asn	Gly	Ile	Leu	Ser	Phe	Lys	Ser	Phe	Gln	Ser	Val	Asn	Lys
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Glu	Val	Ile	Asp	Asn	Leu	Leu	Lys	Thr	Ile	Ser	Pro	Leu	Lys	Asn	Lys
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Ala	Glu	Phe	Leu	Asn	Leu	Ile	Asn	Lys	Asp	Tyr	Gln	Ile	Phe	Thr	Glu
		755					760					765			
Val	Gln	Ala	Val	Ile	Asp	Glu	Ile	Cys	Lys	Gln	Lys	Thr	Phe	Ile	Tyr
	770					775					780				
Phe	Pro	Ile	Ser	Asn	Val	Glu	Leu	Glu	Lys	Glu	Met	Gly	Asp	Lys	Asp
785					790					795					800

Lys Pro Leu Cys Leu Phe Gln Ile Ser Asn Lys Asp Leu Ser Phe Ala
795 800 805 810 815
Lys Thr Phe Ser Ala Asn Leu Arg Lys Lys Arg Gly Ala Glu Asn Leu
820 825 830
His Thr Met Leu Phe Lys Ala Leu Met Glu Gly Asn Gln Asp Asn Leu
835 840 845
Asp Leu Gly Ser Gly Ala Ile Phe Tyr Arg Ala Lys Ser Leu Asp Gly
850 855 860
Asn Lys Pro Thr His Pro Ala Asn Glu Ala Ile Lys Cys Arg Asn Val
865 870 875 880
Ala Asn Lys Asp Lys Val Ser Leu Phe Thr Tyr Asp Ile Tyr Lys Asn
885 890 895
Arg Arg Tyr Met Glu Asn Lys Phe Leu Phe His Leu Ser Ile Val Asn
900 905 910
Asn Tyr Lys Ala Ala Asn Asp Ser Ala Gln Leu Asn Ser Ser Ala Thr
915 920 925 930
Glu Tyr Ile Arg Lys Ala Asp Asp Leu His Ile Ile Gly Ile Asp Arg
935 940
Gly Glu Arg Asn Leu Leu Tyr Tyr Ser Val Ile Asp Met Lys Gly Asn
945 950 955 960
Ile Val Glu Gln Asp Ser Leu Asn Ile Ile Asn Asp Met Asp Leu Glu
965 970 975
Thr Asp Tyr His Asp Leu Leu Asp Lys Arg Glu Lys Glu Arg Lys Ala
980 985 990
Asn Arg Gln Asn Trp Glu Ala Val Glu Gly Ile Lys Asp Leu Lys Lys
995 1000 1005
Gly Tyr Leu Ser Gln Ala Val His Gln Ile Ala Gln Leu Met Leu
1010 1015 1020
Lys Tyr Asn Ala Ile Ile Ala Leu Glu Asp Leu Gly Gln Met Phe
1025 1030 1035
Val Thr Arg Gly Gln Lys Ile Glu Lys Ala Val Tyr Gln Gln Phe
1040 1045 1050
Glu Lys Ser Leu Val Asp Lys Leu Ser Tyr Leu Val Asp Lys Lys
1055 1060 1065
Arg Pro Tyr Asn Glu Leu Gly Gly Ile Leu Lys Ala Tyr Gln Leu
1070 1075 1080
Ala Ser Ser Ile Thr Lys Asn Asn Ser Asp Lys Gln Asn Gly Phe
1085 1090 1095
Leu Phe Tyr Val Pro Ala Trp Asn Thr Ser Lys Ile Asp Pro Val
1100 1105 1110
Thr Gly Phe Thr Asp Leu Leu Arg Pro Lys Ala Met Thr Ile Lys
1115 1120 1125
Glu Ala Gln Asp Phe Phe Gly Ala Phe Asp Asn Ile Ser Tyr Asn
1130 1135 1140
Asp Lys Gly Tyr Phe Glu Phe Glu Thr Asn Tyr Asp Lys Phe Lys
1145 1150 1155
Ile Arg Met Lys Ser Ala Gln Thr Arg Trp Thr Ile Cys Thr Phe
1160 1165 1170
Gly Asn Arg Ile Lys Arg Lys Lys Asp Lys Asn Tyr Trp Asn Tyr
1175 1180 1185
Glu Glu Val Glu Leu Thr Glu Glu Phe Lys Lys Leu Phe Lys Asp
1190 1195 1200
Ser Asn Ile Asp Tyr Glu Asn Cys Asn Leu Lys Glu Glu Ile Gln
1205 1210 1215
Asn Lys Asp Asn Arg Lys Phe Phe Asp Asp Leu Ile Lys Leu Leu
1220 1225 1230

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Gln Leu Thr Leu Gln Met Arg Asn Ser Asp Asp Lys Gly Asn Asp
        1135                1140                1145

Tyr Ile Ile Ser Pro Val Ala Asn Ala Glu Gly Gln Phe Phe Asp
    1150                1155                1160

Ser Arg Asn Gly Asp Lys Lys Leu Pro Leu Asp Ala Asp Ala Asn
1165                1170                1175

Gly Ala Tyr Asn Ile Ala Arg Lys Gly Leu Trp Asn Ile Arg Gln
            1180                1185                1190

Ile Lys Gln Thr Lys Asn Asp Lys Lys Leu Asn Leu Ser Ile Ser
        1195                1200                1205

Ser Thr Glu Trp Leu Asp Phe Val Arg Glu Lys Pro Tyr Leu
    1210                1215                1220
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<210> 661
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 661
Cys His Lys Lys Lys Lys Lys Lys His Cys
1   5   10

<210> 662
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 662
Gly Leu Phe His Ala Ile Ala His Phe Ile His Gly Gly Trp His Gly
1   5   10   15
Leu Ile His Gly Trp Tyr Gly
            20

<210> 663
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 861
Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly
1 5 10 15
Met Ile Asp Gly Trp Tyr Gly
20

<210> 862
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 862
Gly Ile Gly Ala Val Leu Lys Val Leu Thr Thr Gly Leu Pro Ala Leu
1 5 10 15
Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln
20

<210> 863
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 863
Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln
1 5 10

<210> 864
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 864
Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
1 5 10 15

<210> 865
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 867
Gly Trp Thr Leu Asn Ser Ala Gly Tyr Leu Leu Gly Lys Ile Asn Leu
1 5 10 15
Lys Ala Leu Ala Ala Leu Ala Lys Lys Ile Leu
20 25

<210> 868
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 868
Trp Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala Glu His
1 5 10 15
Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
20 25 30

<210> 869
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 869
Trp Glu Ala Lys Leu Ala Lys Ala Leu Ala Lys Ala Leu Ala Lys His
1 5 10 15
Leu Ala Lys Ala Leu Ala Lys Ala Leu Lys Ala Cys Glu Ala
20 25 30

<210> 870
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 870
Gly Leu Phe Glu Ala Leu Leu Glu Leu Leu Glu Ser Leu Trp Glu Leu
1 5 10 15
Leu Leu Glu Ala
20

<210> 871
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 871
Gly Leu Phe Lys Ala Leu Leu Lys Leu Leu Lys Ser Leu Trp Lys Leu
1 5 10 15
Leu Leu Lys Ala
20

<210> 872
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 872
Gly Leu Phe Arg Ala Leu Leu Arg Leu Leu Arg Ser Leu Trp Arg Leu
1 5 10 15
Leu Leu Arg Ala
20

<210> 873
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 873
Cys Trp Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1 5 10 15
Lys Lys Lys Lys Gly Ala Gly Ala Gly Ala Gly Ala
20 25

<210> 874
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 674
Lys Lys Lys Arg Lys
1 5

<210> 675
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 675
Lys Arg Phe Arg Phe
1 5

<210> 676
<211> 14
<212> PRT
<213> Xenopus sp.

<400> 676
Val Arg Lys Lys Arg Lys Thr Glu Glu Glu Ser Pro Leu Lys Asp Lys
1 5 10 15
Asp Ala Lys Lys Ser Lys Gln Glu
20

<210> 677
<211> 24
<212> PRT
<213> Mus sp.

<400> 677
Arg Leu Arg Arg Asp Ala Gly Gly Arg Gly Gly Val Tyr Glu His Leu
1 5 10 15
Gly Gly Ala Pro Arg Arg Arg Lys
20

<210> 678
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 678
Lys Arg Lys Gly Asp Glu Val Asp Gly Val Asp Glu Cys Ala Lys Lys
1 5 10 15
Ser Lys Lys

<210> 87
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 87
His Ser Asp Gly Thr Phe Thr Ser Glu Leu Ser Arg Leu Arg Asp Ser
1 5 10 15
Ala Arg Leu Gln Arg Leu Leu Gln Gly Leu Val
20

<210> 88
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 88
Asn Pro Val Val Gly Tyr Ile Gly Glu Arg Pro Gln Tyr Arg Asp Leu
1 5 10

<210> 89
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 89
Glu Leu Tyr Glu Asn Lys Pro Arg Arg Pro Tyr Ile Leu
1 5 10

<210> 90
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 90
Leu Ser Ile Pro Pro Lys Ala
1 5

<210> 883
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 883
Phe Glu Thr Pro Pro Glu Leu
1 5

<210> 884
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 884
Leu Thr Pro Ala Thr Ala Ile
1 5

<210> 885
<211> 97
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 885
gguguuagcc uugcguuccg guuuuagagc uaugcug 97

<210> 886
<211> 97
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 886
cguguubggg uaacuuggcc guuuuagagc uaugcug 97

<210> 887
<211> 97

<210> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 887
ggaggaggcc uaggaaaggca guuuuagagc uaugcug 37

<210> 888
<211> 37
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 888
gaaggaggaa ggccaguaag guuuuagagc uaugcug 37

<210> 889
<211> 37
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 889
accaccgggu aauggaaggc guuuuagagc uaugcug 37

<210> 890
<211> 37
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 890
cgacuucgaa aaugugcucg guuuuagagc uaugcug 37

<210> 891
<211> 37
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 891
gagugaccac agggaaaaug guuuuagagc uaugaug 37

<210> 892
<211> 37
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 892
uacggcaca uucuugaagu guuuuagagc uaugcug 37

<210> 893
<211> 37
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 893
ggaagccagg aagaaggcca guuuuagagc uaugcug 37

<210> 894
<211> 37
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 894
ucuuugccca gagcauccag guuuuagagc uaugcug 37

<210> 895
<211> 37
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 895
cuaggagaua cacccccacc guuuuagagc uaugcug 37

<210> 896
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 896
ggugcuagcc uugcguccag guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 897
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 897
cgugcucggg ugcuucggcc guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 898
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 898
gccgucccuc ucggaacgca guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 899
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 899
ggacgaggac ggcgacuacg guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 900
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 900
acccacggga aauggaggcc guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 901
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 901
cgacuuuggag aaugugcccg guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 902
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 902
gagugaccac cgggaaaucg guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 903
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 903
cucgggcaca uucucgaagu guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 904
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 904
ggaagccagg aagaaggcca guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 905
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 905
ucuuugccca gagcauccag guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 906
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 906
cuaggagaua caccuccacc guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 907
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 907
gucaccucca augacuaggg guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 908
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 908
cgaaccguac acauucaacg guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> 909
<211> 43
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 909
uaauuucuac ucuuguagau ucaucugugc ccccucccuc cug 43

<210> 910
<211> 44
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 910
uaauuucuac ucuaaguaga uucaucugug ccccucccuc ccug 44

<210> 911
<211> 43
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 911
uaauuucuac ucuuguagau ccccagggcu cccguggaac cug 43

<210> 911
<211> 44
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 911
uaauuucuac ucuaaguaga ucccagagca ucccguggaa ccug 44

<210> 913
<211> 43
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 913
uaauuucuac ucuuguagau cccgugggca cucuguaugc ugg 43

<210> 914
<211> 44
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 914
uaauuucuac ucuaaguaga ucccgugggc acucuguaug cugg 44

<210> 915
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 915

Met	Val	Ser	Lys	Gly	Glu	Glu	Asp	Asn	Met	Ala	Ile	Ile	Lys	Glu	Phe
1				5					10					15	
Met	Arg	Phe	Lys	Val	His	Met	Glu	Gly	Ser	Val	Asn	Gly	His	Glu	Phe
			20					25					30		
Glu	Ile	Glu	Gly	Glu	Gly	Glu	Gly	Arg	Pro	Tyr	Glu	Gly	Thr	Gln	Thr
		35					40					45			
Ala	Lys	Leu	Lys	Val	Thr	Lys	Gly	Gly	Pro	Leu	Pro	Phe	Ala	Trp	Asp
	50					55					60				

Ile 65	Leu	Ser	Pro	Gln	Phe 70	Met	Tyr	Gly	Ser	Lys 75	Ala	Tyr	Val	Lys	His 80
Pro	Ala	Asp	Ile	Pro 85	Asp	Tyr	Leu	Lys	Leu 90	Ser	Phe	Pro	Glu	Gly 95	Phe
Lys	Trp	Glu	Arg 100	Val	Met	Asn	Phe	Glu 105	Asp	Gly	Gly	Val	Val 110	Thr	Val
Thr	Gln	Asp 115	Ser	Ser	Leu	Gln	Asp 120	Gly	Glu	Phe	Ile	Tyr 125	Lys	Val	Lys
Leu	Arg 130	Gly	Thr	Asn	Phe	Pro 135	Ser	Asp	Gly	Pro	Val 140	Met	Gln	Lys	Lys
Thr 145	Met	Gly	Trp	Glu	Ala 150	Ser	Ser	Glu	Arg	Met 155	Tyr	Pro	Glu	Asp	Gly 160
Ala	Leu	Lys	Gly	Glu 165	Ile	Lys	Gln	Arg	Leu 170	Lys	Leu	Lys	Asp	Gly 175	Gly
His	Tyr	Asp	Ala 180	Glu	Val	Lys	Thr	Thr 185	Tyr	Lys	Ala	Lys	Lys 190	Pro	Val
Gln	Leu	Pro 195	Gly	Ala	Tyr	Asn	Val 200	Asn	Ile	Lys	Leu	Asp 205	Ile	Thr	Ser
His	Asn 210	Glu	Asp	Tyr	Thr	Ile 215	Val	Glu	Gln	Tyr	Glu 220	Arg	Ala	Glu	Gly
Arg 225	His	Ser	Thr	Gly	Gly 230	Met	Asp	Glu	Leu	Tyr 235	Lys				

<210> 916
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 916
Arg Lys Lys Arg Arg Arg Glu Ser Arg Lys Lys Arg Arg Arg Glu Ser
1 5 10 15

<210> 917
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 917
Gly Arg Pro Arg Glu Ser Gly Lys Lys Arg Lys Arg Lys Arg Leu Lys
1 5 10 15
Pro

<210> 918
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 918
Gly Lys Arg Lys Lys Lys Gly Lys Leu Gly Lys Lys Arg Asp Pro
1 5 10 15

<210> 919
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 919
Gly Lys Arg Lys Lys Lys Gly Lys Leu Gly Lys Lys Arg Pro Arg Ser
1 5 10 15
Arg

<210> 920
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 920
Arg Lys Lys Arg Arg Arg Glu Ser Arg Arg Ala Arg Arg Ser Pro Arg
1 5 10 15
His Leu

<210> 921
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 921
Ser Arg Arg Ala Arg Arg Ser Pro Arg Glu Ser Gly Lys Lys Arg Lys
1 5 10 15
Arg Lys Arg

<210> 922
<211> 19

<211> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 922
Val Lys Arg Gly Leu Lys Leu Arg His Val Arg Pro Arg Val Thr Arg
1 5 10 15
Met Asp Val

<210> 923
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 923
Ser Arg Arg Ala Arg Arg Ser Pro Arg His Leu Gly Ser Gly
1 5 10

<210> 924
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 924
Leu Arg Arg Glu Arg Gln Ser Arg Leu Arg Arg Glu Arg Gln Ser Arg
1 5 10 15

<210> 925
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 925
Gly Ala Tyr Asp Leu Arg Arg Arg Glu Arg Gln Ser Arg Leu Arg Arg
1 5 10 15
Arg Glu Arg Gln Ser Arg
20

<210> 926
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 926
Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 927
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 927
Arg Arg Arg Arg Asn Arg Thr Arg Arg Asn Arg Arg Arg Val Arg
1 5 10 15

<210> 928
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 928
Thr Arg Gln Ala Arg Arg Asn Arg Arg Arg Arg Trp Arg Glu Arg Gln
1 5 10 15
Arg

<210> 929
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 929
Thr Arg Arg Gln Arg Thr Arg Arg Ala Arg Arg Asn Arg
1 5 10

<210> 930
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 930
Lys Met Thr Arg Ala Gln Arg Arg Ala Ala Ala Arg Arg Asn Arg Trp
1 5 10 15
Thr Ala Arg

<210> 931
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 931
Asn Ala Lys Thr Arg Arg His Glu Arg Arg Arg Lys Leu Ala Ile Glu
1 5 10 15
Arg

<210> 932
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 932
Met Asp Ala Gln Thr Arg Arg Arg Glu Arg Arg Ala Glu Lys Gln Ala
1 5 10 15
Gln Trp Lys Ala Ala Asn
20

<210> 933
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 933
Thr Ala Lys Thr Arg Tyr Lys Ala Arg Arg Ala Glu Leu Ile Ala Glu
1 5 10 15
Arg Arg

<210> 934
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 934
Thr Arg Arg Asn Lys Arg Asn Arg Ile Gln Glu Gln Leu Asn Arg Lys
1 5 10 15

<210> 935
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 935
Pro Arg Arg Arg Arg Ser Ser Ser Arg Pro Val Arg Arg Arg Arg Arg
1 5 10 15
Pro Arg Val Ser Arg Arg Arg Arg Arg Arg Gly Gly Arg Arg Arg Arg
20 25 30

<210> 936
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 936
Arg Ile Lys Ala Glu Arg Lys Arg Met Arg Asn Arg Ile Ala Ala Ser
1 5 10 15
Lys Ser Arg Lys Arg Lys Leu Glu Arg Ile Ala Arg
20 25

<210> 937
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 937
Lys Arg Arg Ile Arg Arg Glu Arg Asn Lys Met Ala Ala Ala Lys Ser
1 5 10 15
Arg Asn Arg Arg Arg Glu Leu Thr Asp Thr
20 25

<210> 938
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 938
Lys Arg Ala Arg Asn Thr Glu Ala Ala Arg Arg Ser Arg Ala Arg Lys
1 5 10 15
Leu Gln Arg Met Lys Gln
20

<210> 939
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 939
Arg Val Ile Arg Val Trp Phe Gln Asn Lys Arg Cys Lys Asp Lys Lys
1 5 10 15

<210> 940
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 940
Ser Lys Arg Thr Arg Gln Thr Tyr Thr Arg Tyr Gln Thr Leu Glu Leu
1 5 10 15
Glu Lys Glu Phe His Phe Asn Arg Tyr Ile Thr Arg Arg Arg Arg Ile
20 25 30

Asp Ile Ala Asn Ala Leu Ser Leu Ser Glu Arg Gln Ile Lys Ile Trp
35 40 45
Phe Gln Asn Arg Arg Met Lys Ser Lys Lys Asp Arg
50 55 60

<210> 941
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 941
Ser Gln Ile Lys Ile Trp Phe Gln Asn Lys Arg Ala Lys Ile Lys Lys
1 5 10 15

<210> 942
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 942
Arg Gln Val Thr Ile Trp Phe Gln Asn Arg Arg Val Lys Glu Lys Lys
1 5 10 15

<210> 943
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 943
Lys Gln Ile Asn Asn Trp Phe Ile Asn Gln Arg Lys Arg His Trp Lys
1 5 10 15

<210> 944
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 944
Met Gly Leu Gly Leu His Leu Leu Val Leu Ala Ala Ala Leu Gln Gly
1 5 10 15
Ala Lys Lys Lys Arg Lys Val
20

<210> 945
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 945
Met Val Lys Ser Lys Ile Gly Ser Trp Ile Leu Val Leu Phe Val Ala
1 5 10 15
Met Trp Ser Asp Val Gly Leu Cys Lys Lys Arg Pro Lys Pro
20 25 30

<210> 946
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 946
Met Ala Asn Leu Gly Tyr Trp Leu Leu Ala Leu Phe Val Thr Met Trp
1 5 10 15
Thr Asp Val Gly Leu Cys Lys Lys Arg Pro Lys Pro
20 25

<210> 947
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 947
Ala Ala Val Leu Leu Pro Val Leu Leu Ala Ala Pro
1 5 10

<210> 948
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 948
Arg Arg Ile Arg Pro Arg Pro Pro Arg Leu Pro Arg Pro Arg Pro Arg
1 5 10 15
Pro Leu Pro Phe Pro Arg Pro Gly
20

<210> 949
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 949
Val Asp Lys Gly Ser Tyr Leu Pro Arg Pro Thr Pro Pro Arg Pro Ile
1 5 10 15
Tyr Asn Arg Asn
20

<210> 950
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 950
Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val Arg Gly Pro Pro
1 5 10 15
Val Ser Cys Ile Lys Arg
20

<210> 951
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 951
Thr Arg Ser Ser Arg Ala Gly Leu Gln Trp Pro Val Gly Arg Val His
1 5 10 15
Arg Leu Leu Arg Lys
20

<210> 952
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 952
Gly Ile Gly Lys Trp Leu His Ser Ala Lys Lys Phe Gly Lys Ala Phe
1 5 10 15
Val Gly Glu Ile Met Asn Ser
20

<210> 953
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 953
Leu Leu Gly Asp Phe Phe Arg Lys Ser Lys Glu Lys Ile Gly Lys Glu
1 5 10 15
Phe Lys Arg Ile Val Gln Arg Ile Lys Asp Phe Leu Arg Asn Leu Val
20 25 30
Pro Arg Thr Glu Ser Cys
35

