

P-2017-13662 - LISTADO DE SECUENCIAS
LISTADO DE SECUENCIAS

<110> Evonik Degussa GmbH

<120> Método de detección de la enteritis necrótica aviar

<130> 201500092

<160> 17

<170> PatentIn version 3.5

<210> 1

<211> 1884

<212> ADN

<213> Clostridium perfringens

<220>

<221> CDS

<222> (631)..(1884)

<223> gen SAM

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Asn Gly Gln Ile Thr Arg Glu Ile Asn Ala Asp Gln Ile Ser Lys Thr
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Pro Thr Leu Val Glu Phe Leu Arg Ala Gly Tyr Tyr Leu Gly Phe Tyr
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gaa Glu	gat Asp	ggt Gly	gaa Glu	atc Ile 805	aaa Lys	gct Ala	tat Tyr	gaa Glu	tgg Trp 810	gac Asp	ttt Phe	gga Gly	gat Asp	gga Gly 815	gaa Glu	2448
aaa Lys	tct Ser	aat Asn	gag Glu 820	gct Ala	aaa Lys	gcc Ala	act Thr	cat His 825	aag Lys	tat Tyr	aat Asn	aaa Lys	act Thr	gga Gly	gaa Glu	2496
tat Tyr	gaa Glu	gta Val 835	aaa Lys	tta Leu	aca Thr	gtt Val	aca Thr 840	gat Asp	aat Asn	aac Asn	ggt Gly	gga Gly 845	ata Ile	aat Asn	act Thr	2544
gaa Glu	agt Ser 850	aaa Lys	aag Lys	ata Ile	aaa Lys	gta Val 855	gta Val	gaa Glu	gat Asp	aaa Lys	cct Pro 860	gtt Val	gaa Glu	gtt Val	ata Ile	2592
aat Asn 865	gaa Glu	agc Ser	gag Glu	cca Pro	aac Asn 870	aat Asn	gat Asp	ttt Phe	gaa Glu	aag Lys 875	gct Ala	aac Asn	caa Gln	ata Ile	gct Ala 880	2640
aaa Lys	tct Ser	aat Asn	atg Met	tta Leu 885	gtt Val	aag Lys	ggt Gly	act Thr	tta Leu 890	tca Ser	gaa Glu	gag Glu	gat Asp	tat Tyr 895	tca Ser	2688
gat Asp	aaa Lys	tat Tyr	tat Tyr 900	ttt Phe	gat Asp	gta Val	gct Ala	aaa Lys 905	aaa Lys	ggc Gly	aat Asn	gtt Val	aaa Lys 910	atc Ile	act Thr	2736
ctt Leu	aat Asn	aat Asn 915	tta Leu	aat Asn	tca Ser	gta Val	gga Gly 920	ata Ile	act Thr	tgg Trp	aca Thr	ctt Leu	tat Tyr	aaa Lys	gag Glu	2784
gga Gly	gac Asp 930	cta Leu	aac Asn	aat Asn	tat Tyr	gtt Val 935	tta Leu	tat Tyr	gca Ala	act Thr	gga Gly 940	aat Asn	gat Asp	gga Gly	aca Thr	2832
gaa Glu 945	tta Leu	aag Lys	ggt Gly	gaa Glu	aag Lys 950	act Thr	tta Leu	gag Glu	cct Pro	gga Gly 955	aga Arg	tac Tyr	tac Tyr	tta Leu	agt Ser 960	2880
gta Val	tat Tyr	act Thr	tat Tyr	gat Asp 965	aat Asn	caa Gln	tca Ser	gga Gly	gct Ala 970	tac Tyr	aca Thr	gta Val	aat Asn	gta Val 975	aaa Lys	2928
gga Gly	aac Asn	ctt Leu	aaa Lys 980	aat Asn	gaa Glu	gtt Val	aaa Lys	gaa Glu 985	aca Thr	gaa Glu	aag Lys	gat Asp	gct Ala 990	ata Ile	aaa Lys	2976
gaa Glu	gtt Val	gaa Glu 995	aat Asn	aac Asn	aat Asn	gat Asp	ttt Phe 1000	gat Asp	aaa Lys	gct Ala	atg Met	aag Lys 1005	gta Val	gac Asp	agt Ser	3024