<210> 954
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 954
Arg Gly Gly Arg Leu Ser Tyr Ser Arg Arg Arg Phe Ser Thr Ser Thr
1 5 10 15
Gly Arg

<210> 955
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 955
Tyr Lys Gln Cys His Lys Lys Gly Gly Lys Lys Gly Ser Gly
1 5 10

<210> 956
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 956
Ala Leu Trp Lys Thr Leu Leu Lys Lys Val Leu Lys Ala Pro Lys Lys
1 5 10 15
Lys Arg Lys Val
20

<210> 957
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 957
His Ala Arg Ile Lys Pro Thr Phe Arg Arg Leu Lys Trp Lys Tyr Lys
1 5 10 15
Gly Lys Phe Trp
20

<210> 958
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 958
Thr Lys Arg Arg Ile Thr Pro Lys Asp Val Ile Asp Val Arg Ser Val
1 5 10 15
Thr Thr Glu Ile Asn Thr
20

<210> 959
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 959
Arg Gln Gly Ala Ala Arg Val Thr Ser Trp Leu Gly Arg Gln Leu Arg
1 5 10 15
Ile Ala Gly Lys Arg Leu Glu Gly Arg Ser Lys
20 25

<210> 960
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 960
Asn Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr
1 5 10 15
Gln Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro
20 25 30
Val Gln

<210> 961
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 961
Arg His Ser Arg Ile Gly Ile Ile Gln Gln Arg Arg Thr Arg Asn Gly
1 5 10 15

<210> 962
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 962
Lys Leu Ile Lys Gly Arg Thr Pro Ile Lys Phe Gly Lys Ala Asp Cys
1 5 10 15
Asp Arg Pro Pro Lys His Ser Gln Asn Gly Met Gly Lys
20 25

<210> 963
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 963
Pro Leu Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro
1 5 10

<210> 964
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 964
Asp Pro Lys Gly Asp Pro Lys Gly Val Thr Val Thr Val Thr Val Thr
1 5 10 15
Val Thr Gly Lys Gly Asp Pro Lys Pro Asp
20 25

<210> 965
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 965
Arg Arg Ile Pro Asn Arg Arg Pro Arg Arg
1 5 10

<210> 966
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 966
Arg Leu Arg Trp Arg
1 5

<210> 967
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 967
Met Val Arg Arg Phe Leu Val Thr Leu Arg Ile Arg Arg Ala Cys Gly
1 5 10 15
Pro Pro Arg Val Arg Val
20

<210> 968
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 968
Met Val Thr Val Leu Phe Arg Arg Leu Arg Ile Arg Arg Ala Cys Gly
1 5 10 15
Pro Pro Arg Val Arg Val
20

<210> 969
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 969
Leu Leu Ile Ile Leu Arg Arg Arg Ile Arg Lys Gln Ala His Ala His
1 5 10 15
Ser Lys

<210> 970
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 970
Leu Ser Thr Ala Ala Asp Met Gln Gly Val Val Thr Asp Gly Met Ala
1 5 10 15
Ser Gly

<210> 971
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 971
Leu Ser Thr Ala Ala Asp Met Gln Gly Val Val Thr Asp Gly Met Ala
1 5 10 15
Ser Gly Leu Asp Lys Asp Tyr Leu Lys Pro Asp Asp
20 25

<210> 972
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 972
Lys Phe His Thr Phe Pro Gln Thr Ala Ile Gly Val Gly Ala Pro
1 5 10 15

<210> 973
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 973
Val Pro Thr Leu Lys
1 5

<210> 974
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 974
Pro Phe Val Tyr Leu Ile
1 5

<210> 975
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 975
Pro Ile Glu Val Cys Met Tyr Arg Glu Pro
1 5 10

<210> 976
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 976
Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5 10

<210> 977
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 977
Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp Ser Gln Pro Lys
1 5 10 15
Lys Arg Lys Val
20

<210> 978
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 978
Gly Leu Ala Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly
1 5 10 15
Ala Trp Ser Gln Pro Lys Lys Lys Arg Lys Val
20 25

<210> 979
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Aib

<400> 979
Ala Gly Tyr Leu Leu Gly His Ile Asn Leu His His Leu Ala His Leu
1 5 10 15
Xaa His His Ile Leu
20

<210> 980
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 980
Lys Leu Ala Leu Lys Ala Leu Lys Ala Leu Lys Ala Ala Leu Lys Leu
1 5 10 15
Ala

<210> 981
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 981
Arg Arg Trp Trp Arg Arg Trp Arg Arg
1 5

<210> 982
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 982
Gly Leu Trp Arg Ala Leu Trp Arg Leu Leu Arg Ser Leu Trp Arg Leu
1 5 10 15
Leu Trp Arg Ala
20

<210> 983
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 983
Leu Ile Arg Leu Trp Ser His Leu Ile His Ile Trp Phe Gln Asn Arg
1 5 10 15
Arg Leu Lys Trp Lys Lys Lys
20

<210> 984
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 984
Leu Lys Thr Leu Thr Glu Thr Leu Lys Glu Leu Thr Lys Thr Leu Thr
1 5 10 15
Glu Leu

<210> 985
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 985
Pro Pro Arg Pro Pro Arg Pro Pro Arg Pro Pro Arg Pro Pro Arg Pro
1 5 10 15
Pro Arg

<210> 986
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 986
Pro Arg Arg Pro Arg Arg Pro Arg Arg Pro Arg Arg Pro Arg Arg Pro
1 5 10 15
Arg Arg

<210> 987
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 987
Gly Pro Ser Gln Pro Thr Tyr Pro Gly Asp Asp Ala Pro Val Arg Asp
1 5 10 15
Leu Ile Arg Phe Tyr Arg Asp Leu Gln Arg Tyr Leu Asn Val Val Thr
20 25 30
Arg His Arg Tyr
35

<210> 988
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 988
Gly Pro Ser Gln Pro Thr Tyr Pro Gly Asp Asp Ala Pro Val Arg Asp
1 5 10 15

Leu Ile Arg Phe Tyr Arg Asp Leu Arg Arg Tyr Leu Asn Val Val Thr
20 25 30
Arg His Arg Tyr
35

<210> 989
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 989
Gly Pro Ser Gln Pro Thr Tyr Pro Gly Asp Asp Ala Pro Val Arg Asp
1 5 10 15
Leu Arg Arg Phe Tyr Arg Asp Leu Arg Arg Tyr Leu Asn Val Val Thr
20 25 30
Arg His Arg Tyr
35

<210> 990
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Proline-based mimic of leucine

<220>
<221> MOD_RES
<222> (3)..(4)
<223> Proline-based mimic of lysine or arginine

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Proline-based mimic of leucine

<220>
<223> See specification as filed for detailed description of substitutions and preferred embodiments

<400> 990
Gly Xaa Xaa Xaa Xaa
1 5

<210> 991
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 991
Val Arg Leu Pro Pro Pro Val Arg Leu Pro Pro Pro Val Arg Leu Pro
1 5 10 15
Pro Pro

<210> 992
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 992
Val Glu Leu Pro Pro Pro Val Glu Leu Pro Pro Pro Val Glu Leu Pro
1 5 10 15
Pro Pro

<210> 993
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 993
Phe Lys Ile Tyr Asp Lys Lys Val Arg Thr Arg Val Val Lys His
1 5 10 15

<210> 994
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 994
Arg Ala Ser Lys Arg Asp Gly Ser Trp Val Lys Lys Leu His Arg Ile
1 5 10 15
Leu Glu

<210> 995
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 995
Lys Gly Thr Tyr Lys Lys Lys Leu Met Arg Ile Pro Leu Lys Gly Thr
1 5 10 15

<210> 996
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 996
Leu Tyr Lys Lys Gly Pro Ala Lys Lys Gly Arg Pro Pro Leu Arg Gly
1 5 10 15
Trp Phe His

<210> 997
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 997
His Ser Pro Ile Ile Pro Leu Gly Thr Arg Phe Val Cys His Gly Val
1 5 10 15
Thr

<210> 998
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 998
Tyr Thr Ala Ile Ala Trp Val Lys Ala Phe Ile Arg Lys Leu Arg Lys
1 5 10 15

<210> 999
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 999
Ile Ala Trp Val Lys Ala Phe Ile Arg Lys Leu Arg Lys Gly Pro Leu
1 5 10 15
Gly

<210> 1000
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1000
Arg Leu Ser Gly Met Asn Glu Val Leu Ser Phe Arg Trp Leu
1 5 10

<210> 1001
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1001
Ser Asp Leu Trp Glu Met Met Met Val Ser Leu Ala Cys Gln Tyr
1 5 10 15

<210> 1002
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1002
Val Thr Trp Thr Pro Gln Ala Trp Phe Gln Trp Val
1 5 10

<210> 1003
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1003
Gly Ser Pro Trp Gly Leu Gln His His Pro Pro Arg Thr
1 5 10

<210> 1004
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1004
Gly Pro Phe His Phe Tyr Gln Phe Leu Phe Pro Pro Val
1 5 10

<210> 1005
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1005
Thr Ser Pro Leu Asn Ile His Asn Gly Gln Lys Leu
1 5 10

<210> 1006
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1006
Cys Ala Tyr His Arg Leu Arg Arg Cys
1 5

<210> 1007
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1007
Arg Cys Gly Arg Ala Ser Arg Cys Arg Val Arg Trp Met Arg Arg Arg
1 5 10 15
Arg Ile

<210> 1008
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1008
Pro Tyr Ser Arg Pro His Val Gln Leu Trp Tyr Pro Asn Arg Glu Ser
1 5 10 15
Cys Arg Ser Leu Ile Arg Ser Leu Gly Pro
20 25

<210> 1009
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1009
Pro Leu Ile Leu Leu Arg Leu Leu Arg Gly Gln Phe
1 5 10

<210> 1010
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1010
Pro Leu Ile Tyr Leu Arg Leu Leu Arg Gly Gln Phe
1 5 10

<210> 1011
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1011
Lys Leu Trp Met Arg Trp Tyr Ser Pro Thr Thr Arg Arg Tyr Gly
1 5 10 15

<210> 1012
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1012
Gly Leu Phe His Ala Leu Leu His Leu Leu His Ser Leu Trp His Leu
1 5 10 15
Leu Leu His Ala
20

<210> 1013
<211> 1401
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1013
Cys Asp Lys Lys Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val
1 5 10 15
Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
20 25 30
Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
35 40 45
Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
50 55 60
Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Ser
65 70 75 80
Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
85 90 95
Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
100 105 110
His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
115 120 125

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
130 135 140
Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145 150 155 160
Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
165 170 175
Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
180 185 190
Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
195 200 205
Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
210 215 220
Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225 230 235 240
Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
245 250 255
Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260 265 270
Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
275 280 285
Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
290 295 300
Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305 310 315 320
Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335
Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350
Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365
Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380
Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385 390 395 400
Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
405 410 415
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
420 425 430
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
450 455 460
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465 470 475 480
Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
485 490 495
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
500 505 510
Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
515 520 525
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
530 535 540
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545 550 555 560
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
565 570 575

Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
580 585 590
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
595 600 605
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
610 615 620
Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640
His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
645 650 655
Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670
Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700
Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720
His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735
Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750
Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765
Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780
Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800
Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815
Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830
Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
835 840 845
Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860
Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880
Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910
Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925
Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945 950 955 960
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975
Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990
Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005
Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
1010 1015 1020

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Lys Ser  Glu Gln Glu Ile Gly  Lys Ala Thr Ala Lys  Tyr Phe Phe
    1025                1030                1035
Tyr Ser  Asn Ile Met Asn Phe  Phe Lys Thr Glu Ile  Thr Leu Ala
    1040                1045                1050
Asn Gly  Glu Ile Arg Lys Arg  Pro Leu Ile Glu Thr  Asn Gly Glu
    1055                1060                1065
Thr Gly  Glu Ile Val Trp Asp  Lys Gly Arg Asp Phe  Ala Thr Val
    1070                1075                1080
Arg Lys  Val Leu Ser Met Pro  Gln Val Asn Ile Val  Lys Lys Thr
    1085                1090                1095
Glu Val  Gln Thr Gly Gly Phe  Ser Lys Glu Ser Ile  Leu Pro Lys
    1100                1105                1110
Arg Asn  Ser Asp Lys Leu Ile  Ala Arg Lys Lys Asp  Trp Asp Pro
    1115                1120                1125
Lys Lys  Tyr Gly Gly Phe Asp  Ser Pro Thr Val Ala  Tyr Ser Val
    1130                1135                1140
Leu Val  Val Ala Lys Val Glu  Lys Gly Lys Ser Lys  Lys Leu Lys
    1145                1150                1155
Ser Val  Lys Glu Leu Leu Gly  Ile Thr Ile Met Glu  Arg Ser Ser
    1160                1165                1170
Phe Glu  Lys Asn Pro Ile Asp  Phe Leu Glu Ala Lys  Gly Tyr Lys
    1175                1180                1185
Glu Val  Lys Lys Asp Leu Ile  Ile Lys Leu Pro Lys  Tyr Ser Leu
    1190                1195                1200
Phe Glu  Leu Glu Asn Gly Arg  Lys Arg Met Leu Ala  Ser Ala Gly
    1205                1210                1215
Glu Leu  Gln Lys Gly Asn Glu  Leu Ala Leu Pro Ser  Lys Tyr Val
    1220                1225                1230
Asn Phe  Leu Tyr Leu Ala Ser  His Tyr Glu Lys Leu  Lys Gly Ser
    1235                1240                1245
Pro Glu  Asp Asn Glu Gln Lys  Gln Leu Phe Val Glu  Gln His Lys
    1250                1255                1260
His Tyr  Leu Asp Glu Ile Ile  Glu Gln Ile Ser Glu  Phe Ser Lys
    1265                1270                1275
Arg Val  Ile Leu Ala Asp Ala  Asn Leu Asp Lys Val  Leu Ser Ala
    1280                1285                1290
Tyr Asn  Lys His Arg Asp Lys  Pro Ile Arg Glu Gln  Ala Glu Asn
    1295                1300                1305
Ile Ile  His Leu Phe Thr Leu  Thr Asn Leu Gly Ala  Pro Ala Ala
    1310                1315                1320
Phe Lys  Tyr Phe Asp Thr Thr  Ile Asp Arg Lys Arg  Tyr Thr Ser
    1325                1330                1335
Thr Lys  Glu Val Leu Asp Ala  Thr Leu Ile His Gln  Ser Ile Thr
    1340                1345                1350
Gly Leu  Tyr Glu Thr Arg Ile  Asp Leu Ser Gln Leu  Gly Gly Asp
    1355                1360                1365
Ala Tyr  Pro Tyr Asp Val Pro  Asp Tyr Ala Ser Leu  Gly Ser Gly
    1370                1375                1380
Ser Pro  Lys Lys Lys Arg Lys  Val Glu Asp Pro Lys  Lys Lys Arg
    1385                1390                1395
Lys Val  Asp
    1400
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<210> 1014
<211> 4203

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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atcaccgacg agtacaaggt gcccagcaag aaattcaagg tgctgggcaa caccgaccgg 120
cacagcatca agaagaacct gatcggcgcc ctgctgttcg acagcggaga aacagccgag 180
gccacccggc tgaagagaac cgccagaaga agatacacca gacggaagaa ccggatcagc 240
tatctgcaag agatcttcag caacgagatg gccaaggtgg acgacagctt cttccacaga 300
ctggaagagt ccttcctggt ggaagaggat aagaagcacg agcggcaccc catcttcggc 360
aacatcgtgg acgaggtggc ctaccacgag aagtacccca ccatctacca cctgagaaag 420
aaactggtgg acagcaccga caaggccgac ctgcggctga tctatctggc cctggcccac 480
atgatcaagt tccggggcca cttcctgatc gagggcgacc tgaaccccga caacagcgac 540
gtggacaagc tgttcatcca gctggtgcag acctacaacc agctgttcga ggaaaacccc 600
atcaacgcca gcggcgtgga cgccaaggcc atcctgtctg ccagactgag caagagcaga 660
cggctggaaa atctgatcgc ccagctgccc ggcgagaaga agaatggcct gttcggcaac 720
ctgattgccc tgagcctggg cctgaccccc aacttcaaga gcaacttcga cctggccgag 780
gatgccaaac tgcagctgag caaggacacc tacgacgacg acctggacaa cctgctggcc 840
cagatcggcg accagtacgc cgacctgttt ctggccgcca agaacctgtc cgacgccatc 900
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ggctacatcg atggcggagc cagccaggaa gagttctaca agttcatcaa gcccatcctg 1140
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aagcagcgga ccttcgacaa cggcagcatc ccccaccaga tccacctggg agagctgcac 1260
gccattctgc ggcggcagga agattttac ccattcctga aggacaaccg ggaaaagatc 1320
gagaagatcc tgaccttccg catcccctac tacgtgggcc ctctggccag gggaaacagc 1380
agattcgcct ggatgaccag aaagagcgag gaaaccatca ccccctggaa cttcgaggaa 1440
gtggtggaca agggcgccag cgcccagagc ttcatcgagc ggatgaccaa cttcgataag 1500
aacctgccca acgagaaggt gctgcccaag cacagcctgc tgtacgagta cttcaccgtg 1560
tacaacgagc tgaccaaagt gaaatacgtg accgagggaa tgagaaagcc cgccttcctg 1620
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gtgaagcagc tgaaagagga ctacttcaag aaaatcgagt gcttcgactc cgtggaaatc 1740
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cacctgttcg acgacaaagt gatgaagcag ctgaagcggc ggagatacac cggctggggc 1980
aggctgagcc ggaagctgat caacggcatc cgggacaagc agtccggcaa gacaatcctg 2040
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aagctggtgt ccgatttccg gaaggatttc cagttttaca aagtgcgcga gatcaacaac 2940

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taccctaagc tggaaagcga gttcgtgtac ggcgactaca aggtgtacga cgtgcggaag 3060
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cctctgatcg agacaaacgg cgaaacaggc gagatcgtgt gggataaggg ccgggacttt 3240
gccaccgtgc ggaaagtgct gtctatgccc caagtgaata tcgtgaaaaa gaccgaggtg 3300
cagacaggcg gcttcagcaa agagtctatc ctgcccaaga ggaacagcga caagctgatc 3360
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tactccctgt tcgagctgga aaacggccgg aagagaatgc tggcctctgc cggcgaactg 3660
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cagcacaaac actacctgga cgagatcatc gagcagatca gcgagttctc caagagagtg 3840
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gaggtgctgg acgccaccct gatccaccag agcatcaccg gcctgtacga gacacggatc 4080
gacctgtctc agctgggagg cgacgcctat ccctatgacg tgcccgatta tgccagcctg 4140
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gac 4203