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aat agc aaa ata gtt gga aca tta agc aat gat gat ctt aag gat	3069
Asn Ser Lys Ile Val Gly Thr Leu Ser Asn Asp Asp Leu Lys Asp	
1010 1015 1020	
att tat agc ata gat ata caa aat cca agt gac tta aac ata gta	3114
Ile Tyr Ser Ile Asp Ile Gln Asn Pro Ser Asp Leu Asn Ile Val	
1025 1030 1035	
gtt gaa aac tta gat aat ata aaa atg aac tgg tta tta tat tca	3159
Val Glu Asn Leu Asp Asn Ile Lys Met Asn Trp Leu Leu Tyr Ser	
1040 1045 1050	
gct gat gat tta agt aac tat gtg gat tac gct aat gca gat gga	3204
Ala Asp Asp Leu Ser Asn Tyr Val Asp Tyr Ala Asn Ala Asp Gly	
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aat aaa tta agt aac act tgt aag tta aat cca ggt aaa tat tac	3249
Asn Lys Leu Ser Asn Thr Cys Lys Leu Asn Pro Gly Lys Tyr Tyr	
1070 1075 1080	
tta tgt gtt tat caa ttt gaa aac tca ggt act gga aat tac aca	3294
Leu Cys Val Tyr Gln Phe Glu Asn Ser Gly Thr Gly Asn Tyr Thr	
1085 1090 1095	
gta aac tta caa aac aaa taa	3315
Val Asn Leu Gln Asn Lys	
1100	

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 <211> 1104
 <212> PRT
 <213> Clostridium perfringens

<400> 6

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

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

Glu Leu Asn Asn Glu Val Ala Thr Asp Asn Asn Arg Pro Leu Gly Pro
 65 70 75 80

Ser Ile Ala Pro Ser Arg Ala Arg Asn Asn Lys Ile Tyr Thr Phe Asp
 85 90 95

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

Ile Ser Tyr Glu Asn Val Pro Asp Leu Phe Asn Phe Asn Asp Gly Ser
 115 120 125

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

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Phe Val Val Lys Ala Gly Asp Lys Val Thr Glu Glu Lys Ile Lys Arg
405 410 415

Leu Tyr Trp Ala Ser Lys Glu Val Lys Ala Gln Phe Met Arg Val Val
420 425 430

Gln Asn Asp Lys Ala Leu Glu Glu Gly Asn Pro Asp Asp Ile Leu Thr
435 440 445

Val Val Ile Tyr Asn Ser Pro Glu Glu Tyr Lys Leu Asn Arg Ile Ile
450 455 460

Asn Gly Phe Ser Thr Asp Asn Gly Gly Ile Tyr Ile Glu Asn Ile Gly
465 470 475 480

Thr Phe Phe Thr Tyr Glu Arg Thr Pro Glu Glu Ser Ile Tyr Thr Leu
485 490 495

Glu Glu Leu Phe Arg His Glu Phe Thr His Tyr Leu Gln Gly Arg Tyr
500 505 510

Val Val Pro Gly Met Trp Gly Gln Gly Glu Phe Tyr Gln Glu Gly Val
515 520 525

Leu Thr Trp Tyr Glu Glu Gly Thr Ala Glu Phe Phe Ala Gly Ser Thr
530 535 540

Arg Thr Asp Gly Ile Lys Pro Arg Lys Ser Val Thr Gln Gly Leu Ala
545 550 555 560

Tyr Asp Arg Asn Asn Arg Met Ser Leu Tyr Gly Val Leu His Ala Lys
565 570 575

Tyr Gly Ser Trp Asp Phe Tyr Asn Tyr Gly Phe Ala Leu Ser Asn Tyr
580 585 590

Met Tyr Asn Asn Asn Met Gly Met Phe Asn Lys Met Thr Asn Tyr Ile
595 600 605

Lys Asn Asn Asp Val Ser Gly Tyr Lys Asp Tyr Ile Ala Ser Met Ser
610 615 620

Ser Asp Tyr Gly Leu Asn Asp Lys Tyr Gln Asp Tyr Met Asp Ser Leu
625 630 635 640

Leu Asn Asn Ile Asp Asn Leu Asp Val Pro Leu Val Ser Asp Glu Tyr
645 650 655

Val Asn Gly His Glu Ala Lys Asp Ile Asn Glu Ile Thr Asn Asp Ile
660 665 670

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Lys Glu Val Ser Asn Ile Lys Asp Leu Ser Ser Asn Val Glu Lys Ser
675 680 685