<210> 1015
<211> 1658
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1015

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            20                  25                  30
Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
        35                  40                  45
Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
    50                  55                  60
Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Ser
65                  70                  75                  80
Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
                85                  90                  95
Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
            100                 105                 110
His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
        115                 120                 125
His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
    130                 135                 140
Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145                 150                 155                 160
Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
                165                 170                 175
```

Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
180 185 190
Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
195 200 205
Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
210 215 220
Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225 230 235 240
Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
245 250 255
Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260 265 270
Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
275 280 285
Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
290 295 300
Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305 310 315 320
Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335
Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350
Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365
Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380
Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385 390 395 400
Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
405 410 415
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
420 425 430
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
450 455 460
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465 470 475 480
Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
485 490 495
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
500 505 510
Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
515 520 525
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
530 535 540
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545 550 555 560
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
565 570 575
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
580 585 590
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
595 600 605
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
610 615 620

Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640
His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
645 650 655
Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670
Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700
Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720
His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735
Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750
Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765
Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780
Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800
Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815
Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830
Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
835 840 845
Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860
Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880
Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910
Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925
Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945 950 955 960
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975
Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990
Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005
Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
1010 1015 1020
Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
1025 1030 1035
Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
1040 1045 1050
Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
1055 1060 1065

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Arg Lys  Val Leu Ser Met Pro  Gln Val Asn Ile Val  Lys Lys Thr
    1085                1090                1095
Glu Val  Gln Thr Gly Gly Phe  Ser Lys Glu Ser Ile  Leu Pro Lys
    1100                1105                1110
Arg Asn  Ser Asp Lys Leu Ile  Ala Arg Lys Lys Asp  Trp Asp Pro
    1115                1120                1125
Lys Lys  Tyr Gly Gly Phe Asp  Ser Pro Thr Val Ala  Tyr Ser Val
    1130                1135                1140
Leu Val  Val Ala Lys Val Glu  Lys Gly Lys Ser Lys  Lys Leu Lys
    1145                1150                1155
Ser Val  Lys Glu Leu Leu Gly  Ile Thr Ile Met Glu  Arg Ser Ser
    1160                1165                1170
Phe Glu  Lys Asn Pro Ile Asp  Phe Leu Glu Ala Lys  Gly Tyr Lys
    1175                1180                1185
Glu Val  Lys Lys Asp Leu Ile  Ile Lys Leu Pro Lys  Tyr Ser Leu
    1190                1195                1200
Phe Glu  Leu Glu Asn Gly Arg  Lys Arg Met Leu Ala  Ser Ala Gly
    1205                1210                1215
Glu Leu  Gln Lys Gly Asn Glu  Leu Ala Leu Pro Ser  Lys Tyr Val
    1220                1225                1230
Asn Phe  Leu Tyr Leu Ala Ser  His Tyr Glu Lys Leu  Lys Gly Ser
    1235                1240                1245
Pro Glu  Asp Asn Glu Gln Lys  Gln Leu Phe Val Glu  Gln His Lys
    1250                1255                1260
His Tyr  Leu Asp Glu Ile Ile  Glu Gln Ile Ser Glu  Phe Ser Lys
    1265                1270                1275
Arg Val  Ile Leu Ala Asp Ala  Asn Leu Asp Lys Val  Leu Ser Ala
    1280                1285                1290
Tyr Asn  Lys His Arg Asp Lys  Pro Ile Arg Glu Gln  Ala Glu Asn
    1295                1300                1305
Ile Ile  His Leu Phe Thr Leu  Thr Asn Leu Gly Ala  Pro Ala Ala
    1310                1315                1320
Phe Lys  Tyr Phe Asp Thr Thr  Ile Asp Arg Lys Arg  Tyr Thr Ser
    1325                1330                1335
Thr Lys  Glu Val Leu Asp Ala  Thr Leu Ile His Gln  Ser Ile Thr
    1340                1345                1350
Gly Leu  Tyr Glu Thr Arg Ile  Asp Leu Ser Gln Leu  Gly Gly Asp
    1355                1360                1365
Ala Tyr  Pro Tyr Asp Val Pro  Asp Tyr Ala Ser Leu  Gly Ser Gly
    1370                1375                1380
Ser Pro  Lys Lys Lys Arg Lys  Val Glu Asp Pro Lys  Lys Lys Arg
    1385                1390                1395
Lys Val  Asp Gly Ile Gly Ser  Gly Ser Asn Gly Ser  Ser Gly Ser
    1400                1405                1410
Val Ser  Lys Gly Glu Glu Asp  Asn Met Ala Ile Ile  Lys Glu Phe
    1415                1420                1425
Met Arg  Phe Lys Val His Met  Glu Gly Ser Val Asn  Gly His Glu
    1430                1435                1440
Phe Glu  Ile Glu Gly Glu Gly  Glu Gly Arg Pro Tyr  Glu Gly Thr
    1445                1450                1455
Gln Thr  Ala Lys Leu Lys Val  Thr Lys Gly Gly Pro  Leu Pro Phe
    1460                1465                1470
Ala Trp  Asp Ile Leu Ser Pro  Gln Phe Met Tyr Gly  Ser Lys Ala
    1475                1480                1485
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Tyr Val  Lys His Pro Ala Asp  Ile Pro Asp Tyr Leu  Lys Leu Ser
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    1505                1510                1515
Gly Gly  Val Val Thr Val Thr  Gln Asp Ser Ser Leu  Gln Asp Gly
    1520                1525                1530
Glu Phe  Ile Tyr Lys Val Lys  Leu Arg Gly Thr Asn  Phe Pro Ser
    1535                1540                1545
Asp Gly  Pro Val Met Gln Lys  Lys Thr Met Gly Trp  Glu Ala Ser
    1550                1555                1560
Ser Glu  Arg Met Tyr Pro Glu  Asp Gly Ala Leu Lys  Gly Glu Ile
    1565                1570                1575
Lys Gln  Arg Leu Lys Leu Lys  Asp Gly Gly His Tyr  Asp Ala Glu
    1580                1585                1590
Val Lys  Thr Thr Tyr Lys Ala  Lys Lys Pro Val Gln  Leu Pro Gly
    1595                1600                1605
Ala Tyr  Asn Val Asn Ile Lys  Leu Asp Ile Thr Ser  His Asn Glu
    1610                1615                1620
Asp Tyr  Thr Ile Val Glu Gln  Tyr Glu Arg Ala Glu  Gly Arg His
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Ser Thr  Gly Gly Met Asp Glu  Leu Tyr Lys Gly Ser  Pro Lys Lys
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Lys Arg  Lys Val Glu
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<210> 1016
<211> 4974
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1016

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atgatcaaga gatacgacga gcaccaccag gacctgaccc tgctgaaagc tctcgtgcgg    1020
cagcagctgc ctgagaagta caaagagatt ttcttcgacc agagcaagaa cggctacgcc    1080
ggctacatcg atggcggagc cagccaggaa gagttctaca agttcatcaa gcccatcctg    1140
gaaaagatgg acggcaccga ggaactgctc gtgaagctga acagagagga cctgctgcgg    1200
aagcagcgga ccttcgacaa cggcagcatc ccccaccaga tccacctggg agagctgcac    1260
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<210> 1017
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 1017
gccatcccct tctgtgaatg ttagac 26

<210> 1018
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 1018
ggagattgga gacacggaga gcag 24

<210> 1019
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 1019
ccagctccca gccaggattc 20

<210> 1020
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 1020
atcgtgccaa gcgaagagc 19

<210> 1021
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 1021
tgatggcctt ggacagttac c 21

<210> 1022
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 1022
ggtccagatg gagagagacc a 21

<210> 1023
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1023
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<210> 1024
<211> 1658
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> MOD_RES
<222> (168)..(168)
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<400> 1024
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35 40 45
Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
50 55 60
Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
65 70 75 80
Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
85 90 95
Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
100 105 110
His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
115 120 125
His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
130 135 140
Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145 150 155 160
Met Ile Lys Phe Arg Gly His Xaa Leu Ile Glu Gly Asp Leu Asn Pro
165 170 175
Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
180 185 190
Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
195 200 205
Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
210 215 220
Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225 230 235 240
Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
245 250 255
Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260 265 270
Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
275 280 285
Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
290 295 300
Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305 310 315 320
Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335
Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350
Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365
Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380
Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385 390 395 400
Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
405 410 415
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
420 425 430
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
450 455 460

Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465 470 475 480
Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
485 490 495
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
500 505 510
Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
515 520 525
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
530 535 540
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545 550 555 560
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
565 570 575
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
580 585 590
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
595 600 605
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
610 615 620
Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640
His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
645 650 655
Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670
Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700
Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720
His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735
Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750
Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765
Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780
Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800
Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815
Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830
Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
835 840 845
Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860
Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880
Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910

Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925
Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945 950 955 960
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975
Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990
Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005
Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
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Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
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1055 1060 1065
Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080
Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
1085 1090 1095
Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
1100 1105 1110
Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
1115 1120 1125
Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
1130 1135 1140
Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
1145 1150 1155
Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
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Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
1175 1180 1185
Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
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Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly
1205 1210 1215
Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
1220 1225 1230
Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser
1235 1240 1245
Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys
1250 1255 1260
His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys
1265 1270 1275
Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala
1280 1285 1290
Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn
1295 1300 1305
Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala
1310 1315 1320
Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser
1325 1330 1335

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Ala Tyr  Pro Tyr Asp Val Pro  Asp Tyr Ala Ser Leu  Gly Ser Gly
    1370                1375                1380
Ser Pro  Lys Lys Lys Arg Lys  Val Glu Asp Pro Lys  Lys Lys Arg
    1385                1390                1395
Lys Val  Asp Gly Ile Gly Ser  Gly Ser Asn Gly Ser  Ser Gly Ser
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Val Ser  Lys Gly Glu Glu Asp  Asn Met Ala Ile Ile  Lys Glu Phe
    1415                1420                1425
Met Arg  Phe Lys Val His Met  Glu Gly Ser Val Asn  Gly His Glu
    1430                1435                1440
Phe Glu  Ile Glu Gly Glu Gly  Glu Gly Arg Pro Tyr  Glu Gly Thr
    1445                1450                1455
Gln Thr  Ala Lys Leu Lys Val  Thr Lys Gly Gly Pro  Leu Pro Phe
    1460                1465                1470
Ala Trp  Asp Ile Leu Ser Pro  Gln Phe Met Tyr Gly  Ser Lys Ala
    1475                1480                1485
Tyr Val  Lys His Pro Ala Asp  Ile Pro Asp Tyr Leu  Lys Leu Ser
    1490                1495                1500
Phe Pro  Glu Gly Phe Lys Trp  Glu Arg Val Met Asn  Phe Glu Asp
    1505                1510                1515
Gly Gly  Val Val Thr Val Thr  Gln Asp Ser Ser Leu  Gln Asp Gly
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Glu Phe  Ile Tyr Lys Val Lys  Leu Arg Gly Thr Asn  Phe Pro Ser
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Asp Gly  Pro Val Met Gln Lys  Lys Thr Met Gly Trp  Glu Ala Ser
    1550                1555                1560
Ser Glu  Arg Met Tyr Pro Glu  Asp Gly Ala Leu Lys  Gly Glu Ile
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Lys Gln  Arg Leu Lys Leu Lys  Asp Gly Gly His Tyr  Asp Ala Glu
    1580                1585                1590
Val Lys  Thr Thr Tyr Lys Ala  Lys Lys Pro Val Gln  Leu Pro Gly
    1595                1600                1605
Ala Tyr  Asn Val Asn Ile Lys  Leu Asp Ile Thr Ser  His Asn Glu
    1610                1615                1620
Asp Tyr  Thr Ile Val Glu Gln  Tyr Glu Arg Ala Glu  Gly Arg His
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Lys Arg  Lys Val Glu
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<210> 1025
<211> 1368
<212> PRT
<213> Streptococcus pyogenes

<400> 1025

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50 55 60
Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Ser
65 70 75 80
Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
85 90 95
Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
100 105 110
His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
115 120 125
His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
130 135 140
Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145 150 155 160
Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
165 170 175
Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
180 185 190
Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
195 200 205
Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
210 215 220
Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225 230 235 240
Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
245 250 255
Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260 265 270
Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
275 280 285
Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
290 295 300
Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305 310 315 320
Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335
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340 345 350
Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365
Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380
Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385 390 395 400
Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
405 410 415
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
420 425 430
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
450 455 460
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465 470 475 480

Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
485 490 495
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
500 505 510
Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
515 520 525
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
530 535 540
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545 550 555 560
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
565 570 575
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
580 585 590
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
595 600 605
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
610 615 620
Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640
His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
645 650 655
Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670
Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700
Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720
His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735
Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750
Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765
Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780
Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800
Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815
Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830
Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
835 840 845
Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860
Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880
Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910
Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925

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Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
    930                 935                 940
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945                 950                 955                 960
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
                965                 970                 975
Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
            980                 985                 990
Val Gly Thr Ala Leu Ile Lys Lys  Tyr Pro Lys Leu Glu  Ser Glu Phe
        995                 1000                1005
Val Tyr  Gly Asp Tyr Lys Val  Tyr Asp Val Arg Lys  Met Ile Ala
    1010                1015                1020
Lys Ser  Glu Gln Glu Ile Gly  Lys Ala Thr Ala Lys  Tyr Phe Phe
    1025                1030                1035
Tyr Ser  Asn Ile Met Asn Phe  Phe Lys Thr Glu Ile  Thr Leu Ala
    1040                1045                1050
Asn Gly  Glu Ile Arg Lys Arg  Pro Leu Ile Glu Thr  Asn Gly Glu
    1055                1060                1065
Thr Gly  Glu Ile Val Trp Asp  Lys Gly Arg Asp Phe  Ala Thr Val
    1070                1075                1080
Arg Lys  Val Leu Ser Met Pro  Gln Val Asn Ile Val  Lys Lys Thr
    1085                1090                1095
Glu Val  Gln Thr Gly Gly Phe  Ser Lys Glu Ser Ile  Leu Pro Lys
    1100                1105                1110
Arg Asn  Ser Asp Lys Leu Ile  Ala Arg Lys Lys Asp  Trp Asp Pro
    1115                1120                1125
Lys Lys  Tyr Gly Gly Phe Asp  Ser Pro Thr Val Ala  Tyr Ser Val
    1130                1135                1140
Leu Val  Val Ala Lys Val Glu  Lys Gly Lys Ser Lys  Lys Leu Lys
    1145                1150                1155
Ser Val  Lys Glu Leu Leu Gly  Ile Thr Ile Met Glu  Arg Ser Ser
    1160                1165                1170
Phe Glu  Lys Asn Pro Ile Asp  Phe Leu Glu Ala Lys  Gly Tyr Lys
    1175                1180                1185
Glu Val  Lys Lys Asp Leu Ile  Ile Lys Leu Pro Lys  Tyr Ser Leu
    1190                1195                1200
Phe Glu  Leu Glu Asn Gly Arg  Lys Arg Met Leu Ala  Ser Ala Gly
    1205                1210                1215
Glu Leu  Gln Lys Gly Asn Glu  Leu Ala Leu Pro Ser  Lys Tyr Val
    1220                1225                1230
Asn Phe  Leu Tyr Leu Ala Ser  His Tyr Glu Lys Leu  Lys Gly Ser
    1235                1240                1245
Pro Glu  Asp Asn Glu Gln Lys  Gln Leu Phe Val Glu  Gln His Lys
    1250                1255                1260
His Tyr  Leu Asp Glu Ile Ile  Glu Gln Ile Ser Glu  Phe Ser Lys
    1265                1270                1275
Arg Val  Ile Leu Ala Asp Ala  Asn Leu Asp Lys Val  Leu Ser Ala
    1280                1285                1290
Tyr Asn  Lys His Arg Asp Lys  Pro Ile Arg Glu Gln  Ala Glu Asn
    1295                1300                1305
Ile Ile  His Leu Phe Thr Leu  Thr Asn Leu Gly Ala  Pro Ala Ala
    1310                1315                1320
Phe Lys  Tyr Phe Asp Thr Thr  Ile Asp Arg Lys Arg  Tyr Thr Ser
    1325                1330                1335
```

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Thr Lys  Glu Val Leu Asp Ala  Thr Leu Ile His Gln  Ser Ile Thr
    1340                1345                1350
Gly Leu  Tyr Glu Thr Arg Ile  Asp Leu Ser Gln Leu  Gly Gly Asp
    1355                1360                1365
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<210> 1026
<211> 1658
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1026

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Met Asp Lys Lys Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val
1               5                  10                  15
Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
            20                  25                  30
Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
        35                  40                  45
Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
    50                  55                  60
Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Ser
65                  70                  75                  80
Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
                85                  90                  95
Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
            100                 105                 110
His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
        115                 120                 125
His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
    130                 135                 140
Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145                 150                 155                 160
Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
                165                 170                 175
Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
            180                 185                 190
Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
        195                 200                 205
Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
    210                 215                 220
Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225                 230                 235                 240
Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
                245                 250                 255
Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
            260                 265                 270
Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
        275                 280                 285
Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
    290                 295                 300
Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305                 310                 315                 320
```

Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335
Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350
Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365
Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380
Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385 390 395 400
Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
405 410 415
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
420 425 430
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
450 455 460
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465 470 475 480
Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
485 490 495
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
500 505 510
Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
515 520 525
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
530 535 540
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545 550 555 560
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
565 570 575
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
580 585 590
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
595 600 605
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
610 615 620
Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640
His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
645 650 655
Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670
Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700
Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720
His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735
Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750
Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765

Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780
Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800
Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815
Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830
Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
835 840 845
Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860
Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880
Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910
Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925
Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945 950 955 960
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975
Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990
Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005
Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
1010 1015 1020
Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
1025 1030 1035
Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
1040 1045 1050
Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
1055 1060 1065
Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080
Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
1085 1090 1095
Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
1100 1105 1110
Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
1115 1120 1125
Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
1130 1135 1140
Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
1145 1150 1155
Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
1160 1165 1170
Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
1175 1180 1185
Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
1190 1195 1200

Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly
1205 1210 1215
Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
1220 1225 1230
Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser
1235 1240 1245
Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys
1250 1255 1260
His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys
1265 1270 1275
Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala
1280 1285 1290
Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn
1295 1300 1305
Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala
1310 1315 1320
Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser
1325 1330 1335
Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr
1340 1345 1350
Gly Leu Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp
1355 1360 1365
Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Gly Ser Gly
1370 1375 1380
Ser Pro Lys Lys Lys Arg Lys Val Glu Asp Pro Lys Lys Lys Arg
1385 1390 1395
Lys Val Asp Gly Ile Gly Ser Gly Ser Asn Gly Ser Ser Gly Ser
1400 1405 1410
Val Ser Lys Gly Glu Glu Asp Asn Met Ala Ile Ile Lys Glu Phe
1415 1420 1425
Met Arg Phe Lys Val His Met Glu Gly Ser Val Asn Gly His Glu
1430 1435 1440
Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro Tyr Glu Gly Thr
1445 1450 1455
Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu Pro Phe
1460 1465 1470
Ala Trp Asp Ile Leu Ser Pro Gln Phe Met Tyr Gly Ser Lys Ala
1475 1480 1485
Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser
1490 1495 1500
Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp
1505 1510 1515
Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly
1520 1525 1530
Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser
1535 1540 1545
Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser
1550 1555 1560
Ser Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile
1565 1570 1575
Lys Gln Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu
1580 1585 1590
Val Lys Thr Thr Tyr Lys Ala Lys Lys Pro Val Gln Leu Pro Gly
1595 1600 1605
Ala Tyr Asn Val Asn Ile Lys Leu Asp Ile Thr Ser His Asn Glu
1610 1615 1620

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Asp Tyr  Thr Ile Val Glu Gln  Tyr Glu Arg Ala Glu  Gly Arg His
    1625                1630                1635
Ser Thr  Gly Gly Met Asp Glu  Leu Tyr Lys Gly Ser  Pro Lys Lys
    1640                1645                1650
Lys Arg  Lys Val Glu
    1655
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<210> 1027
<211> 1368
<212> PRT
<213> Streptococcus pyogenes

<400> 1027

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Met Asp Lys Lys Tyr Ser Ile Gly Leu Ala Ile Gly Thr Asn Ser Val
1               5                  10                  15
Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
            20                  25                  30
Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
        35                  40                  45
Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
    50                  55                  60
Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
65                  70                  75                  80
Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
                85                  90                  95
Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
            100                 105                 110
His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
        115                 120                 125
His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
    130                 135                 140
Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145                 150                 155                 160
Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
                165                 170                 175
Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
            180                 185                 190
Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
        195                 200                 205
Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
    210                 215                 220
Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225                 230                 235                 240
Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
                245                 250                 255
Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
            260                 265                 270
Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
        275                 280                 285
Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
    290                 295                 300
Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305                 310                 315                 320
Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
                325                 330                 335
```

Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350
Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365
Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380
Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385 390 395 400
Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
405 410 415
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
420 425 430
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
450 455 460
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465 470 475 480
Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
485 490 495
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
500 505 510
Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
515 520 525
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
530 535 540
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545 550 555 560
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
565 570 575
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
580 585 590
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
595 600 605
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
610 615 620
Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640
His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
645 650 655
Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670
Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700
Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720
His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735
Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750
Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765
Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780

Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800
Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815
Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830
Leu Ser Asp Tyr Asp Val Asp Ala Ile Val Pro Gln Ser Phe Leu Lys
835 840 845
Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860
Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880
Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910
Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925
Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945 950 955 960
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975
Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990
Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005
Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
1010 1015 1020
Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
1025 1030 1035
Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
1040 1045 1050
Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
1055 1060 1065
Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080
Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
1085 1090 1095
Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
1100 1105 1110
Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
1115 1120 1125
Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
1130 1135 1140
Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
1145 1150 1155
Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
1160 1165 1170
Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
1175 1180 1185
Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
1190 1195 1200
Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly
1205 1210 1215

Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
1220 1225 1230
Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser
1235 1240 1245
Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys
1250 1255 1260
His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys
1265 1270 1275
Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala
1280 1285 1290
Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn
1295 1300 1305
Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala
1310 1315 1320
Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser
1325 1330 1335
Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr
1340 1345 1350
Gly Leu Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp
1355 1360 1365

<210> 1028
<211> 69
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1028
cagcauagca aguuaaaaua aggcuagucc guuaucaacu ugaaaaagug gcaccgaguc 60
ggugcuuuu 69

<210> 1029
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1029
His His His His His Trp Tyr Gly
1 5

<210> 1030
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1030
Pro Met Leu Lys Glu
1 5

<210> 1031
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1031
Val Pro Ala Leu Arg
1 5

<210> 1032
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1032
Val Ser Ala Leu Lys
1 5

<210> 1033
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1033
Ile Pro Ala Leu Lys
1 5

<210> 1034
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1034
Gln Leu Ala Leu Gln Leu Ala Leu Gln Ala Leu Gln Ala Ala Leu Gln
1 5 10 15
Leu Ala

<210> 1035
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1035
Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile His Arg Gly Val Pro
1 5 10 15

<210> 1036
<211> 17
<212> PRT
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<210> 1037
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<210> 1038
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Pro Leu Ala Glu Ile Asp Gly Ile Glu Leu Thr Tyr
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<210> 1039
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Arg His Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
1 5 10 15

<210> 1040
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1 5

<210> 1041
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Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 1042
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1 5 10

<210> 1043
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1 5 10

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Pro Pro Arg Pro Pro Arg Pro Pro Arg Pro Pro Arg Pro Pro Arg
1 5 10 15

<210> 1046
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<210> 1047
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1 5 10

<210> 1048
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<210> 1049
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<223> Cys(NPys)

<220>
<223> C-term OH

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1 5 10 15
Leu Leu Leu His Ala
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<210> 1050
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<223> C-term OH

<400> 1050
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1 5 10 15
Leu Leu His Ala
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<210> 1051
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<223> Cys(NPys)

<220>
<223> C-term OH

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1 5 10 15
Leu Leu His Ala Cys
20

<210> 1052
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<212> PRT
<213> Artificial Sequence

<220>
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<223> His(Trt)

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1 5 10 15
Leu Leu His Ala
20

<210> 1053
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<220>
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<220>
<223> C-term Wang resin

<400> 1053

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1				5					10					15	

Leu	Leu	Leu	His	Ala
			20	

<210> 1054
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<220>
<223> C-term OH

<400> 1054
Cys Gly Leu Phe His Ala Leu Leu His Leu Leu His Ser Leu Trp His
1 5 10 15
Leu Leu Leu His Ala
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<210> 1055
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<400> 1055
Gly Leu Phe His Ala Leu Leu His Leu Leu His Ser Leu Trp His Leu
1 5 10 15
Leu Leu His Ala
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<210> 1056
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<220>
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<220>
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<400> 1056
Gly Leu Phe His Ala Leu Leu His Leu Leu His Ser Leu Trp His Leu
1 5 10 15
Leu Leu His Ala
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<210> 1057
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<220>
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<222> (14)..(14)
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<220>
<221> MOD_RES
<222> (21)..(21)
<223> Cys(Trt)

<220>
<223> C-term CTC resin

<400> 1057
Gly Leu Phe His Ala Leu Leu His Leu Leu His Ser Leu Trp His Leu
1 5 10 15
Leu Leu His Ala Cys
20

<210> 1058
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> N-term H

<220>
<223> C-term OH

<400> 1058
Gly Leu Phe His Ala Leu Leu His Leu Leu His Ser Leu Trp His Leu
1 5 10 15
Leu Leu His Ala Cys
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<210> 1059
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<220>
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<220>
<223> N-term Ac

<400> 1059
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1 5 10 15
Leu Leu Leu His Ala
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<210> 1060
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<220>
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1 5 10 15
Leu Leu His Ala
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<210> 1061
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<212> PRT
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<220>
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Gly Leu Phe His Ala Leu Leu His Leu Leu His Ser Leu Trp His Leu
1 5 10 15
Leu Leu His Ala Cys
20