Gln Phe Phe Thr Thr Tyr Asp Met Arg Gly Thr Tyr Val Gly Gly Arg
690 695 700

Ser Gln Gly Glu Glu Asn Asp Trp Lys Asp Met Asn Ser Lys Leu Asn
705 710 715 720

Asp Met Leu Lys Glu Leu Ser Lys Lys Ser Trp Asn Gly Tyr Lys Thr
725 730 735

Val Thr Ala Tyr Phe Val Asn His Lys Val Asp Glu Asn Gly Asn Tyr
740 745 750

Val Tyr Asp Val Val Phe His Gly Met Asn Thr Asp Thr Asn Thr Asp
755 760 765

Val His Val Asn Lys Glu Pro Lys Ala Val Ile Lys Ser Asp Ser Ser
770 775 780

Val Ile Val Glu Glu Glu Ile Asn Phe Asp Gly Thr Glu Ser Lys Asp
785 790 795 800

Glu Asp Gly Glu Ile Lys Ala Tyr Glu Trp Asp Phe Gly Asp Gly Glu
805 810 815

Lys Ser Asn Glu Ala Lys Ala Thr His Lys Tyr Asn Lys Thr Gly Glu
820 825 830

Tyr Glu Val Lys Leu Thr Val Thr Asp Asn Asn Gly Gly Ile Asn Thr
835 840 845

Glu Ser Lys Lys Ile Lys Val Val Glu Asp Lys Pro Val Glu Val Ile
850 855 860

Asn Glu Ser Glu Pro Asn Asn Asp Phe Glu Lys Ala Asn Gln Ile Ala
865 870 875 880

Lys Ser Asn Met Leu Val Lys Gly Thr Leu Ser Glu Glu Asp Tyr Ser
885 890 895

Asp Lys Tyr Tyr Phe Asp Val Ala Lys Lys Gly Asn Val Lys Ile Thr
900 905 910

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

Gly Asp Leu Asn Asn Tyr Val Leu Tyr Ala Thr Gly Asn Asp Gly Thr
930 935 940

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Glu Leu Lys Gly Glu Lys Thr Leu Glu Pro Gly Arg Tyr Tyr Leu Ser
945 950 955 960

Val Tyr Thr Tyr Asp Asn Gln Ser Gly Ala Tyr Thr Val Asn Val Lys
965 970 975

Gly Asn Leu Lys Asn Glu Val Lys Glu Thr Glu Lys Asp Ala Ile Lys
980 985 990

Glu Val Glu Asn Asn Asn Asp Phe Asp Lys Ala Met Lys Val Asp Ser
995 1000 1005

Asn Ser Lys Ile Val Gly Thr Leu Ser Asn Asp Asp Leu Lys Asp
1010 1015 1020

Ile Tyr Ser Ile Asp Ile Gln Asn Pro Ser Asp Leu Asn Ile Val
1025 1030 1035

Val Glu Asn Leu Asp Asn Ile Lys Met Asn Trp Leu Leu Tyr Ser
1040 1045 1050

Ala Asp Asp Leu Ser Asn Tyr Val Asp Tyr Ala Asn Ala Asp Gly
1055 1060 1065

Asn Lys Leu Ser Asn Thr Cys Lys Leu Asn Pro Gly Lys Tyr Tyr
1070 1075 1080

Leu Cys Val Tyr Gln Phe Glu Asn Ser Gly Thr Gly Asn Tyr Thr
1085 1090 1095

Val Asn Leu Gln Asn Lys
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<210> 7

<211> 1001

<212> ADN

<213> Clostridium perfringens

<400> 7

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tatcttttca gtttttgatc cagttttaat tttggctatt tttaaagttag ttttccaagg	180
atagaaaagt tctattcctt ctgaagttaa aaaatctaaa actaagtggg atatatatcc	240
agctataaat cctattgaaa ttattaataa tattatgttg aagttactaa catttaaaat	300
aatatataag gtaataacta ttaaagatag acatagtaaa ctatgagtaa agccacgatg	360
tctacattta ctacctatat gctttgaaag aaaaggatac atttgactaa ttgaagattt	420
tctttgatct atacaggaa atagagatcc tatataagaa aaatgaaaaa ataatgctat	480
taataaaatt ttataagcta tatcatatgg aaataagaac aggcttaaaa ttgtatttaa	540

P-2017-13662 - LISTADO DE SECUENCIAS

cattattaaa gaaatgcata cgcctccagt tgaatgagtt tcttttgtca taaaatctcc	600
tttaaaaaata attatcatta gtttatatta aaaatattat cataatattc attttacata	660
aagaagaaaa aaataaaaaat cctaaaaata gagtggacag ttctatttct aggatcaata	720
gttatggtgg taattttatg taaggttttt tactaaatta aagtaaaatc attaataagt	780
aattatttat ttttaattac aattatggaa tatgcaattg aaaatattga tattaagca	840
agtatgggac ttataatatt tgaaacaact tctaaagatg taaaataaga tactctttgt	900
tcaatatata aagctatgct atttttaagt attaaggag aaaaaagagt tattaatgta	960
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 <211> 960
 <212> ADN
 <213> Clostridium perfringens

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 <223> n is a, c, g, t or u

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atagtcatta tcaaactctt gatattcaac tattattaca gattcttttag catttttagg	180
tgctgttaat gctaaagcca tattgggtga aaatccacca gaaattaatg ttgataaatc	240
tctatcatct gtgaaattht tatcaccatt attatacaat cttgatttca tgaataattg	300
atttcataa atagcatgat aagaatctat attataaccg tccttagtct caacaaatth	360
tatatcccat gatgctaaat ttgcatcatc thttctthga attgtthcta aatcaggthg	420
thcatagctt atagtattht ggacattata tgaagcattt attccagcac cagcagthth	480
tccttcaaca gatatattac cgcctataga ataaccaatt gaattanata catctththt	540
atctatagth ttaggaatag aatttgctat attattatth acatcagcac ththtacatt	600
aattctataa gthtcaggcc atttcattth tccgtaatat ttagaaccaa aaatctgtht	660
atcagaaggt ataaatcctt cttaaattth taaagcagth thcttatcag aatgaggatc	720
thcaataaat gthccactta aagthgcctt ccaacctth tgtgaagcgg tatcactaga	780
agtatattth atagcttctt thccatttht thttattatt thtccactta gattthtcaa	840
ctcaattthg thtatgtcat ttaattcact tgcaaaaact tgagthtgag ttgaaaaaag	900
gcttgacta attacactg taagaactag tgtaattgaa ataattthta atctthtcaa	960

<210> 9
 <211> 562
 <212> ADN
 <213> Clostridium perfringens

<400> 9

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tgtataaaaa tcataagtta aattgctcta tataatatat ccaaataaga ttaattttat	180
gaaatagaaa tgaaaaaagt tctgcaaagt gcagaacttt taatttatga ataaacttgc	240
gttaattatc aattatctat tcattttttg agcttttctt gcttttctgc aagctgggca	300
tctaactgga tcgttttcaa atcctttttc tttgaagaat tcttgttctc ctacagttaa	360
tacgaattct tttccacagt ctttacaac taaattttta tcttccattt cttttacctc	420
ctgtaaaatt tactaggtac gtttgagatc tataactataa aactaataaa ataaatttta	480
caggacagaa ataaagtaca tatctactaa atttttttt atatatattgat tatatcatat	540
agaaaaaaga atacaatact tt	562

<210> 10
 <211> 84
 <212> RNA
 <213> Gallus gallus

<400> 10 gucugucaua cucuagcagc acguaaaauu ugguguuaaa acuguaaaua ucuccaguau	60
uaacugugcu gcugaaguua ggcu	84

<210> 11
 <211> 68
 <212> RNA
 <213> Gallus gallus

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aacaggag	68

<210> 12
 <211> 63
 <212> RNA
 <213> Gallus gallus

<400> 12 uguuaaagcu aaucgugaua gggguuuuuu ccucugaaug acuccuacau guuagcauuu	60
aca	63

<210> 13
 <211> 76
 <212> RNA
 <213> Gallus gallus

<400> 13 gagaugacau gcuucuuuau auccccaauu ggauuaggcu gcuauggaau guaaggaagu	60
gugugguuuc agggag	76

<210> 14
 <211> 77
 <212> PRT

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<213> Clostridium perfringens

<400> 14

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Asp Arg Ala Pro Thr Val Glu Phe Arg Asn Phe Asn Gly Ser Leu Asn
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Glu Lys Gln Ile Gln Asp Asn Ile Lys Met Ala Ala Gly Ile Ile Asn
35 40 45