<210> 1062
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<220>
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<220>
<221> MOD_RES
<222> (1)..(1)
<223> Gly(propargyl)

<400> 1062
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1 5 10 15
Leu Leu Leu His Ala
20

<210> 1063
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<220>
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<220>
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<400> 1063
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1 5 10 15
Leu Leu His Ala
20

<210> 1064
<211> 31
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<220>
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1 5 10 15
His Leu Ala Lys Ala Leu Ala Lys Ala Leu Lys Ala Cys Glu Ala
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<210> 1065
<211> 31
<212> PRT
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<220>
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<220>
<223> C-term OH

<400> 1065
Trp Glu Ala Lys Leu Ala Lys Ala Leu Ala Lys Ala Leu Ala Lys His
1 5 10 15
Leu Ala Lys Ala Leu Ala Lys Ala Leu Lys Ala Ser Glu Ala Cys
20 25 30

<210> 1066
<211> 31
<212> PRT
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<220>
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<220>
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<220>
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<222> (1)..(1)
<223> Cys(NPys)

<400> 1066
Cys Trp Glu Ala Lys Leu Ala Lys Ala Leu Ala Lys Ala Leu Ala Lys
1 5 10 15
His Leu Ala Lys Ala Leu Ala Lys Ala Leu Lys Ala Ser Glu Ala
20 25 30

<210> 1067
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> N-term PEG

<400> 1067
Trp Glu Ala Lys Leu Ala Lys Ala Leu Ala Lys Ala Leu Ala Lys His
1 5 10 15
Leu Ala Lys Ala Leu Ala Lys Ala Leu Lys Ala Ser Glu Ala
20 25 30

<210> 1068
<211> 6
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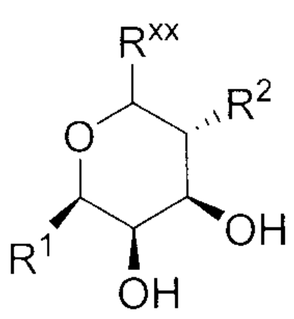
<220>
<223> Description of Artificial Sequence: Synthetic 6xHis tag

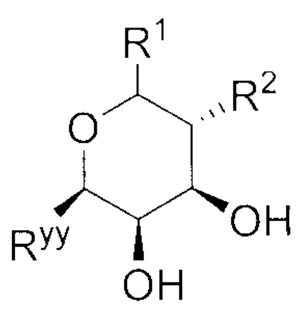
<400> 1068
His His His His His His
1 5

What is claimed is:

1. A compound of Formula (A-1), (A-2), or (A-3):

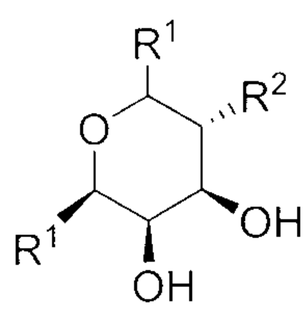


(A-1)



(A-2)

or



(A-3),

or a pharmaceutically acceptable salt thereof,

wherein:

R^{xx} is -H, -alkyl, -cycloalkyl, -alkenyl, alkynyl, -aryl, -heteroaryl, $-OR^5$, $-N(R^4)-R^5$, $-SR^5$,

wherein a $-CH_2-$ group of said R^{xx} may each be independently replaced with a heteroatom group selected from –O-, -S-, $-N(R^4)-$ and wherein a $-CH_3$ of said R^{xx} may be replaced with a heteroatom group selected from $-N(R^4)_2$, $-OR^4$, and $-S(R^4)$ wherein the heteroatom groups are separated by at least 2 carbon atoms, and wherein the alkyl, alkenyl, alkynyl, and cycloalkyl may each be substituted with one or more halo atoms;

R^{yy} is–CN,$-CH_2-CN$,-C≡CH, $-CH_2-N_3$, $-CH_2-NH_2$, $-CH2-N(R^4)-S(O)_2-R^5$, $-CH_2-CO_2H$,$-CO_2H$, $-CH_2-OH$, $-CH_2-SH$, $-CH=CH-R^5$, $-CH_2-R^5$, $-CH_2-S-R^5$, $-CH_2-N(R^4)-R^5$, $-CH_2-N(R^4)-C(O)-R^5$, $-CH_2-N(R^4)-C(O)-O-R^5$, $-CH_2-N(R^4)-C(O)-N(R^4)-R^5$, $-CH_2-O-R^5$, $-CH_2-O-C(O)-R^5$,

$-CH_2-O-C(O)-N(R^4)-R^5$, $-CH_2-O-C(O)-O-R^5$, $-CH_2-S(O)-R^5$, $-CH_2-S(O)_2-R^5$,

$-CH_2-S(O)_2-N(R^4)-R^5$, $-C(O)-NH_2$, $-C(O)-O-R^5$, $-C(O)-N(R^4)-R^5$, or aryl or heteroaryl, wherein the aryl or heteroaryl is optionally substituted with R^5;

each R^1 is independently –CN,$-CH_2-CN$,-C≡CH, $-CH_2-N_3$, $-CH_2-NH_2$, $-CH_2-N(R^4)-S(O)_2-R^5$, $-CH_2-CO_2H$, $-CO_2H$, $-CH_2-OH$, $-CH_2-SH$, $-CH=CH-R^5$, $-CH_2-R^5$, $-CH_2-S-R^5$, $-CH_2-N(R^4)-R^5$,

$-CH_2-N(R^4)-C(O)-R^5$, $-CH_2-N(R^4)-C(O)-O-R^5$, $-CH_2-N(R^4)-C(O)-N(R^4)-R^5$, $-CH_2-O-R^5$, $-CH_2-O-C(O)-R^5$, $-CH_2-O-C(O)-N(R^4)-R^5$, $-CH_2-O-C(O)-O-R^5$, $-CH_2-S(O)-R^5$, $-CH_2-S(O)_2-R^5$, $-CH_2-S(O)_2-N(R^4)-R^5$, $-C(O)-NH_2$, $-C(O)-O-R^5$, $-C(O)-N(R^4)-R^5$, or aryl or heteroaryl, wherein the aryl or heteroaryl is optionally substituted with R^5,

or R^1 is –Z-X-Y, -Z-Y, -X-Y, –Z-X^+Y^-, –X^+Y^-, –Z-X^-Y^+, –X^-Y^+, or –Y;

X is a linker;

X^+ is a positively charged linker;

X^- is a negatively charged linker;

Y is a ribonucleoprotein or endonuclease comprising a site-directed modifying polypeptide, or Y is a site-directed modifying polypeptide, or Y is Cas9 ribonucleoprotein, or Y is a Cas9 protein, or Y is a single guide RNA sequence (sgRNA) or Y is a dual guide RNA sequence comprising a CRISPR RNA (crRNA) and a trans-activating crRNA (tracrRNA);

Y^+ is a positively charged ribonucleoprotein or endonuclease comprising a site-directed modifying polypeptide, or Y^+ a positively charged site-directed modifying polypeptide, or Y^+ is a positively charged Cas9 protein;

Y^- is a negatively charged ribonucleoprotein or endonuclease comprising a site-directed modifying polypeptide, or Y^- is a negatively charged site-directed modifying polypeptide, or Y^- is a negatively charged Cas9 ribonucleoprotein, or Y^- is a negatively charged sgRNA, or Y^- is a negatively charged dual guide RNA sequence comprising a CRISPR RNA (crRNA) and a trans-activating crRNA (tracrRNA);

Z is absent or is -C≡C-, -CH=CH-, –CH_2-, -CH_2-O-, -C(O)-N(R^4)-, -CH_2-S-, -CH_2-S(O)-, -CH_2-$S(O)_2$-, -CH_2-$S(O)_2$-N(R^4)-, -C(O)-O-, -CH_2-N(R^4)-, -CH_2-N(R^4)-C(O)-, -CH_2-N(R^4)-$S(O)_2$-, -CH_2-N(R^4)-C(O)-O-, -CH_2-N(R^4)-C(O)-N(R^4)-, -CH_2-O-C(O)-, -CH_2-O-C(O)-N(R^4)-, -CH_2-O-C(O)-O-, or aryl or heteroaryl, wherein the aryl or heteroaryl is optionally substituted with R^5;

R^2 is-OH, -N_3, -N(R^3)$_2$, –N(R^3)-C(O)-R^3 , –N(R^3)-C(O)-N(R^3)$_2$, –N(R^3)-C(O)-OR^3, –N(R^3)-$S(O)_2$-R^3 , tetrazole, or triazole, wherein the tetrazole and triazole are optionally substituted with R^3;

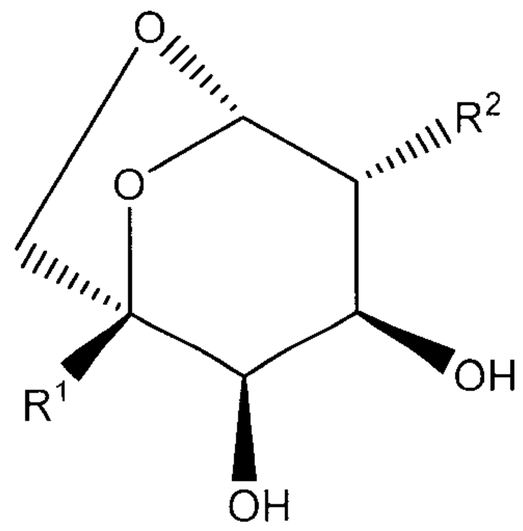
each R^3 is independently –H, -(C_1-C_5)alkyl, halo-substituted (C_1-C_5)alkyl, halo substituted (C_3-C_6)cycloalkyl, -(C_1-C_5)alkenyl, -(C_1-C_5)alkynyl, halo substituted -(C_1-C_5)alkenyl, halo substituted -(C_1-C_5)alkynyl, or (C_3-C_6)cycloalkyl, wherein a –CH_2- group of the alkyl or cycloalkyl may each be independently replaced with a heteroatom group selected from –O-, -S-, and -N(R^4)- and -CH_3 of the alkyl may each be independently replaced with a

heteroatom group selected from $-N(R^4)_2$, $-OR^4$, and $-S(R^4)$ wherein the heteroatom groups are separated by at least 2 carbon atoms;

each R^4 is independently –H, -(C_1-C_{20})alkyl, -(C_1-C_{20})alkenyl, -(C_1-C_{20})alkynyl, or (C_3-C_6)cycloalkyl wherein one to six $-CH_2-$ groups of the alkyl or cycloalkyl separated by at least two carbon atoms may each be independently replaced with a heteroatom independently selected from –O-, -S-, or $-N(R^4)-$, and $-CH_3$ of the alkyl may each be independently replaced with a heteroatom group selected from $-N(R^4)_2$, $-OR^4$, and $-S(R^4)$ wherein the heteroatom groups are separated by at least 2 carbon atoms; and wherein the alkyl, alkenyl, alkynyl, and cycloalkyl may be substituted with halo atoms;

each R^5 is independently –H, (C_3-C_{20})cycloalkyl, -(C_1-C_{60})alkenyl, -(C_1-C_{60})alkynyl, or (C_1-C_{60})alkyl wherein one to six $-CH_2-$ groups of the cycloalkyl or one to 20 $-CH_2-$ groups of the alkyl may each be independently replaced with heteroatoms independently selected from –O-, -S-, and $-N(R^4)-$ wherein the heteroatoms are separated by at least two carbon atoms, and $-CH_3$ of the alkyl may each be independently replaced with a heteroatom group selected from $-N(R^4)_2$, $-OR^4$, and $-S(R^4)$ wherein the heteroatom groups are separated by at least 2 carbon atoms; and wherein the alkyl, alkenyl, alkynyl, and cycloalkyl may be substituted with halo atoms.

2. A compound of Formula (B):



(B),

or a pharmaceutically acceptable salt thereof,

wherein:

R^1 is $-Z-X-Y$, -Z-Y, -X-Y, $-Z-X^+Y^-$, $-X^+Y^-$, $-Z-X^-Y^+$, $-X^-Y^+$, or –Y;

X is a linker;

X^+ is a positively charged linker;

X^- is a negatively charged linker;

Y is a ribonucleoprotein or endonuclease comprising a site-directed modifying polypeptide, or Y is a site-directed modifying polypeptide, or Y is Cas9 ribonucleoprotein, or Y is a Cas9 protein, or Y is a single guide RNA sequence (sgRNA) or Y is a dual guide RNA sequence comprising a CRISPR RNA (crRNA) and a trans-activating crRNA (tracrRNA);

Y^+ is a positively charged ribonucleoprotein or endonuclease comprising a site-directed modifying polypeptide, or Y^+ a positively charged site-directed modifying polypeptide, or Y^+ is a positively charged Cas9 protein;

Y^- is a negatively charged ribonucleoprotein or endonuclease comprising a site-directed modifying polypeptide, or Y^- is a negatively charged site-directed modifying polypeptide, or Y^- is a negatively charged Cas9 ribonucleoprotein, or Y^- is a negatively charged sgRNA, or Y^- is a negatively charged dual guide RNA sequence comprising a CRISPR RNA (crRNA) and a trans-activating crRNA (tracrRNA);

Z is absent or is -C≡C-, -CH=CH-, $-CH_2-$, $-CH_2-O-$, $-C(O)-N(R^4)-$, $-CH_2-S-$, $-CH_2-S(O)-$, $-CH_2-S(O)_2-$, $-CH_2-S(O)_2-N(R^4)-$, $-C(O)-O-$, $-CH_2-N(R^4)-$, $-CH_2-N(R^4)-C(O)-$, $-CH_2-N(R^4)-S(O)_2-$, $-CH_2-N(R^4)-C(O)-O-$, $-CH_2-N(R^4)-C(O)-N(R^4)-$, $-CH_2-O-C(O)-$, $-CH_2-O-C(O)-N(R^4)-$, $-CH_2-O-C(O)-O-$, or aryl or heteroaryl, wherein the aryl or heteroaryl is optionally substituted with R^5;

R^2 is -OH, $-N_3$, $-N(R^3)_2$, $-N(R^3)-C(O)-R^3$, $-N(R^3)-C(O)-N(R^3)_2$, $-N(R^3)-C(O)-OR^3$, $-N(R^3)-S(O)_2-R^3$, tetrazole, or triazole, wherein the tetrazole and triazole are optionally substituted with R^3;

each R^3 is independently –H, $-(C_1-C_5)$alkyl, halo-substituted (C_1-C_5)alkyl, halo substituted (C_3-C_6)cycloalkyl, $-(C_1-C_5)$alkenyl, $-(C_1-C_5)$alkynyl, halo substituted $-(C_1-C_5)$alkenyl, halo substituted $-(C_1-C_5)$alkynyl, or (C_3-C_6)cycloalkyl, wherein a $-CH_2-$ group of the alkyl or cycloalkyl may each be independently replaced with a heteroatom group selected from –

O-,

-S-, and $-N(R^4)-$ and $-CH_3$ of the alkyl may each be independently replaced with a

heteroatom group selected from $-N(R^4)_2$, $-OR^4$, and $-S(R^4)$ wherein the heteroatom groups are separated by at least 2 carbon atoms;

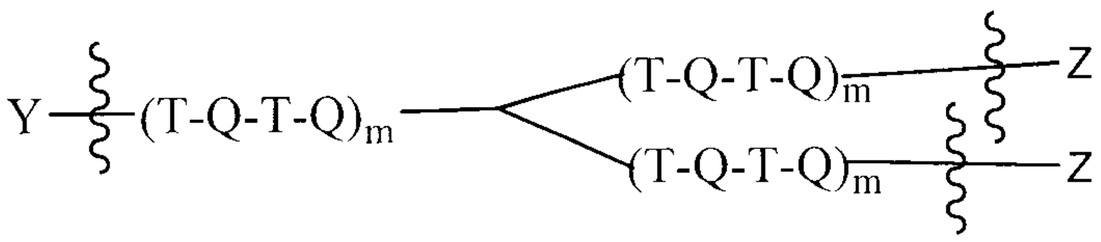
each R^4 is independently –H, -(C_1-C_{20})alkyl, -(C_1-C_{20})alkenyl, -(C_1-C_{20})alkynyl, or (C_3-C_6)cycloalkyl wherein one to six $-CH_2-$ groups of the alkyl or cycloalkyl separated by at least two carbon atoms may each be independently replaced with a heteroatom independently selected from –O-, -S-, or $-N(R^4)-$, and $-CH_3$ of the alkyl may each be independently replaced with a heteroatom group selected from $-N(R^4)_2$, $-OR^4$, and $-S(R^4)$ wherein the heteroatom groups are separated by at least 2 carbon atoms; and wherein the alkyl, alkenyl, alkynyl, and cycloalkyl may be substituted with halo atoms;

each R^5 is independently –H, (C_3-C_{20})cycloalkyl, -(C_1-C_{60})alkenyl, -(C_1-C_{60})alkynyl, or (C_1-C_{60})alkyl wherein one to six $-CH_2-$ groups of the cycloalkyl or one to 20 $-CH_2-$ groups of the alkyl may each be independently replaced with heteroatoms independently selected from –O-, -S-, and $-N(R^4)-$ wherein the heteroatoms are separated by at least two carbon atoms, and $-CH_3$ of the alkyl may each be independently replaced with a heteroatom group selected from $-N(R^4)_2$, $-OR^4$, and $-S(R^4)$ wherein the heteroatom groups are separated by at least 2 carbon atoms; and wherein the alkyl, alkenyl, alkynyl, and cycloalkyl may be substituted with halo atoms.

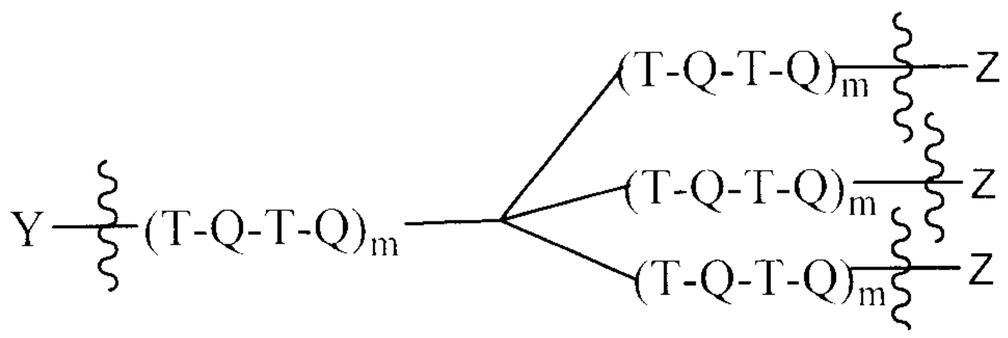
3. The compound according to claim 1 or 2, wherein R^2 is $-NH-C(O)-CH_3$.