Ala Ala Glu Lys Ala Arg Phe Arg Asp Thr Glu Asp Glu Ile Phe Lys
50 55 60

Lys Arg Gly Asn Ile Leu Lys Asn Thr Ser Ile Leu Gly
65 70 75

<210> 15

<211> 196

<212> PRT

<213> Clostridium perfringens

<400> 15

Met Thr Lys Glu Thr His Ser Thr Gly Gly Val Cys Ile Ser Leu Ile
1 5 10 15

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20 25 30

Tyr Lys Ile Leu Leu Ile Ala Leu Phe Phe His Phe Ser Tyr Ile Gly
35 40 45

Ser Leu Phe Pro Asp Ile Asp Gln Arg Lys Ser Ser Ile Ser Gln Met
50 55 60

Tyr Pro Phe Leu Ser Lys His Ile Gly Ser Lys Cys Arg His Arg Gly
65 70 75 80

Phe Thr His Ser Leu Leu Cys Leu Ser Leu Ile Val Leu Thr Leu Tyr
85 90 95

Ile Ile Leu Asn Val Ser Asn Phe Asn Ile Ile Leu Leu Ile Ile Ser
100 105 110

Ile Gly Phe Ile Ala Gly Tyr Ile Ser His Leu Val Leu Asp Phe Leu
115 120 125

Thr Ser Glu Gly Ile Glu Leu Phe Tyr Pro Trp Lys Thr Asn Phe Lys
130 135 140

Ile Ala Lys Ile Lys Thr Gly Ser Lys Thr Glu Lys Ile Ile Asn Lys

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145 150 155 160

Ile Leu Lys Ile Phe Asn Phe Leu Leu Ile Ile Tyr Asn Ile Val Leu
165 170 175

Ile Leu Ser Asp Ile Leu Gly Ile Asn Ile Leu Ser Phe Ile Ser Lys
180 185 190

Ser Thr Leu Phe
195

<210> 16
<211> 5628
<212> ADN
<213> Clostridium perfringens

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<221> CDS
<222> (673)..(5628)
<223> gen TpeL

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aaattactta attattctag acagcacgta aaccaaataa aaaatagagc attaaaaaat 180
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gttaattgtg gattcagaac tgtttaaaat tatggctact caaggagctt ttgctttact 300
attttcctac ttgttatattt atgtattaaa agaaaatagc aaaagagaag aaaattatca 360
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aaaaaataaa ttgaataata attagaaaaa atttataaaa aatataaatt ttaaattttt 480
atttacaataa tttaaaatta gaactcttta tataatgtat aagaaattta attctaagta 540
tataaaatac taaaggaggg ttaagaagaa taaaatttga aaggaaaaaa tttgtgcaaa 600
ttcaaattta taattagatt gaaggaggga tttgatgtaa atataaatta agttttacat 660
caacaataat at atg ggg tta atg tca aaa gaa caa tta att ata tta gca 711
Met Gly Leu Met Ser Lys Glu Gln Leu Ile Ile Leu Ala
1 5 10

aaa aat tca agt cca aaa gaa gga gaa tat aaa aaa att tta gaa tta 759
Lys Asn Ser Ser Pro Lys Glu Gly Glu Tyr Lys Lys Ile Leu Glu Leu
15 20 25

cta gat gaa tat aat tta tta aat aat tct gtt gaa aaa aat agt ata 807
Leu Asp Glu Tyr Asn Leu Leu Asn Asn Ser Val Glu Lys Asn Ser Ile
30 35 40 45

gat tta tat tta aaa ctt aat gaa tta tct aaa tca att gat att tat 855
Asp Leu Tyr Leu Lys Leu Asn Glu Leu Ser Lys Ser Ile Asp Ile Tyr
50 55 60

tta aaa aaa tat aag aat tca aag aga aat aat gca tta tat caa tta 903
Leu Lys Lys Tyr Lys Asn Ser Lys Arg Asn Asn Ala Leu Tyr Gln Leu
65 70 75

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aaa Lys	tct Ser	gat Asp 80	tta Leu	aca Thr	aag Lys	gaa Glu	ggt Val 85	att Ile	gaa Glu	ata Ile	aaa Lys	gat Asp 90	act Thr	aat Asn	tta Leu	951
aaa Lys	cct Pro 95	ttg Leu	gaa Glu	aaa Lys	aat Asn	att Ile 100	cat His	ttt Phe	ggt Val	tgg Trp	ggt Val 105	gga Gly	gga Gly	atg Met	ata Ile	999
aat Asn 110	aat Asn	ata Ile	tct Ser	att Ile	gat Asp 115	tat Tyr	ata Ile	aat Asn	caa Gln	tgg Trp 120	aaa Lys	gat Asp	att Ile	aat Asn	agc Ser 125	1047
gat Asp	tat Tyr	gaa Glu	act Thr	att Ile 130	ata Ile	tgg Trp	tat Tyr	gat Asp	agt Ser 135	gaa Glu	gct Ala	ttg Leu	tta Leu	gta Val 140	aat Asn	1095
ata Ile	tta Leu	aaa Lys	aaa Lys 145	gct Ala	ata Ile	ata Ile	gac Asp	tca Ser 150	tca Ser	aat Asn	aaa Lys	gaa Glu	ggt Val 155	tta Leu	act Thr	1143
aaa Lys	tat Tyr	gaa Glu 160	tca Ser	gta Val	tta Leu	aat Asn	gat Asp 165	aat Asn	agc Ser	ttt Phe	gat Asp 170	tca Ser	aat Asn	aaa Lys	ttt Phe	1191
tat Tyr	aga Arg 175	gaa Glu	aga Arg	atg Met	gaa Glu	ggt Val 180	att Ile	ttt Phe	aga Arg	aag Lys	caa Gln 185	aaa Lys	gag Glu	ttt Phe	aat Asn	1239
aat Asn 190	tat Tyr	tat Tyr	aat Asn	aca Thr	aat Asn 195	gat Asp	aac Asn	tat Tyr	act Thr	aaa Lys 200	tct Ser	tta Leu	aat Asn	gat Asp	gta Val 205	1287
att Ile	aaa Lys	ggt Val	tat Tyr	tta Leu 210	ata Ile	gaa Glu	aaa Lys	tat Tyr	tta Leu 215	aaa Lys	act Thr	gat Asp	gaa Glu	gaa Glu 220	tta Leu	1335
gaa Glu	aaa Lys	tat Tyr	att Ile 225	aat Asn	gaa Glu	agt Ser	aaa Lys	gaa Glu 230	ggt Val	ttt Phe	aag Lys	gct Ala 235	aat Asn	gga Gly	gct Ala	1383
aaa Lys	gat Asp	ata Ile 240	aga Arg	gaa Glu	tac Tyr	gat Asp	ata Ile 245	cta Leu	gat Asp	gat Asp	ggt Val	gaa Glu 250	tta Leu	aaa Lys	tca Ser	1431
ata Ile	tat Tyr 255	gag Glu	caa Gln	gag Glu	tta Leu	tta Leu 260	atg Met	aga Arg	ttt Phe	aat Asn	tta Leu 265	gca Ala	tct Ser	gca Ala	tca Ser	1479
gat Asp 270	att Ile	att Ile	aga Arg	gtg Val	att Ile 275	gta Val	tta Leu	aat Asn	aaa Lys	tta Leu 280	ggg Gly	ggg Gly	att Ile	tat Tyr	tta Leu 285	1527
gat Asp	gta Val	gat Asp	gtg Val	ctt Leu 290	cct Pro	gga Gly	ata Ile	aaa Lys	aaa Lys 295	cat His	att Ile	ttt Phe	aaa Lys	gat Asp 300	att Ile	1575
aat Asn	aaa Lys	cct Pro	aca Thr 305	aat Asn	att Ile	tct Ser	gaa Glu	aat Asn 310	aaa Lys	tgg Trp	caa Gln	atg Met 315	att Ile	caa Gln	tta Leu	1623
gaa Glu	act Thr	att Ile 320	atg Met	aaa Lys	tat Tyr	aaa Lys	caa Gln 325	tat Tyr	ata Ile	aaa Lys	gga Gly	tat Tyr 330	aca Thr	gaa Glu	aat Asn	1671
tca Ser	ttt Phe 335	aaa Lys	aat Asn	tta Leu	cca Pro	agt Ser 340	gat Asp	ttg Leu	cag Gln	gaa Glu	atg Met 345	tta Leu	caa Gln	gaa Glu	aaa Lys	1719