4. The compound according to claim 1 or 2, where R^1 is –Z-X-Y.

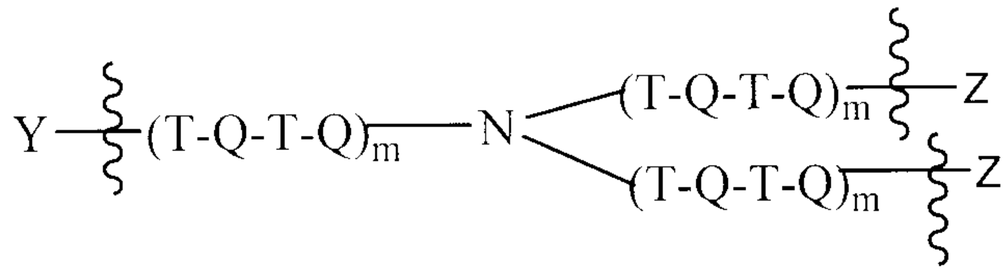
5. The compound according to claim 4, wherein R^1 is –Z-X-Y that is selected from the group consisting of L1 to L10:



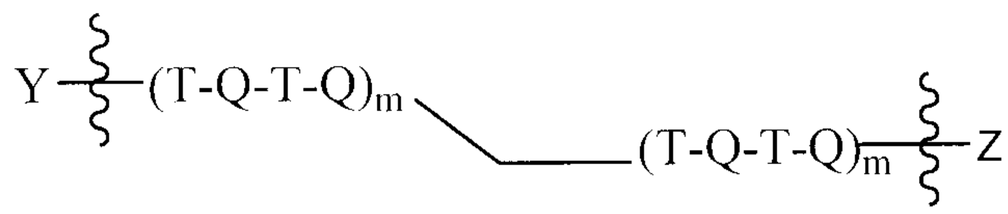
L1



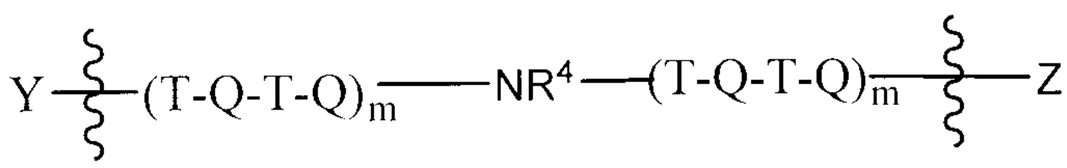
L2



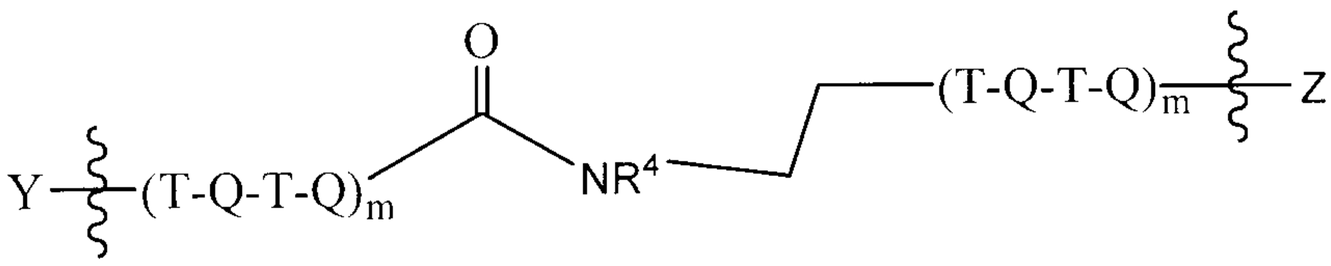
L3



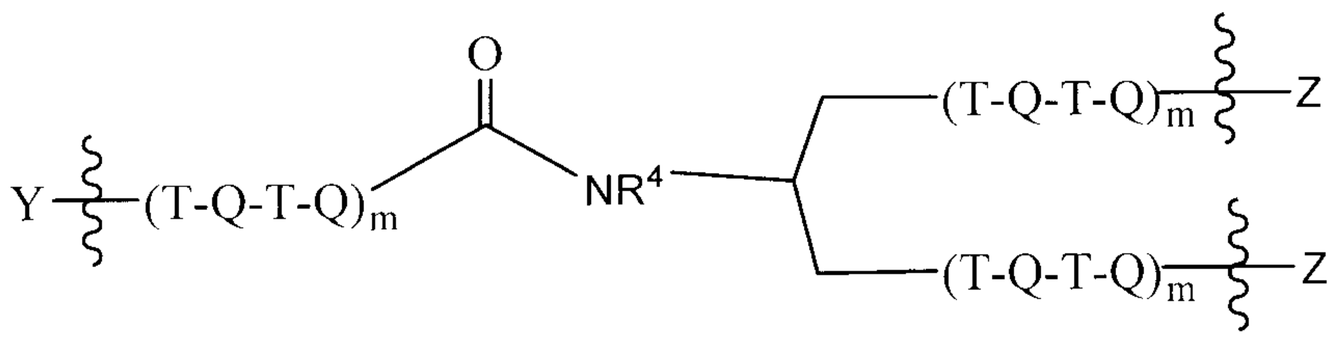
L4



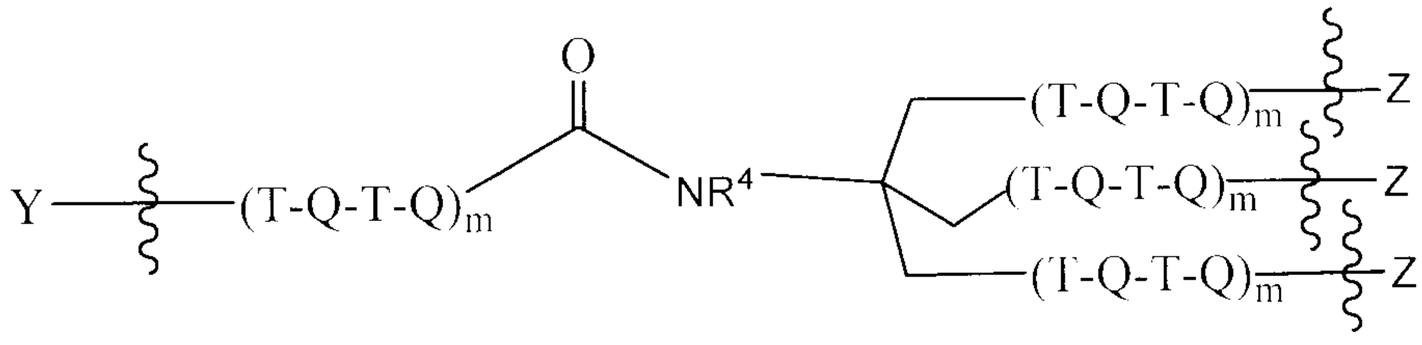
L5



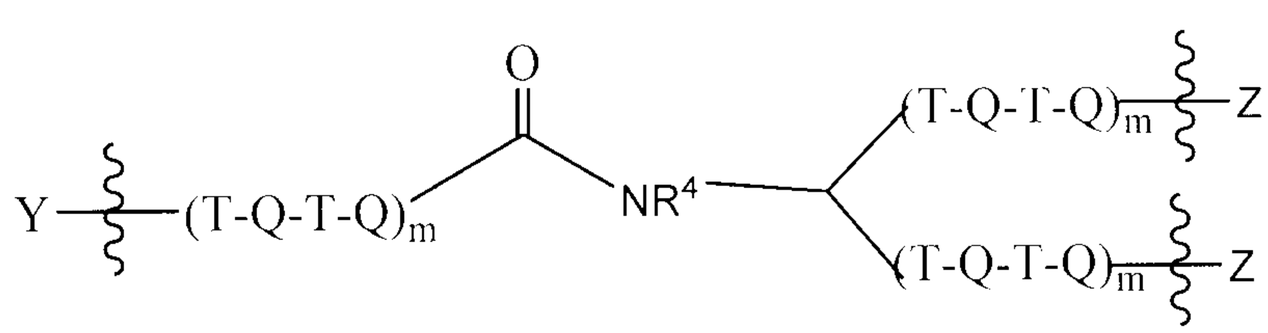
L6



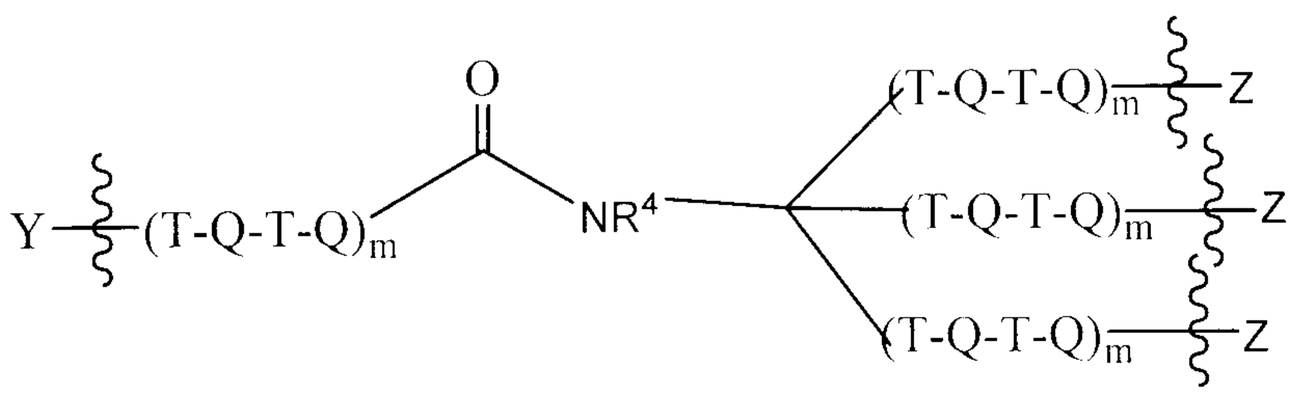
L7



L8



L9



L10,

wherein each T is independently absent or is (C_1-C_{10}) alkylene, (C_2-C_{10}) alkenylene, or (C_2-C_{10}) alkynylene, wherein one or more carbon groups of said T may each independently be replaced with a heteroatom group independently selected from –O-, -S-, and -N(R^4)- wherein the heteroatom groups are separated by at least 2 carbon atoms, and wherein alkylene, alkenylene, and alkynylene may each be independently substituted with one or more halo atoms;

each Q is independently absent or is C(O), C(O)-NR^4, NR^4-C(O),O-C(O)-NR^4, NR^4-C(O)-O, -CH_2-, a heteroaryl, or a heteroatom group selected from O, S, S-S, S(O), $S(O)_2$, and NR^4, wherein at least two carbon atoms separate the heteroatom groups O, S, S-S, S(O), $S(O)_2$ and NR^4 from any other heteroatom group;

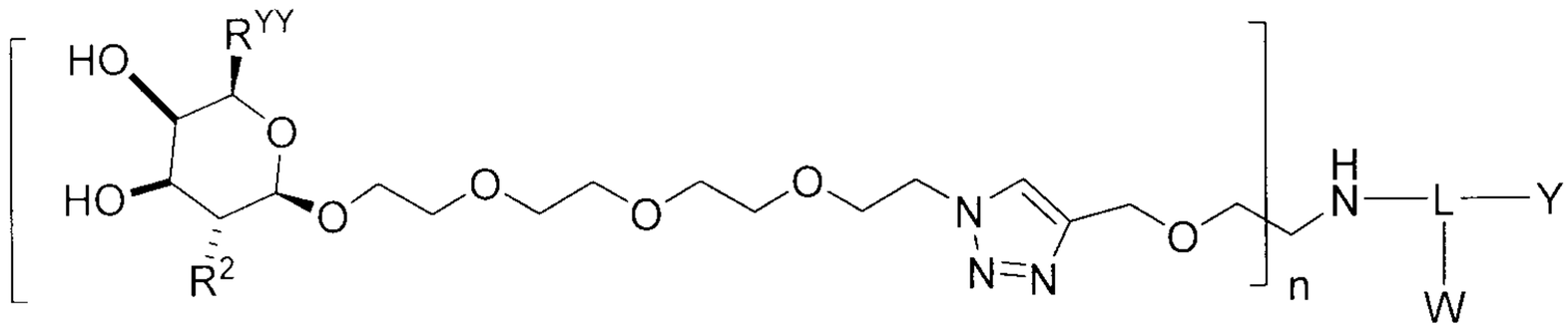
each R^4 is independently –H, -(C_1-C_{20})alkyl, or (C_3-C_6)cycloalkyl wherein one to six -CH_2- groups of the alkyl or cycloalkyl separated by at least two carbon atoms may each be independently replaced with –O-, -S-, or -N(R^4)-, and -CH_3 of the alkyl may be replaced

with a heteroatom group selected from –N(R^4)2, -OR^4, and –S(R^4) wherein the heteroatom groups are separated by at least 2 carbon atoms; and wherein the alkyl and cycloalkyl may be substituted with halo atoms; and

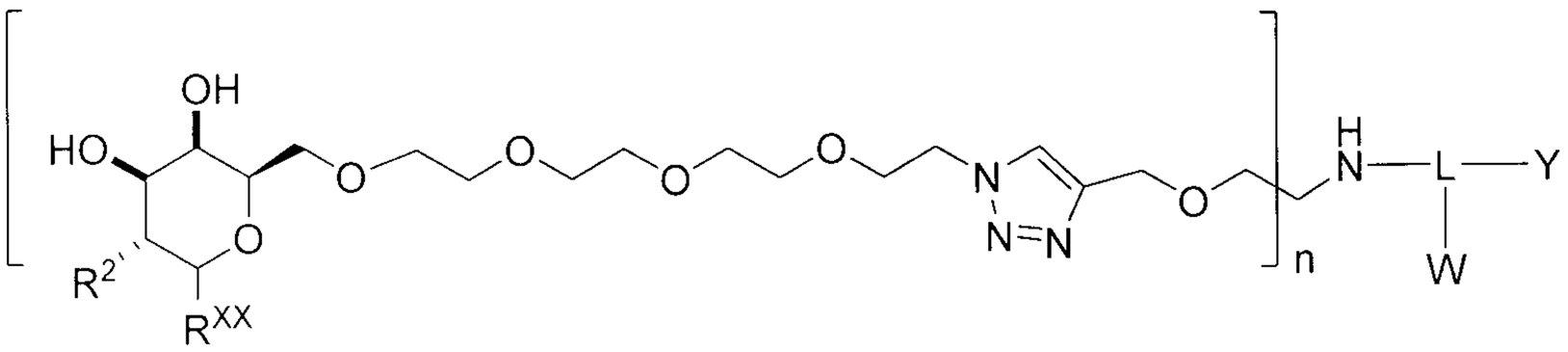
each m is independently 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10,11,12,13,14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40.

6. The compound according to claim 5, wherein said X comprises a disulfide bond.

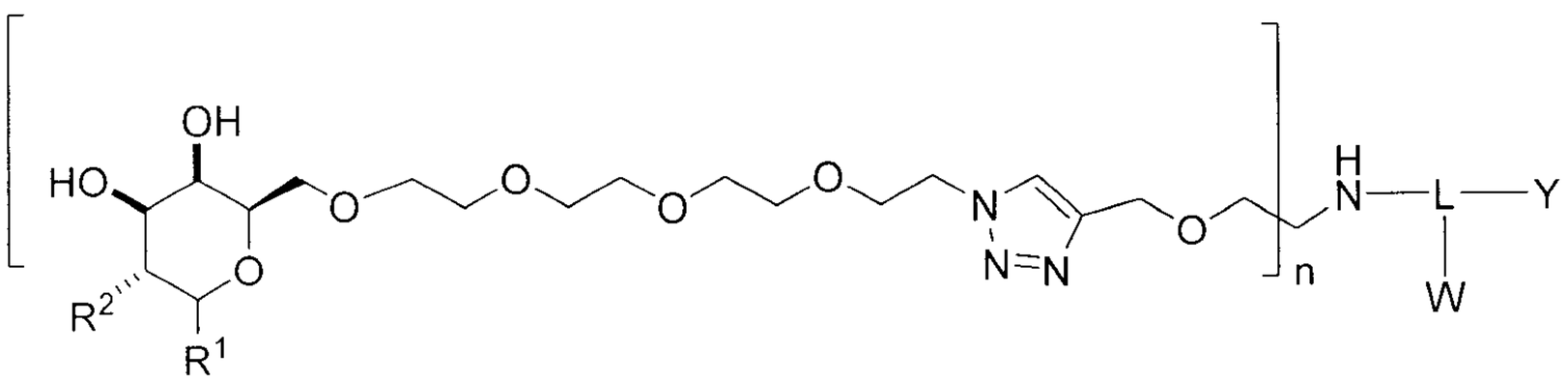
7. The compound according to claim 1, wherein said compound has a formula of Formula (C-1), (C-2), (C-3) or (C4):



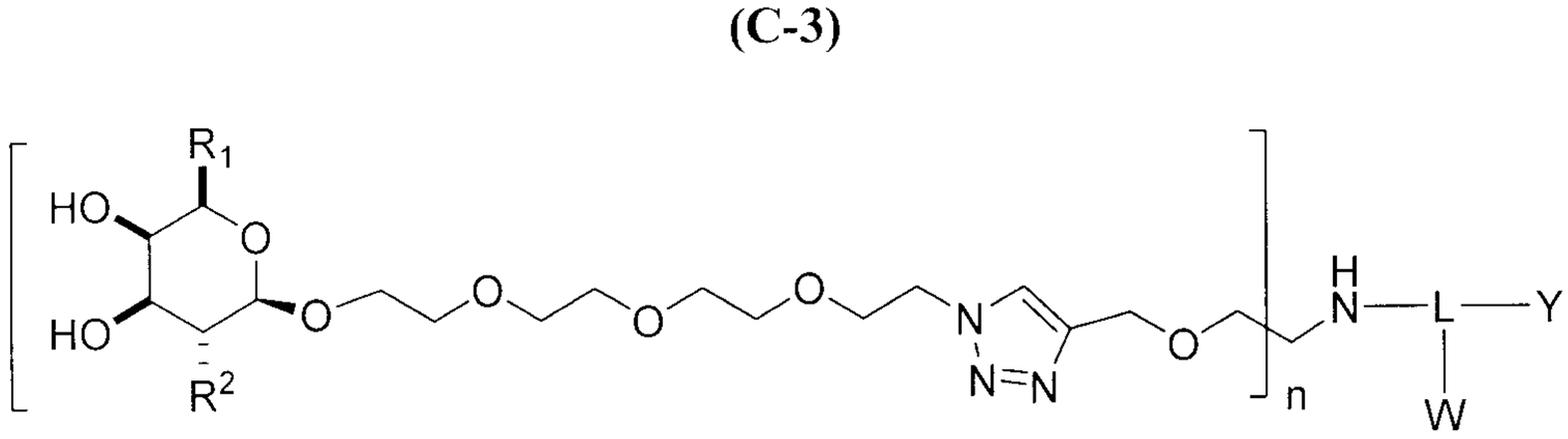
(C-1)



(C-2)



(C-3)



(C-4),

or a pharmaceutically acceptable salt thereof,

wherein:

n is 1, 2, or 3;

W is absent or a peptide;

L is $–(T\text{-}Q\text{-}T\text{-}Q)_m$-, wherein:

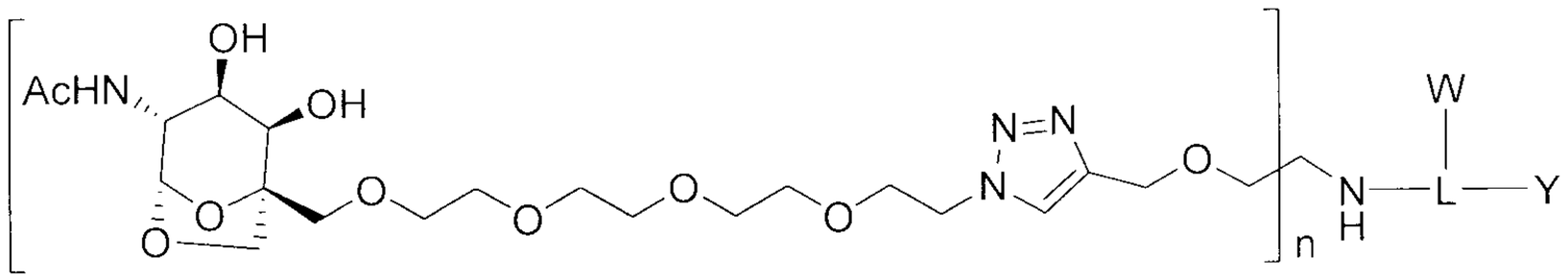
each T is independently absent or is $(C_1\text{-}C_{10})$ alkylene, $(C_2\text{-}C_{10})$ alkenylene, or $(C_2\text{-}C_{10})$ alkynylene, wherein one or more carbon groups of said T may each independently be replaced with a heteroatom group independently selected from –O-, -S-, and $-N(R^4)$- wherein the heteroatom groups are separated by at least 2 carbon atoms, and wherein alkylene, alkenylene, and alkynylene may each be independently substituted with one or more halo atoms;

each Q is independently absent or is C(O), $C(O)\text{-}NR^4$, $NR^4\text{-}C(O)$,$O\text{-}C(O)\text{-}NR^4$, $NR^4\text{-}C(O)\text{-}O$, $-CH_2$-, a heteroaryl, or a heteroatom group selected from O, S, S-S, S(O), $S(O)_2$, and NR^4, wherein at least two carbon atoms separate the heteroatom groups O, S, S-S, S(O), $S(O)_2$ and NR^4 from any other heteroatom group;

each R^4 is independently –H, $-(C_1\text{-}C_{20})$alkyl, or $(C_3\text{-}C_6)$cycloalkyl wherein one to six $-CH_2$- groups of the alkyl or cycloalkyl separated by at least two carbon atoms may be replaced with –O-, -S-, or $-N(R^4)$-, and $-CH_3$ of the alkyl may each be independently replaced with a heteroatom group selected from $–N(R^4)_2$, $-OR^4$, and $–S(R^4)$ wherein the heteroatom groups are separated by at least 2 carbon atoms; and wherein the alkyl and cycloalkyl may be substituted with halo atoms; and

each m is independently 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10,11,12,13,14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40.

8. The compound according to claim 2, wherein said compound has a formula of Formulae (E):



(E),

or a pharmaceutically acceptable salt thereof,

wherein:

n is 1, 2 or 3;

W is absent or is a peptide;

L is $-(T\text{-}Q\text{-}T\text{-}Q)_m$-, wherein:

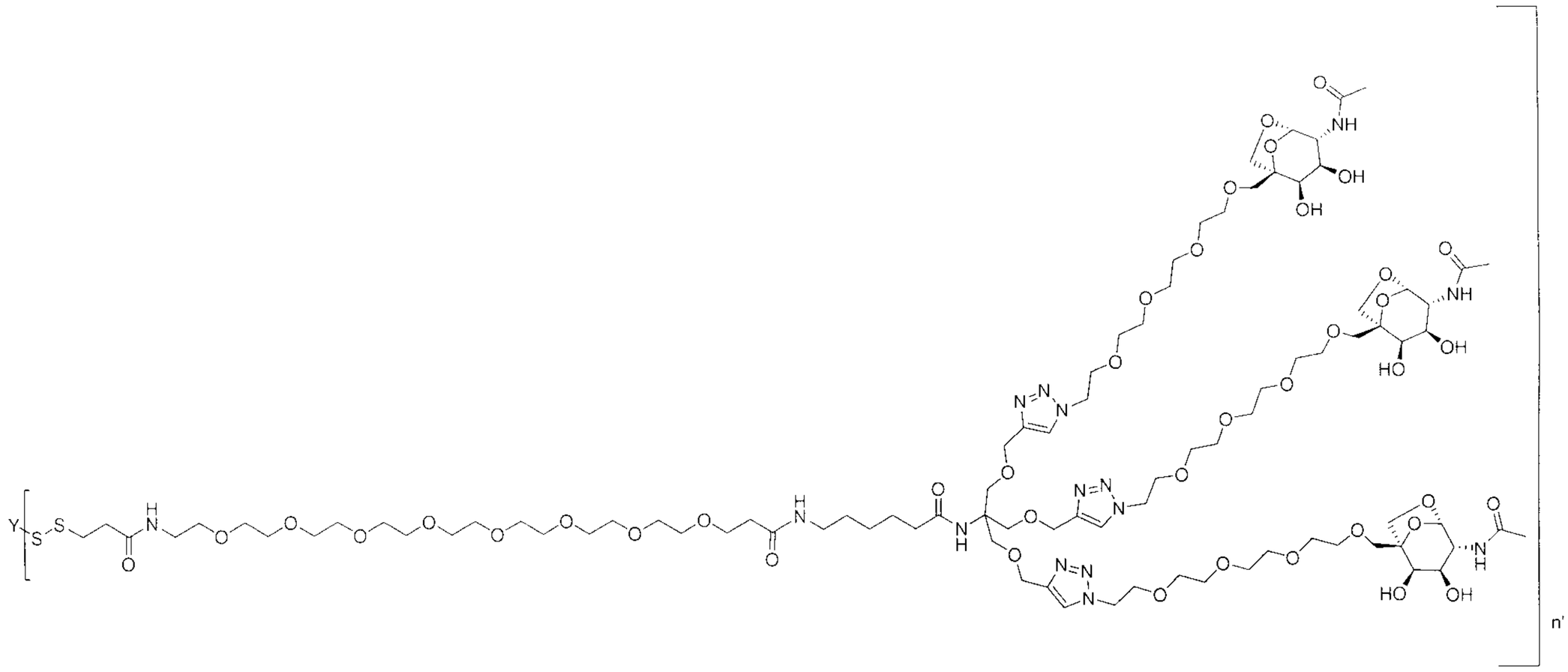
each T is independently absent or is (C_1-C_{10}) alkylene, (C_2-C_{10}) alkenylene, or (C_2-C_{10}) alkynylene, wherein one or more carbon groups of said T may each independently be replaced with a heteroatom group independently selected from –O-, -S-, and -N(R^4)- wherein the heteroatom groups are separated by at least 2 carbon atoms;

each Q is independently absent or is C(O), C(O)-NR^4, NR^4-C(O),O-C(O)-NR^4, NR^4-C(O)-O, -CH_2-, a heteroaryl, or a heteroatom group selected from O, S, S-S, S(O), $S(O)_2$, and NR^4, wherein at least two carbon atoms separate the heteroatom groups O, S, S-S, S(O), $S(O)_2$ and NR^4 from any other heteroatom group;

each R^4 is independently –H, -(C_1-C_{20})alkyl, or (C_3-C_6)cycloalkyl wherein one to six -CH_2- groups of the alkyl or cycloalkyl separated by at least two carbon atoms may each be independently replaced with –O-, -S-, or -N(R^4)-, and -CH_3 of the alkyl may be replaced with a heteroatom group selected from –N(R^4)$_2$, -OR^4, and –S(R^4) wherein the heteroatom groups are separated by at least 2 carbon atoms; and wherein the alkyl and cycloalkyl may be substituted with halo atoms; and

each m is independently 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10,11,12,13,14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40.