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gtt Val 350	gtt Val 350	gaa Glu 350	aaa Lys 350	aat Asn 350	ctt Leu 355	aaa Lys 355	agt Ser 355	gat Asp 355	ata Ile 355	ttt Phe 360	cag Gln 360	aga Arg 360	tta Leu 360	ggg Gly 365	gat Asp 365	1767
ata Ile 370	ttt Phe 370	att Ile 370	tca Ser 370	gaa Glu 370	tta Leu 370	gat Asp 370	aca Thr 370	aaa Lys 370	ata Ile 375	gct Ala 375	ttt Phe 375	atg Met 375	ttt Phe 380	ggg Gly 380	aaa Lys 380	1815
att Ile 385	gct Ala 385	aat Asn 385	caa Gln 385	gta Val 385	tta Leu 385	ata Ile 385	tct Ser 385	aaa Lys 390	aaa Lys 390	aat Asn 390	tca Ser 390	tac Tyr 390	tca Ser 395	tta Leu 395	aat Asn 395	1863
tta Leu 400	ata Ile 400	att Ile 400	aat Asn 400	caa Gln 400	atc Ile 400	aag Lys 405	aat Asn 405	aga Arg 405	tat Tyr 405	aat Asn 405	att Ile 410	att Ile 410	aat Asn 410	aaa Lys 410	tgt Cys 410	1911
tta Leu 415	tct Ser 415	tcg Ser 415	gct Ala 415	att Ile 415	gaa Glu 420	aaa Lys 420	gga Gly 420	tca Ser 420	aat Asn 420	ttt Phe 425	aat Asn 425	aat Asn 425	aca Thr 425	gtt Val 425	gat Asp 425	1959
ata Ile 430	ttc Phe 430	att Ile 430	caa Gln 430	caa Gln 430	tta Leu 435	aat Asn 435	gaa Glu 435	ttc Phe 435	tat Tyr 440	gtt Val 440	aat Asn 440	gaa Glu 440	ggc Gly 440	ttt Phe 445	ttt Phe 445	2007
gtt Val 450	agt Ser 450	aaa Lys 450	gta Val 450	atg Met 450	gga Gly 450	tat Tyr 450	tta Leu 450	ggg Gly 455	gat Asp 455	gga Gly 455	tat Tyr 455	atg Met 455	cct Pro 460	gat Asp 460	atg Met 460	2055
aga Arg 465	gcg Ala 465	aca Thr 465	ctt Leu 465	aat Asn 465	ata Ile 465	agt Ser 465	ggg Gly 470	cca Pro 470	gga Gly 470	ata Ile 470	tat Tyr 470	aca Thr 475	gct Ala 475	gct Ala 475	tat Tyr 475	2103
tat Tyr 480	gat Asp 480	tta Leu 480	tta Leu 480	tat Tyr 480	ttt Phe 480	aat Asn 480	gag Glu 485	agg Arg 485	tca Ser 485	tta Leu 485	aat Asn 485	cct Pro 490	caa Gln 490	att Ile 490	tta Leu 490	2151
caa Gln 495	gaa Glu 495	gat Asp 495	ttg Leu 495	aaa Lys 495	tat Tyr 500	ttt Phe 500	gaa Glu 500	gtt Val 500	cca Pro 500	caa Gln 500	gct Ala 505	cta Leu 505	ata Ile 505	tca Ser 505	caa Gln 505	2199
caa Gln 510	aca Thr 510	gaa Glu 510	caa Gln 510	gaa Glu 510	ata Ile 515	aat Asn 515	agt Ser 515	tca Ser 515	tgg Trp 520	aca Thr 520	ttt Phe 520	aat Asn 520	caa Gln 520	gtt Val 525	aaa Lys 525	2247
tca Ser 530	caa Gln 530	ata Ile 530	gaa Glu 530	tat Tyr 530	aaa Lys 530	aag Lys 530	cta Leu 535	gta Val 535	gaa Glu 535	aaa Lys 535	tat Tyr 535	act Thr 540	aat Asn 540	aaa Lys 540	tca Ser 540	2295
tta Leu 545	agt Ser 545	gaa Glu 545	aat Asn 545	gat Asp 545	aaa Lys 545	cta Leu 550	aat Asn 550	ttt Phe 550	aat Asn 550	gag Glu 550	aat Asn 550	aaa Lys 555	atc Ile 555	att Ile 555	gat Asp 555	2343
aaa Lys 560	gta Val 560	gaa Glu 560	tta Leu 560	cta Leu 560	aat Asn 560	cga Arg 565	att Ile 565	aat Asn 565	agt Ser 565	aat Asn 565	aat Asn 570	tta Leu 570	att Ile 570	aat Asn 570	ttt Phe 570	2391
gat Asp 575	gat Asp 575	aaa Lys 575	gaa Glu 575	tac Tyr 575	tta Leu 580	aga Arg 580	tat Tyr 580	ata Ile 580	att Ile 580	caa Gln 585	tta Leu 585	caa Gln 585	ggg Gly 585	gat Asp 585	aaa Lys 585	2439
gta Val 590	agt Ser 590	tat Tyr 590	gag Glu 590	gct Ala 595	gca Ala 595	ata Ile 595	aat Asn 595	tta Leu 595	ttt Phe 600	att Ile 600	aaa Lys 600	aat Asn 600	cct Pro 605	tca Ser 605	aat Asn 605	2487
tca Ser 610	ata Ile 610	cta Leu 610	gtt Val 610	caa Gln 610	gaa Glu 610	att Ile 610	aat Asn 615	aat Asn 615	ata Ile 615	agc Ser 615	tac Tyr 615	tat Tyr 615	ttt Phe 620	aat Asn 620	tca Ser 620	2535