9. The compound according to claim 8, wherein said compound has the formula



.

wherein n' is 1 or 2

or a pharmaceutically acceptable salt thereof.

10. The compound according to claim 1 or 2, wherein Y is a Cas9 ribonucleoprotein comprising:

(1) a first element comprising a recognition element comprising either a dual guide RNA sequence comprising a CRISPR RNA (crRNA) and a trans-activating crRNA (tracrRNA), or a single guide RNA sequence (sgRNA), wherein when expressed, the guide sequence directs sequence-specific binding of the Cas9 ribonucleoprotein to a target sequence, and the first element optionally comprises one or more endosomal escape agents, and

(2) a second element comprising a Cas9 protein and optionally one or more nuclear localization sequences (NLSs) and optionally one or more fluorescent proteins, and one or more endosomal escape agents;

wherein said first element is associated with said second element.

11. The compound according to claim 10, wherein Y comprises one or two NLSs and each of said NLSs comprises the amino acid sequence PKKKRKV (SEQ ID NO: 830).

12. The compound according to claim 1 or 2, wherein said Y comprises a Cas9 protein that is at least about 75 percent, at least about 80 percent, at least about 85 percent, at least about 90 percent, at least about 95 percent, at least about 96 percent, at least about 97 percent, at least about 98 percent, at least about 99 percent or 100 percent amino acid sequence

identity to a Cas9 protein derived from *S. aureus, S. pneumoniae, S. pyogenes, S. thermophilus, N. meningitidis* or *A. ebreus.*

13. The compound according to claim 1 or 2, wherein said Y comprises a Cas9 protein that is at least about 75 percent, at least about 80 percent, at least about 85 percent, at least about 90 percent, at least about 95 percent, at least about 96 percent, at least about 97 percent, at least about 98 percent, at least about 99 percent or 100 percent amino acid sequence identity to a sequence selected from: *S. pyogenes* Cas9 (wild type) (SEQ ID NO:848), *S. pyogenes* Cas9 - mutation M1C (SEQ ID NO:849), *S. pyogenes* Cas9 - mutation M1C & C80S (SEQ ID NO:850), *S. pyogenes* Cas9 nickase - mutation D10A (SEQ ID NO:851), *S. pyogenes* Cas9 nickase - mutation H840A (SEQ ID NO:852), *S. pyogenes* Cas9 nickase – mutations E923P & T924P (SEQ ID NO:853), *Acidovorax ebreus* Cas9 (SEQ ID NO:854), Acid mine drainage bacteria Ga0052161_JGI Cas9 (SEQ ID NO:855), *S. pyogenes* Cas9 null - mutation D10A& H840A (SEQ ID NO:1027), and Uranium mine bacteria FW106_JGI Cas9 (SEQ ID NO:856).

14. The compound according to claim 1 or 2, wherein said compound further comprises an endosomal escape agent.

15. The compound according to claim 14, wherein said endosomal escape agent is peptide ppTG21: GLFHALLHLLHSLWHLLLHA (SEQ ID NO: 1012).

16. A composition comprising a compound according to any one of claims 1 to 15 and an endosomal escape agent, wherein said compound and the endosomal escape agent are co-incubated to form the composition.

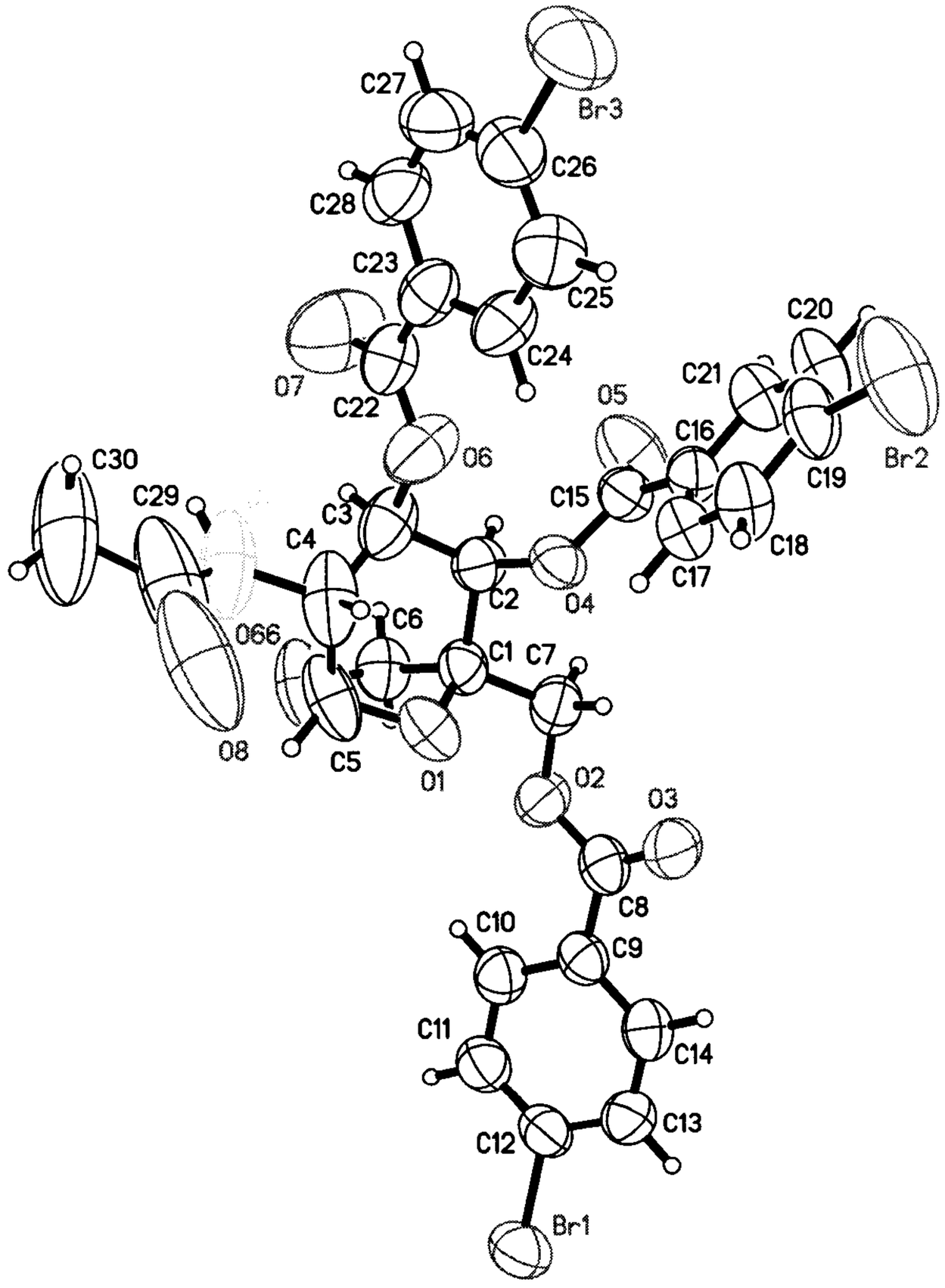
17. A pharmaceutical composition comprising a compound of any one of claims 1 to 15 and a pharmaceutically acceptable carrier, excipient or diluent.

18. A composition comprising a ribonucleoprotein and an endosomal escape agent.

19. The composition of claim 18, wherein said ribonucleoprotein is a Cas9 ribonucleoprotein or a Cpf1 ribonucleoprotein.

20. A pharmaceutical composition comprising a composition according to claim 18 and a pharmaceutically acceptable carrier, excipient or diluent.

FIG. 1


C27
Br3
C26
C28
C23
C25
C24
O7
C22
O6
C30
C29
C3
C4
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O4
C15
O5
C16
C21
C20
C19
Br2
C18
C17
O66
C6
C1
C7
O8
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O1
O2
O3
C8
C10
C9
C11
C14
C12
C13
Br1

FIG. 2

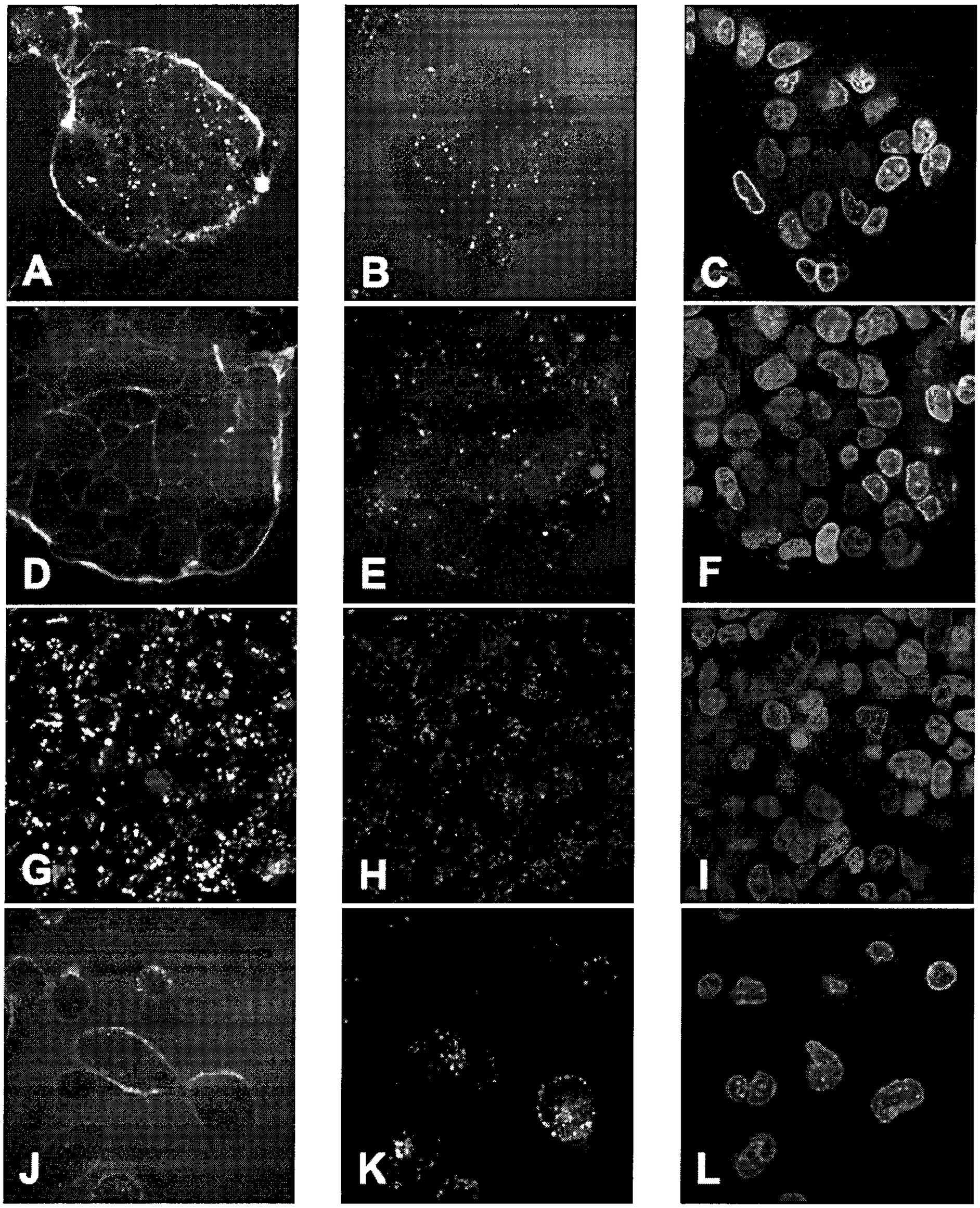
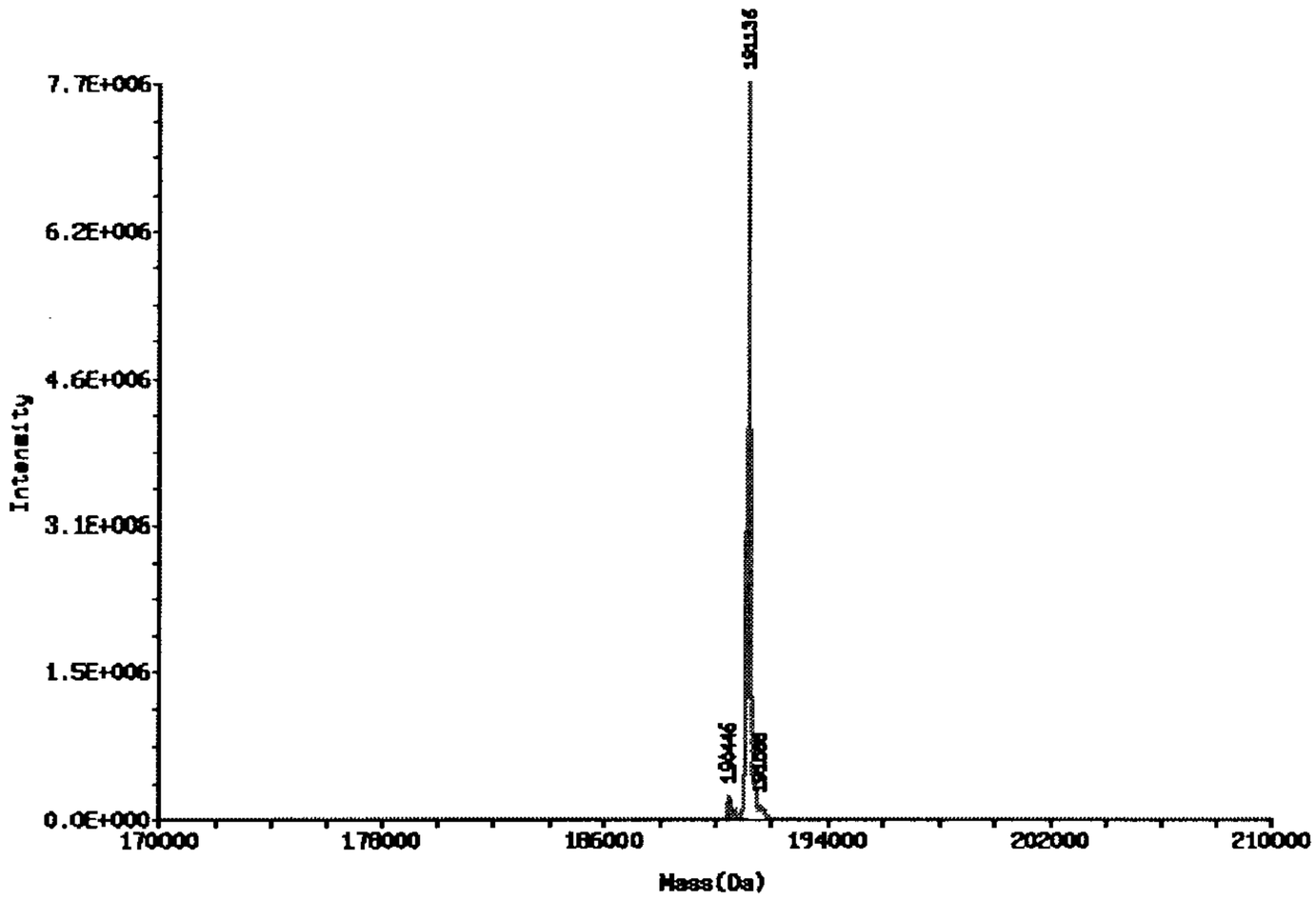
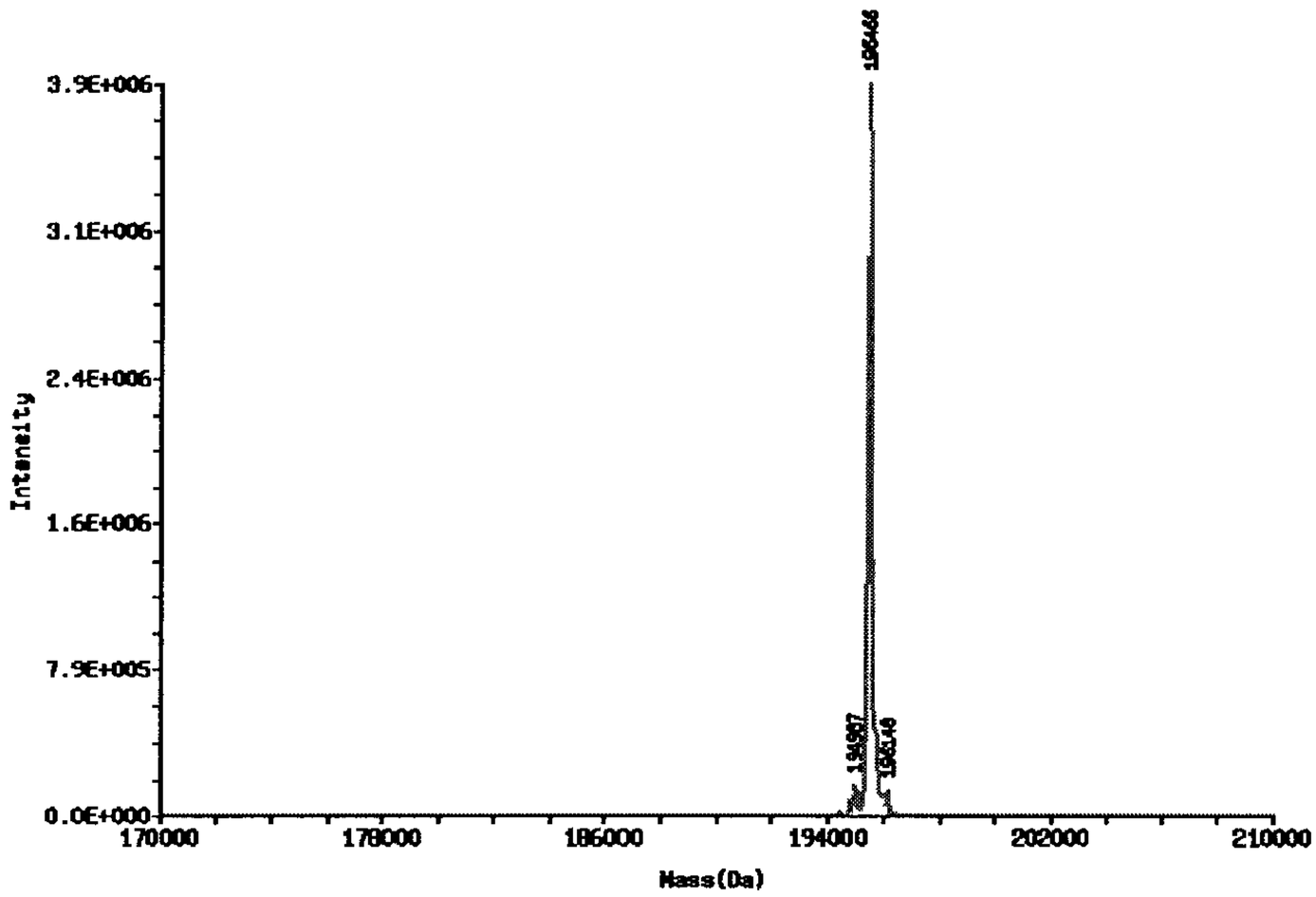


FIG. 3


7.7E+006
6.2E+006
4.6E+006
3.1E+006
1.5E+006
0.0E+000
Intensity
170000
178000
186000
194000
202000
210000
Mass(Da)
194136
194446
195088

(A)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3.1E+006
2.4E+006
1.6E+006
7.9E+005
0.0E+000
Intensity
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178000
186000
194000
202000
210000
Mass(Da)
194446
194987
195548

(B)

FIG. 4

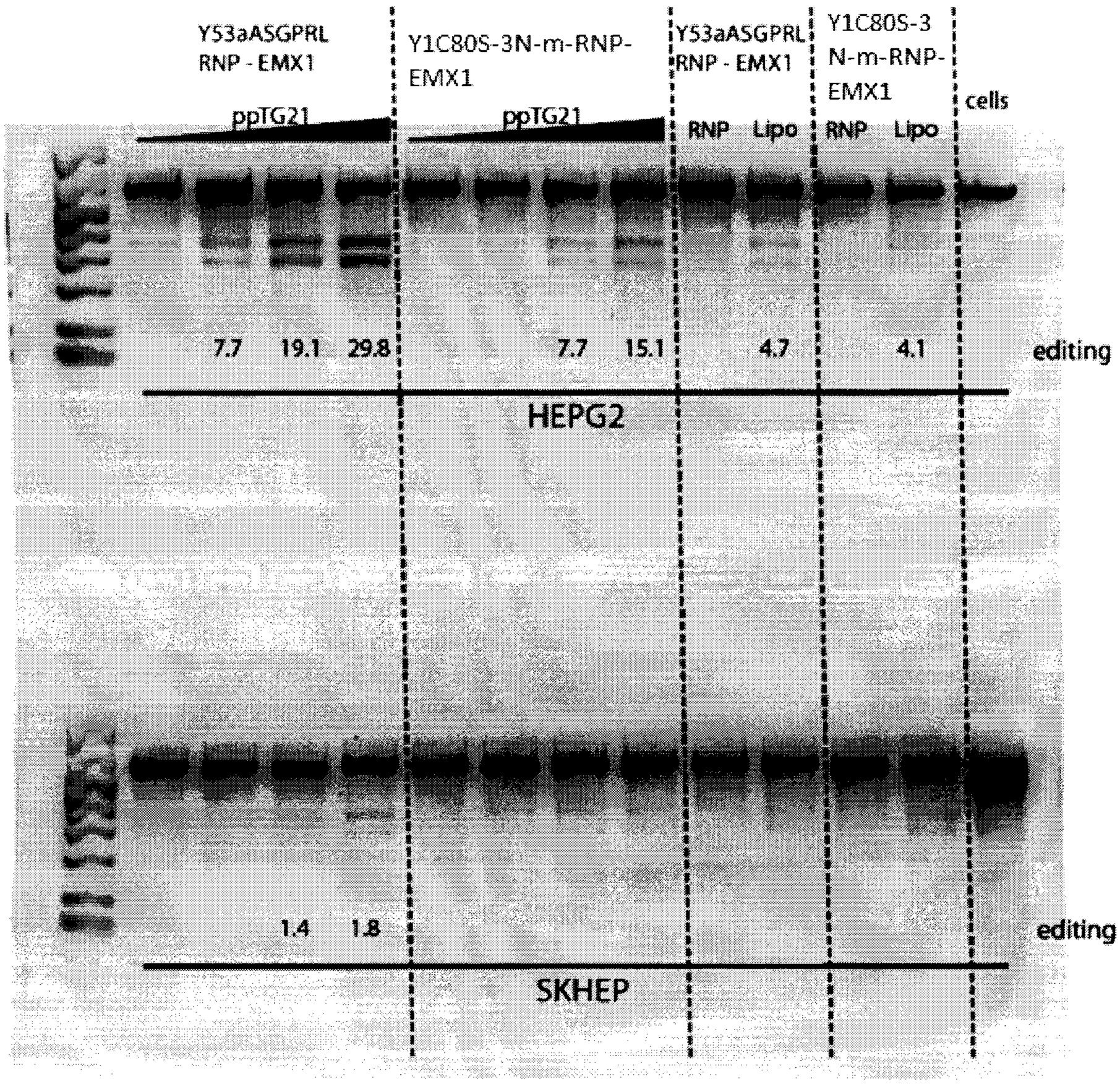

Y53aASGPRL RNP - EMX1
Y1C80S-3N-m-RNP-EMX1
Y53aASGPRL RNP - EMX1
Y1C80S-3 N-m-RNP-EMX1
cells
ppTG21
ppTG21
RNP
Lipo
RNP
Lipo
7.7
19.1
29.8
7.7
15.1
4.7
4.1
editing
HEPG2
1.4
1.8
editing
SKHEP

FIG. 5

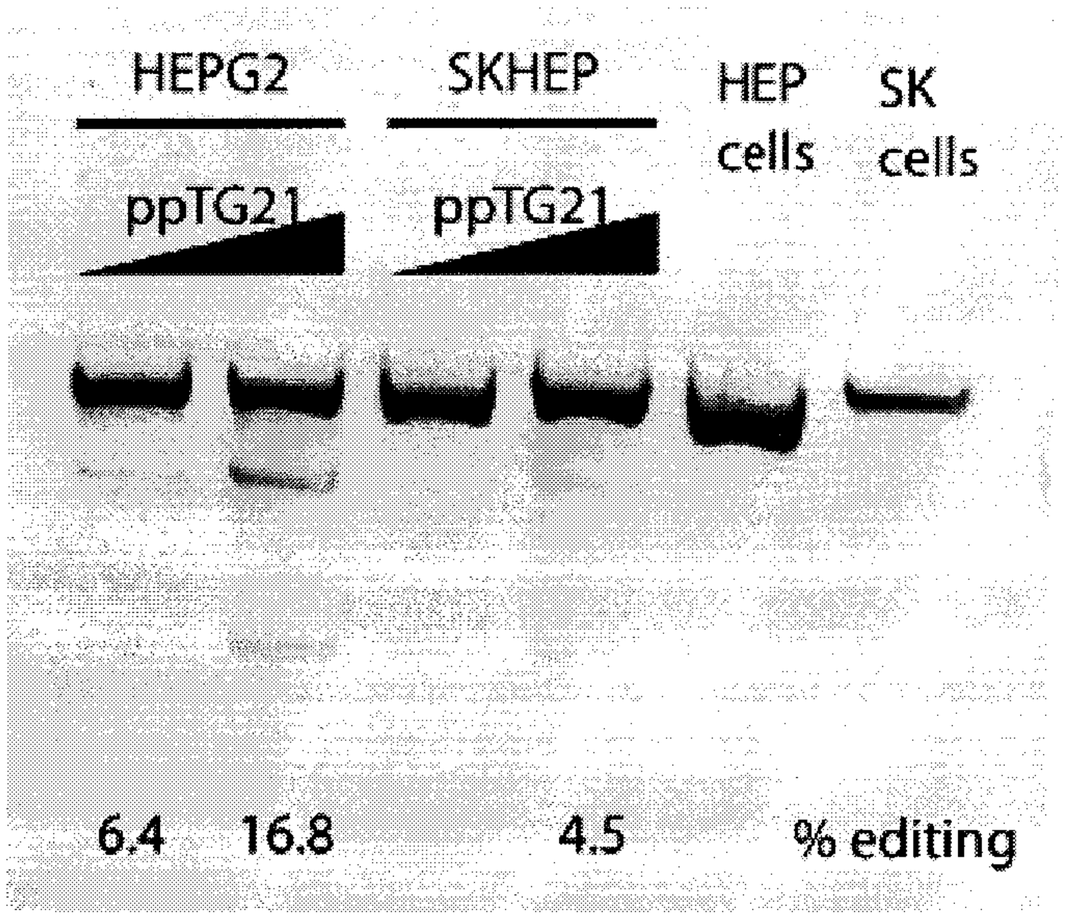

HEPG2
SKHEP
HEP cells
SK cells
ppTG21
ppTG21
6.4
16.8
4.5
% editing

FIG. 6

S. pyogenes Cas9 (wild type) (amino acid sequence) (SEQ ID NO:848):

MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEA
TRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIV
DEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHXLIEGDLNPDNSDVDKL
FIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLG
LTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRV
NTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQ
EEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPF
LKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK
TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILE
DIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKT
ILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQT
VKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPV
ENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSD
KNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQL
VETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYH
HAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNI
MNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTG
GFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELL
GITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELA
LPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK
VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSI
TGLYETRIDLSQLGGD

S. pyogenes Cas9 3NLS mCherry (amino acid sequence) (SEQ ID NO:1024):

MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEA
TRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIV
DEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHXLIEGDLNPDNSDVDKL
FIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLG
LTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRV
NTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQ
EEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPF
LKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK
TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILE
DIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKT
ILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQT
VKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPV
ENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSD
KNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQL
VETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYH
HAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNI
MNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTG
GFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELL

GITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELA
LPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK
VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSI
TGLYETRIDLSQLGGDAYPYDVPDYASLGSGSPKKKRKVEDPKKKRKVDGIGSGSNGSSGS
VSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFA
WDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGE
FIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAE
VKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYKGSPKK
KRKVE

S. pyogenes Cas9 - mutation M1C (amino acid sequence) (SEQ ID NO:849):

CDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEAT
RLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVD
EVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFI
QLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLT
PNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNT
EITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF
YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKD
NREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTN
FDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRK
VTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVL
TLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDF
LKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV
DELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHD
AYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFK
TEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESI
LPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIME
RSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKY
VNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAY
NKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYE
TRIDLSQLGGD

S. pyogenes Cas9 - mutation C80S (amino acid sequence) (SEQ ID NO:1025):

MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEA
TRLKRTARRRYTRRKNRISYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVD
EVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFI
QLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLT
PNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNT
EITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF
YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKD
NREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTN
FDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRK
VTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVL
TLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDF

LKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV
DELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHD
AYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFK
TEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESI
LPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIME
RSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKY
VNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAY
NKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYE
TRIDLSQLGGD

S. pyogenes Cas9 - mutation C80S 3NLS mCherry (amino acid sequence) (SEQ ID NO:1026):

MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEA
TRLKRTARRRYTRRKNRISYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVD
EVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFI
QLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLT
PNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNT
EITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF
YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKD
NREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTN
FDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRK
VTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVL
TLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDF
LKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV
DELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHD
AYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFK
TEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESI
LPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIME
RSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKY
VNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAY
NKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYE
TRIDLSQLGGDAYPYDVPDYASLGSGSPKKKRKVEDPKKKRKVDGIGSGSNGSSGSVSKGE
EDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILS
PQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKV
KLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTY
KAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYKGSPKKKRKVE

S. pyogenes Cas9 - mutation M1C & C80S (amino acid sequence) (SEQ ID NO:850):

CDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEAT
RLKRTARRRYTRRKNRISYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDE
VAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQ
LVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTP

NFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEI
TKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFY
KFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDN
REKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNF
DKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRK
VTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVL
TLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDF
LKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV
DELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHD
AYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFK
TEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESI
LPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIME
RSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKY
VNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAY
NKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYE
TRIDLSQLGGD

S. pyogenes Cas9 - mutation M1C & C80S 2NLS (amino acid sequence) (SEQ ID NO:1013):

CDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEAT
RLKRTARRRYTRRKNRISYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDE
VAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQ
LVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTP
NFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEI
TKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFY
KFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDN
REKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNF
DKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRK
VTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVL
TLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDF
LKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV
DELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHD
AYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFK
TEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESI
LPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIME
RSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKY
VNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAY
NKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYE
TRIDLSQLGGDAYPYDVPDYASLGSGSPKKKRKVEDPKKKRKVD

S. pyogenes Cas9 - mutation M1C & C80S 2NLS (nucleotide sequence) (SEQ ID NO:1014):
TGCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCG
TGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGA

CCGGCACAGCATCAAGAAGAACCTGATCGGCGCCCTGCTGTTCGACAGCGGAGAAACA
GCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAAC
CGGATCAGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCT
TCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCA
CCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCT
ACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTA
TCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGA
ACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCA
GCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCT
GCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGA
AGAAGAATGGCCTGTTCGGCAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTC
AAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACG
ACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTG
GCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCG
AGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCA
GGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAG
ATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATCGATGGCGGAGCCAGCC
AGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGA
ACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAAC
GGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGG
AAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTT
CCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATG
ACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAG
GGCGCCAGCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCA
ACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTACAACGA
GCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGC
GAGCAGAAAAAAGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGA
AGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTC
CGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTA
TCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGT
GCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTAT
GCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCT
GGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGA
CAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATC
CACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGG
GCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGG
CATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAG
CCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAG
AAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGC
CAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACC
TGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCG
GCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCA
TCGATAACAAAGTGCTGACTCGGAGCGACAAGAACCGGGGCAAGAGCGACAACGTGC
CCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGCCAGCTGCTGAATGCCAA
GCTGATTACCCAGAGGAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGC
GAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAA
AGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAACGACAA
ACTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGG
AAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACG

CCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAG
CGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGC
GAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACT
TTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGA
GACAAACGGCGAAACAGGCGAGATCGTGTGGGATAAGGGCCGGGACTTTGCCACCGTG
CGGAAAGTGCTGTCTATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAG
GCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGACAAGCTGATCGCCAG
AAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTAT
TCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGA
AAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGA
CTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCT
AAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCG
AACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTG
GCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGT
TTGTGGAACAGCACAAACACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTC
CAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAGGTGCTGAGCGCCTACAACAAG
CACAGAGACAAGCCTATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGA
CCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGG
TACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCC
TGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGACGCCTATCCCTATGACGTG
CCCGATTATGCCAGCCTGGGCAGCGGCTCCCCCAAGAAAAAACGCAAGGTGGAAGATC
CTAAGAAAAAGCGGAAAGTGGAC

S. pyogenes Cas9 - mutation M1C & C80S 3NLS and mCherry (amino acid sequence) (SEQ ID NO:1015):

CDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEAT
RLKRTARRRYTRRKNRISYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDE
VAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQ
LVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTP
NFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEI
TKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFY
KFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDN
REKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNF
DKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRK
VTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVL
TLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDF
LKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV
DELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQ
LQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRG
KSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHD
AYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFK
TEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESI
LPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIME
RSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKY
VNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAY
NKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYE
TRIDLSQLGGDAYPYDVPDYASLGSGSPKKKRKVEDPKKKRKVDGIGSGSNGSSGSVSKGE

EDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILS
PQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKV
KLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTY
KAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYKGSPKKKRKVE

S. pyogenes Cas9 - mutation M1C & C80S 3NLS mCherry (nucleotide sequence) (SEQ ID NO:1016):

TGCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCG
TGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGA
CCGGCACAGCATCAAGAAGAACCTGATCGGCGCCCTGCTGTTCGACAGCGGAGAAACA
GCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAAC
CGGATCAGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCT
TCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCA
CCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCT
ACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTA
TCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGA
ACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCA
GCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCT
GCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGA
AGAAGAATGGCCTGTTCGGCAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTC
AAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACG
ACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTG
GCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCG
AGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCA
GGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAG
ATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATCGATGGCGGAGCCAGCC
AGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGA
ACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAAC
GGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGG
AAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTT
CCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATG
ACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAG
GGCGCCAGCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCA
ACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTACAACGA
GCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGC
GAGCAGAAAAAAGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGA
AGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTC
CGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTA
TCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGT
GCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTAT
GCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCT
GGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGA
CAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATC
CACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGG
GCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGG
CATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAG
CCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAG
AAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGC

CAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACC
TGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCG
GCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCA
TCGATAACAAAGTGCTGACTCGGAGCGACAAGAACCGGGGCAAGAGCGACAACGTGC
CCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGCCAGCTGCTGAATGCCAA
GCTGATTACCCAGAGGAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGC
GAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAA
AGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAACGACAA
ACTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGG
AAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACG
CCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAG
CGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGC
GAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACT
TTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGA
GACAAACGGCGAAACAGGCGAGATCGTGTGGGATAAGGGCCGGGACTTTGCCACCGTG
CGGAAAGTGCTGTCTATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAG
GCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGACAAGCTGATCGCCAG
AAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTAT
TCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGA
AAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGA
CTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCT
AAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCG
AACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTG
GCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGT
TTGTGGAACAGCACAAACACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTC
CAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAGGTGCTGAGCGCCTACAACAAG
CACAGAGACAAGCCTATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGA
CCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGG
TACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCC
TGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGACGCCTATCCCTATGACGTG
CCCGATTATGCCAGCCTGGGCAGCGGCTCCCCCAAGAAAAAACGCAAGGTGGAAGATC
CTAAGAAAAAGCGGAAAGTGGACGGCATTGGTAGTGGGAGCAACGGCAGCAGCGGAT
CCGTGAGCAAGGGCGAGGAGGATAACATGGCCATCATCAAGGAGTTCATGCGCTTCAA
GGTGCACATGGAGGGCTCCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGA
GGGCCGCCCCTACGAGGGCACCCAGACCGCCAAGCTGAAGGTGACCAAGGGTGGCCCC
CTGCCCTTCGCCTGGGACATCCTGTCCCCTCAGTTCATGTACGGCTCCAAGGCCTACGT
GAAGCACCCCGCCGACATCCCCGACTACTTGAAGCTGTCCTTCCCCGAGGGCTTCAAGT
GGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACCCAGGACTCCTC
CCTCCAGGACGGCGAGTTCATCTACAAGGTGAAGCTGCGCGGCACCAACTTCCCCTCCG
ACGGCCCCGTAATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCTCCGAGCGGATGTA
CCCCGAGGACGGCGCCCTGAAGGGCGAGATCAAGCAGAGGCTGAAGCTGAAGGACGG
CGGCCACTACGACGCTGAGGTCAAGACCACCTACAAGGCCAAGAAGCCCGTGCAGCTG
CCCGGCGCCTACAACGTCAACATCAAGTTGGACATCACCTCCCACAACGAGGACTACA
CCATCGTGGAACAGTACGAACGCGCCGAGGGCCGCCACTCCACCGGCGGCATGGACGA
GCTGTACAAGGGGTCACCTAAGAAAAAACGAAAAGTTGAG

S. pyogenes Cas9 nickase - mutation D10A (amino acid sequence) (SEQ ID NO:851):

MDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEA
TRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIV
DEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKL
FIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLG
LTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRV
NTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQ
EEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPF
LKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK
TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILE
DIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKT
ILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQT
VKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPV
ENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSD
KNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQL
VETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYH
HAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNI
MNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTG
GFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELL
GITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELA
LPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK
VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSI
TGLYETRIDLSQLGGD

S. pyogenes Cas9 nickase - mutation H840A (amino acid sequence) (SEQ ID NO:852):

MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEA
TRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIV
DEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKL
FIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLG
LTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRV
NTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQ
EEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPF
LKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK
TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILE
DIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKT
ILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQT
VKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPV
ENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSD
KNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQL
VETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYH
HAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNI
MNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTG
GFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELL
GITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELA
LPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK
VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSI
TGLYETRIDLSQLGGD

S. pyogenes Cas9 nickase – mutations E923P & T924P (amino acid sequence) (SEQ ID NO:853):

MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEA
TRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIV
DEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKL
FIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLG
LTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRV
NTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQ
EEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPF
LKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK
TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILE
DIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKT
ILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQT
VKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPV
ENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSD
KNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQL
VPPRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHH
AHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIM
NFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGF
SKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGI
TIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELAL
PSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKV
LSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSIT
GLYETRIDLSQLGGD

Acidovorax ebreus Cas9 (amino acid sequence) (SEQ ID NO:854):

MAQHVFGLDIGIASVGWAILGEQRIIDLGVRCFDKAETAKEGDPLNLTRRQARLLRRRLYR
RAWRLTQLSRLLKRKGLIADAKLFAKAPSYGDSAWELRRQGLDRLLTPLEWARVIYHQCK
HRGFHWTSKAEEAKADSDAEGGRVKQGLAHTKALMQAKNYRSAAEMVLAEFPDAQRNK
RGQYDKALSRVLLGEELALLFATQRRLGNPHASDFFEKLILGDGDRKSGLFWQQKPALSGA
DLLKMLGKCTFEKGEYRAPKASFSVERHVWLTRLNNLRIVVDGRSRPLNEAERQAALLLP
YQTETSKYKTLKNAFIKAGLWGDGVRFGGLAYPSQAQIDAEKTKDPEDQFLVKLPAWHEL
RKAFKAAGHEALWQQISTPALDGDPTLLDQIATVLSVYKDGAEVVQQLRQLALPEPAASIA
VLEKISFDKFSSLSLKALRRIVPLMQSGLRYDEAVAQIPEYGHHSQRIEPGAAKHLYLPPFYE
AQRKYAGKGDHIGSMQFRDDADIPRNPVVLRALNQARKVVNALIREYGSPIAVNIEMARD
LSRPLDERNKVKRAQEEFRDRNDRARSEFERDFGYKPKAAAFEKWMLYREQLGQCAYSQ
QPLDIQRVLDDHNYAQVDHALPYSRSYDDSKNNKVLVLTHENQNKGNRTAFEYLTSFPDG
EDGERWRTFVAWVQGNKAYRMAKRNRLLRKNYGVDESKGFIDRNLNDTRYICKFFKNYV
EEHLQLAARADGDTARRCVVVNGQLTAFLRARWGLTKVRGDSDRHHALDAAVVAACTH
GMVKALADYSRRKEISFLQEGFPDPETGEILNPAAFDRARQHFPEPWTHFAHELKARLFTD
DLAALREDMQRLGSYTTEDLGRLRTLFVSRAPQRRSGGAVHKETIYAQPESLKQQGGVIEK
ILLTSLKLQDFDKLLNPESNDHFVEPHRNERLYAAIRQRLEQFGGRADKAFGPDNLFHKPDK
NNQPTGPVVRSIKLVRGKQTGIPIRGGLAKNDSMLRVDIFTKAGKFHLVPVYVHHRVTGLP
NRAIVAFKDEDEWTLIDESFAFLFSVYPNDYVKVTLKKEQQSGYYSGADRSTGAMNLWAH
DRAASVGKDGLIRGIGVKTALSVEKFNVDVLGRIYLAPPETRSGLA

Acid mine drainage bacteria Ga0052161_JGI Cas9 (amino acid sequence) (SEQ ID NO:855):

MADSLSRPWRLALDVGVGSIGWAALNLKRSERSNTPGDKWVACSLLDLGVNLFDSGVED
GIPKNTARRTYKAARHRLQSVKVRKRNLRDVLVAADCLPCDSATSQRSLLKGEPRSASIAL
RDQMVPIDGDGSVAIPAVWAWRWKALRKPGQLTHHELGVILMALASARGQGFSEESDSRT
VAPLVSELQEKISRAGCTAFGDYAAEILAKSPGATIRARNAEPNFVSRQMVLGEFRAIRNAQ
TRLLSPKRWDEIENIIFDQAPLAPPRPGNCPLVKEDVRLERAHPLAQRLKIVQTLRNVRLFDA
DGAVPEDRPTQLTPDEIRKAEKFLSTRKSATAISLFKALGIKSLRSNYHGGSRAEATDLPGNE
TNVAAAREDAFGAAWAAFEPSKQRDIVELALSIRGGRTADEIRAAADTWGISIDAARAFID
MLPKGRAAYGLTATNRLLAVMLEEGLSLFDARDREYPQAAQSRKFCSLPYYAIALPDHVF
DGDPRADETATDEQRYGHVRNPIVHVALNQIRGLVNALVAEFGAPVEITVELAREISLSDDE
KKKLLKSQKERAEMRETAAATIRECGYKPSRDLIDRYVLYCGQDRRLVQGEFAEIKCVYSG
KPIESFKRLFSNDIEIDHIVPRQRSHDDSLANKVLAYRGANRNKLNRTPFEFWGHTEHWAEI
WERAEFAFRKNPKKLARFRETAAQEFTGDFASRHLNDTRYISKMTRLYLERLKGTECVYAT
RGSITGRLRKAWELAKLLPVPAAVQSLIDISRASSRDVPIELKRHDHRHHAIDAALIGLVDH
HTLQYYFEKTESQTDKRFPLPWPTFKEELAERLQGLVVRRRPEHKRGFRYQGQLVEDSRYR
LRRQNEKNVLSSRTSLIGLVIDKFGNLIPGTRSAGIQFSCKEAFESSIMRIDPTGRLITLLNWET
LQAIRNSYLTSRPGDGDSGPLERKKAEREATAFAWKSLCSRAATTAGGISSVRKKIVLEDPV
IVGPEKSAVKSAGYAFAYVIKRNVPNTRYQLFPVAMKDAETDQGPPLKPGEVVVCKLHKG
DMLSLLLESNSLSSPVYCTVQGFKSSGVLTLTTQYNAARNGGRAVNTVPEIESSDGRNAVN
KVFGTWRARIVRPTVLGRLP

Uranium mine bacteria FW106_JGI Cas9 (amino acid sequence) (SEQ ID NO:856):

MGLIIREFSMENKALEQQAAAPMVFGFDIGIASVGWTVLGPTRIIDLGVRAFDKAETAKEGE
PLNLARRTARLMRRRLRRRAWRLTKLARLLKRHGVIDEVALFMPEHPYPHSLWKLRVEAL
DRPLAAEEWARVIYHLCKHRGFHWISRAEEKKAEADSKGEGGKVKQGLAGTKRLMEDKG
YRSAAEMVLAEFPDAQRNKQGDYTKSLSRVLLGDELSLLFTRQRELGNQHATPELQLSVLG
TGDHKSGLFWAQKPALAGDALLGMLGKCTFEKSEYRAPKASFTAERHVWLTRLNNLRVV
ADGRVRPLNEQERQIALRLPYQQASDLTYKQLRAALVKAGVLPDSFRFTGLAYPNATQQS
DSKIKDPEAAPLIRIPAWQEIRLTLKKAGLETEWEGMASLAIDGKPELLDQIAWVLTVFKED
DEVRAELRKLNLPQADKMVEALLDIRFDKFHALSLKALRNIVPHMELGLRYDEACEKAGY
HHSQLFTVGAGTHRYLPPFYSKRDASGRMIFDQELDIPRNPVVLRALNQARKVINALIRHYG
PPSEVRIELARDLSRPFDERKKIQTAQDEYRERNEKEKIRFLEEFSLSGTAKGRDFEKWQLYR
EQQGKCAYSLEALDLHRLFEVGYVEIDHALPYSRSYDDSKNNKVLVLAKENRNKGNQTPY
EYLDGMENTERWRAFASFVESNKTYRVAKRSRLLRKEFGAKESSEFKERNLNDTRYICKFF
KNYVERYLQLAENSEAKRCVVVSGQLTSFLRARWGLIKVREDSDRHHALDAAVVAACSH
GMVKRLSDYARRRELEKVSEGFVDMETGEIVNPAMFRQLEQHFPEPWPNFRHELEARRKID
DPASLRSEIERLGTYSSDVLQILKPLFVSRAVQRRNRGAAHKETIYSQPERLKEQGGVTQKIP
LASLTLKDIDKLIDPHRNEKLYAAIRSRLEAHGGKGDKAFPSNNPLRKPDREGNATGPIVRT
VTMVIDKLSGIPVRGGVAKNDSMLRVDVFTKAGKFHLVPVYVHHSVAKTLPDRAIVQAKD
EDEWTLIDNSFDFCFSLYPNDLIKISQKGKPPLIGYYGSCNRNTGAINLWAHDRSNAIGKNG
LIESVGVKVALNLEKFHVDVLGNIFPAPKEERRGLA

A. sp Cpf1 (amino acid sequence) (SEQ ID NO:857):

MTQFEGFTNLYQVSKTLRFELIPQGKTLKHIQEQGFIEEDKARNDHYKELKPIIDRIYKTYAD
QCLQLVQLDWENLSAAIDSYRKEKTEETRNALIEEQATYRNAIHDYFIGRTDNLTDAINKRH
AEIYKGLFKAELFNGKVLKQLGTVTTTEHENALLRSFDKFTTYFSGFYENRKNVFSAEDIST

AIPHRIVQDNFPKFKENCHIFTRLITAVPSLREHFENVKKAIGIFVSTSIEEVFSFPFYNQLLTQ
TQIDLYNQLLGGISREAGTEKIKGLNEVLNLAIQKNDETAHIIASLPHRFIPLFKQILSDRNTLS
FILEEFKSDEEVIQSFCKYKTLLRNENVLETAEALFNELNSIDLTHIFISHKKLETISSALCDH
WDTLRNALYERRISELTGKITKSAKEKVQRSLKHEDINLQEIISAAGKELSEAFKQKTSEILS
HAHAALDQPLPTTLKKQEEKEILKSQLDSLLGLYHLLDWFAVDESNEVDPEFSARLTGIKLE
MEPSLSFYNKARNYATKKPYSVEKFKLNFQMPTLASGWDVNKEKNNGAILFVKNGLYYL
GIMPKQKGRYKALSFEPTEKTSEGFDKMYYDYFPDAAKMIPKCSTQLKAVTAHFQTHTTPI
LLSNNFIEPLEITKEIYDLNNPEKEPKKFQTAYAKKTGDQKGYREALCKWIDFTRDFLSKYT
KTTSIDLSSLRPSSQYKDLGEYYAELNPLLYHISFQRIAEKEIMDAVETGKLYLFQIYNKDFA
KGHHGKPNLHTLYWTGLFSPENLAKTSIKLNGQAELFYRPKSRMKRMAHRLGEKMLNKK
LKDQKTPIPDTLYQELYDYVNHRLSHDLSDEARALLPNVITKEVSHEIIKDRRFTSDKFFFHV
PITLNYQAANSPSKFNQRVNAYLKEHPETPIIGIDRGERNLIYITVIDSTGKILEQRSLNTIQQF
DYQKKLDNREKERVAARQAWSVVGTIKDLKQGYLSQVIHEIVDLMIHYQAVVVLENLNFG
FKSKRTGIAEKAVYQQFEKMLIDKLNCLVLKDYPAEKVGGVLNPYQLTDQFTSFAKMGTQ
SGFLFYVPAPYTSKIDPLTGFVDPFVWKTIKNHESRKHFLEGFDFLHYDVKTGDFILHFKMN
RNLSFQRGLPGFMPAWDIVFEKNETQFDAKGTPFIAGKRIVPVIENHRFTGRYRDLYPANEL
IALLEEKGIVFRDGSNILPKLLENDDSHAIDTMVALIRSVLQMRNSNAATGEDYINSPVRDL
NGVCFDSRFQNPEWPMDADANGAYHIALKGQLLLNHLKESKDLKLQNGISNQDWLAYIQE
LRN

L. bacterium Cpf1 (amino acid sequence) (SEQ ID NO:858):

MSKLEKFTNCYSLSKTLRFKAIPVGKTQENIDNKRLLVEDEKRAEDYKGVKKLLDRYYLSF
INDVLHSIKLKNLNNYISLFRKKTRTEKENKELENLEINLRKEIAKAFKGNEGYKSLFKKDIIE
TILPEFLDDKDEIALVNSFNGFTTAFTGFFDNRENMFSEEAKSTSIAFRCINENLTRYISNMDI
FEKVDAIFDKHEVQEIKEKILNSDYDVEDFFEGEFFNFVLTQEGIDVYNAIIGGFVTESGEKIK
GLNEYINLYNQKTKQKLPKFKPLYKQVLSDRESLSFYGEGYTSDEEVLEVFRNTLNKNSEIF
SSIKKLEKLFKNFDEYSSAGIFVKNGPAISTISKDIFGEWNVIRDKWNAEYDDIHLKKKAVVT
EKYEDDRRKSFKKIGSFSLEQLQEYADADLSVVEKLKEIIIQKVDEIYKVYGSSEKLFDADFV
LEKSLKKNDAVVAIMKDLLDSVKSFENYIKAFFGEGKETNRDESFYGDFVLAYDILLKVDH
IYDAIRNYVTQKPYSKDKFKLYFQNPQFMGGWDKDKETDYRATILRYGSKYYLAIMDKKY
AKCLQKIDKDDVNGNYEKINYKLLPGPNKMLPKVFFSKKWMAYYNPSEDIQKIYKNGTFK
KGDMFNLNDCHKLIDFFKDSISRYPKWSNAYDFNFSETEKYKDIAGFYREVEEQGYKVSFE
SASKKEVDKLVEEGKLYMFQIYNKDFSDKSHGTPNLHTMYFKLLFDENNHGQIRLSGGAEL
FMRRASLKKEELVVHPANSPIANKNPDNPKKTTTLSYDVYKDKRFSEDQYELHIPIAINKCP
KNIFKINTEVRVLLKHDDNPYVIGIDRGERNLLYIVVVDGKGNIVEQYSLNEIINNFNGIRIKT
DYHSLLDKKEKERFEARQNWTSIENIKELKAGYISQVVHKICELVEKYDAVIALEDLNSGFK
NSRVKVEKQVYQKFEKMLIDKLNYMVDKKSNPCATGGALKGYQITNKFESFKSMSTQNGF
IFYIPAWLTSKIDPSTGFVNLLKTKYTSIADSKKFISSFDRIMYVPEEDLFEFALDYKNFSRTD
ADYIKKWKLYSYGNRIRIFRNPKKNNVFDWEEVCLTSAYKELFNKYGINYQQGDIRALLCE
QSDKAFYSSFMALMSLMLQMRNSITGRTDVDFLISPVKNSDGIFYDSRNYEAQENAILPKN
ADANGAYNIARKVLWAIGQFKKAEDEKLDKVKIAISNKEWLEYAQTSVKH

P. macacae Cpf1 (amino acid sequence) (SEQ ID NO:859):

MKTQHFFEDFTSLYSLSKTIRFELKPIGKTLENIKKNGLIRRDEQRLDDYEKLKKVIDEYHED
FIANILSSFSFSEEILQSYIQNLSESEARAKIEKTMRDTLAKAFSEDERYKSIFKKELVKKDIPV
WCPAYKSLCKKFDNFTTSLVPFHENRKNLYTSNEITASIPYRIVHDNLPKFIQNIEALCELQK
KMGADLYLEMMENLRNVWPSFVKTPDDLCNLKTYNHLMVQSSISEYNRFVGGYSTEDGT

KHQGINEWINIYRQRNKEMRLPGLVFLHKQILAKVDSSSFISDTLENDDQVFCVLRQFRKLF
WNTVSSKEDDAASLKDLFCGLSGYDPEAIYVSDAHLATISKNIFDRWNYISDAIRRKTEVLM
PRKKESVERYAEKISKQIKKRQSYSLAELDDLLAHYSEESLPAGFSLLSYFTSLGGQKYLVS
DGEVILYEEGSNIWDEVLIAFRDLQVILDKDFTEKKLGKDEEAVSVIKKALDSALRLRKFFD
LLSGTGAEIRRDSSFYALYTDRMDKLKGLLKMYDKVRNYLTKKPYSIEKFKLHFDNPSLLS
GWDKNKELNNLSVIFRQNGYYYLGIMTPKGKNLFKTLPKLGAEEMFYEKMEYKQIAEPML
MLPKVFFPKKTKPAFAPDQSVVDIYNKKTFKTGQKGFNKKDLYRLIDFYKEALTVHEWKL
FNFSFSPTEQYRNIGEFFDEVREQAYKVSMVNVPASYIDEAVENGKLYLFQIYNKDFSPYSK
GIPNLHTLYWKALFSEQNQSRVYKLCGGGELFYRKASLHMQDTTVHPKGISIHKKNLNKK
GETSLFNYDLVKDKRFTEDKFFFHVPISINYKNKKITNVNQMVRDYIAQNDDLQIIGIDRGE
RNLLYISRIDTRGNLLEQFSLNVIESDKGDLRTDYQKILGDREQERLRRRQEWKSIESIKDLK
DGYMSQVVHKICNMVVEHKAIVVLENLNLSFMKGRKKVEKSVYEKFERMLVDKLNYLVV
DKKNLSNEPGGLYAAYQLTNPLFSFEELHRYPQSGILFFVDPWNTSLTDPSTGFVNLLGRIN
YTNVGDARKFFDRFNAIRYDGKGNILFDLDLSRFDVRVETQRKLWTLTTFGSRIAKSKKSG
KWMVERIENLSLCFLELFEQFNIGYRVEKDLKKAILSQDRKEFYVRLIYLFNLMMQIRNSDG
EEDYILSPALNEKNLQFDSRLIEAKDLPVDADANGAYNVARKGLMVVQRIKRGDHESIHRI
GRAQWLRYVQEGIVE

P. disiens Cpf1 (amino acid sequence) (SEQ ID NO:860):

MENYQEFTNLFQLNKTLRFELKPIGKTCELLEEGKIFASGSFLEKDKVRADNVSYVKKEIDK
KHKIFIEETLSSFSISNDLLKQYFDCYNELKAFKKDCKSDEEEVKKTALRNKCTSIQRAMRE
AISQAFLKSPQKKLLAIKNLIENVFKADENVQHFSEFTSYFSGFETNRENFYSDEEKSTSIAYR
LVHDNLPIFIKNIYIFEKLKEQFDAKTLSEIFENYKLYVAGSSLDEVFSLEYFNNTLTQKGIDN
YNAVIGKIVKEDKQEIQGLNEHINLYNQKHKDRRLPFFISLKKQILSDREALSWLPDMFKND
SEVIKALKGFYIEDGFENNVLTPLATLLSSLDKYNLNGIFIRNNEALSSLSQNVYRNFSIDEAI
DANAELQTFNNYELIANALRAKIKKETKQGRKSFEKYEEYIDKKVKAIDSLSIQEINELVEN
YVSEFNSNSGNMPRKVEDYFSLMRKGDFGSNDLIENIKTKLSAAEKLLGTKYQETAKDIFK
KDENSKLIKELLDATKQFQHFIKPLLGTGEEADRDLVFYGDFLPLYEKFEELTLLYNKVRNR
LTQKPYSKDKIRLCFNKPKLMTGWVDSKTEKSDNGTQYGGYLFRKKNEIGEYDYFLGISSK
AQLFRKNEAVIGDYERLDYYQPKANTIYGSAYEGENSYKEDKKRLNKVIIAYIEQIKQTNIK
KSIIESISKYPNISDDDKVTPSSLLEKIKKVSIDSYNGILSFKSFQSVNKEVIDNLLKTISPLKNK
AEFLDLINKDYQIFTEVQAVIDEICKQKTFIYFPISNVELEKEMGDKDKPLCLFQISNKDLSFA
KTFSANLRKKRGAENLHTMLFKALMEGNQDNLDLGSGAIFYRAKSLDGNKPTHPANEAIK
CRNVANKDKVSLFTYDIYKNRRYMENKFLFHLSIVQNYKAANDSAQLNSSATEYIRKADD
LHIIGIDRGERNLLYYSVIDMKGNIVEQDSLNIIRNNDLETDYHDLLDKREKERKANRQNWE
AVEGIKDLKKGYLSQAVHQIAQLMLKYNAIIALEDLGQMFVTRGQKIEKAVYQQFEKSLV
DKLSYLVDKKRPYNELGGILKAYQLASSITKNNSDKQNGFLFYVPAWNTSKIDPVTGFTDL
LRPKAMTIKEAQDFFGAFDNISYNDKGYFEFETNYDKFKIRMKSAQTRWTICTFGNRIKRK
KDKNYWNYEEVELTEEFKKLFKDSNIDYENCNLKEEIQNKDNRKFFDDLIKLLQLTLQMRN
SDDKGNDYIISPVANAEGQFFDSRNGDKKLPLDADANGAYNIARKGLWNIRQIKQTKNDK
KLNLSISSTEWLDFVREKPYL

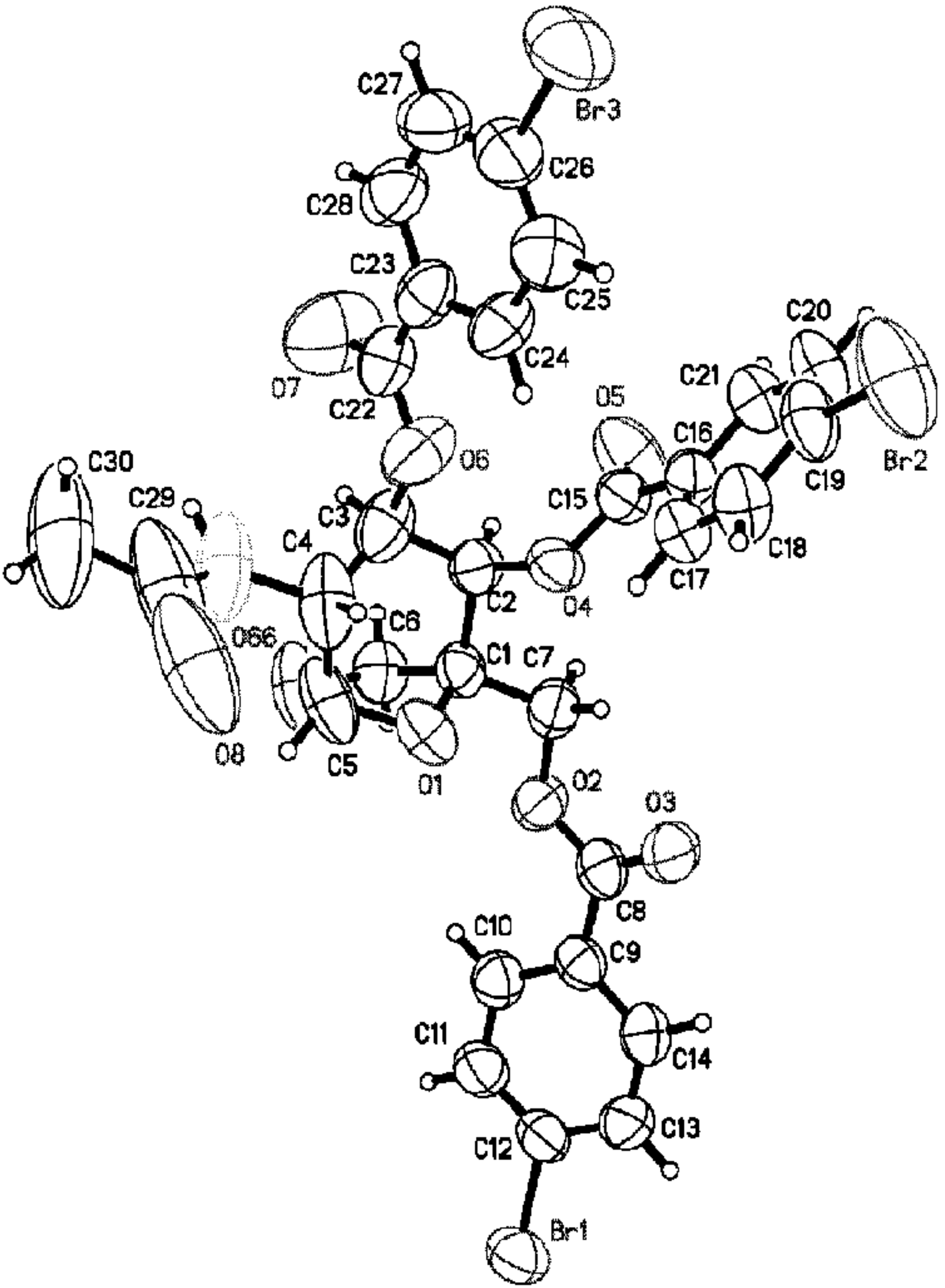
mCherry sequence (SEQ ID NO:915), wherein the initial methionine between brackets was not used for direct fusion to Cas9, but for independent expression:

(M)VSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPL
PFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQ

DGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHY
DAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

S. pyogenes Cas9 null - mutation D10A& H840A (amino acid sequence) (SEQ ID NO:1027):

MDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEA
TRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIV
DEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKL
FIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLG
LTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRV
NTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQ
EEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPF
LKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK
TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILE
DIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKT
ILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQT
VKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPV
ENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSD
KNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQL
VETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYH
HAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNI
MNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTG
GFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELL
GITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELA
LPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK
VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSI
TGLYETRIDLSQLGGD


C27
Br3
C26
C28
C23
C25
C24
O7
C22
O5
C20
C21
C16
Br2
O6
C19
C15
C30
C29
C3
C4
C18
C17
C2
O4
C6
O66
C1
C7
O8
C5
O1
O2
O3
C8
C10
C9
C11
C14
C13
C12
Br1