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gaa Glu	tat Tyr	aaa Lys	tca Ser 625	ata Ile	gat Asp	tct Ser	ata Ile	caa Gln 630	ttt Phe	gat Asp	aat Asn	att Ile	cct Pro 635	gaa Glu	ata Ile	2583
tta Leu	aaa Lys	ggt Gly 640	aaa Lys	aat Asn	aaa Lys	att Ile	aaa Lys 645	tta Leu	aca Thr	ttt Phe	ata Ile	ggt Gly 650	cat His	gga Gly	gaa Glu	2631
gaa Glu 655	gaa Glu	ttt Phe	aat Asn	aca Thr	gag Glu	aga Arg 660	ttt Phe	gct Ala	tca Ser	tta Leu	aca Thr 665	gta Val	aag Lys	gag Glu	ttt Phe	2679
tca Ser 670	aaa Lys	aaa Lys	ata Ile	tat Tyr	aaa Lys 675	gtt Val	tta Leu	gat Asp	atg Met	ata Ile 680	aag Lys	agc Ser	aat Asn	acg Thr	aat Asn 685	2727
gtt Val	aaa Lys	gaa Glu	att Ile	caa Gln 690	ata Ile	gat Asp	ttg Leu	tta Leu	gga Gly 695	tgt Cys	aat Asn	atg Met	ttt Phe	tca Ser 700	tat Tyr	2775
aat Asn	ata Ile	aat Asn	gta Val 705	gaa Glu	gaa Glu	aca Thr	tat Tyr	cct Pro 710	ggg Gly	aaa Lys	tta Leu	tta Leu	aaa Lys 715	gta Val	gta Val	2823
tta Leu	gat Asp	tat Tyr 720	gta Val	gat Asp	aaa Lys	att Ile	tat Tyr 725	aat Asn	gca Ala	gat Asp	att Ile	aaa Lys 730	cca Pro	gaa Glu	ata Ile	2871
aaa Lys 735	ata Ile	agt Ser	gcc Ala	aat Asn	caa Gln	tat Tyr 740	gaa Glu	gtc Val	aga Arg	ata Ile	aat Asn 745	aaa Lys	gat Asp	ggg Gly	aaa Lys	2919
aaa Lys 750	gaa Glu	tta Leu	cta Leu	tct Ser	cat His 755	tca Ser	gga Gly	gag Glu	tgg Trp	ctt Leu 760	tct Ser	aaa Lys	gaa Glu	gaa Glu	gct Ala 765	2967
ata Ile	ata Ile	aaa Lys	gat Asp	att Ile 770	gca Ala	agt Ser	aaa Lys	gaa Glu	att Ile 775	att Ile	tat Tyr	ttt Phe	gat Asp	aca Thr 780	aga Arg	3015
gaa Glu	aat Asn	act Thr	att Ile 785	aaa Lys	gca Ala	gaa Glu	gct Ala 790	aaa Lys	aat Asn	att Ile	atg Met	gag Glu	ttg Leu 795	ata Ile	act Thr	3063
ttt Phe	aga Arg	aat Asn 800	agt Ser	cta Leu	gat Asp	aaa Lys	aaa Lys 805	tta Leu	aat Asn	gat Asp	tta Leu	gaa Glu 810	agt Ser	tta Leu	att Ile	3111
aat Asn 815	aat Asn	aat Asn	ttt Phe	att Ile	gta Val	aat Asn 820	gaa Glu	gta Val	tat Tyr	gaa Glu	caa Gln 825	tta Leu	aca Thr	tca Ser	aat Asn	3159
aat Asn 830	tta Leu	tat Tyr	aga Arg	aca Thr	agt Ser 835	ttt Phe	aga Arg	aat Asn	tct Ser	ttt Phe 840	tta Leu	gat Asp	act Thr	ata Ile	aat Asn 845	3207
ttt Phe	ata Ile	gaa Glu	gat Asp	gtt Val 850	tct Ser	caa Gln	gag Glu	tta Leu	tat Tyr 855	gaa Glu	ata Ile	aag Lys	ata Ile	aaa Lys 860	aat Asn	3255
aat Asn	ata Ile	aac Asn	gat Asp 865	gat Asp	tat Tyr	atc Ile	atg Met	gca Ala 870	tta Leu	gat Asp	gaa Glu	ata Ile	aag Lys 875	caa Gln	gat Asp	3303
aat Asn	aat Asn	att Ile 880	tca Ser	gaa Glu	att Ile	aaa Lys	ttt Phe 885	att Ile	aat Asn	att Ile	aat Asn	tca Ser 890	gga Gly	gaa Glu	ttt Phe	3351

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agg Arg	gtt Val 895	gta Val	aga Arg	gaa Glu	aat Asn	agt Ser 900	agg Arg	tta Leu	att Ile	aat Asn	aaa Lys 905	ttt Phe	aaa Lys	gaa Glu	gat Asp	3399
ttt Phe 910	aaa Lys	ttt Phe	atg Met	att Ile	aat Asn 915	aat Asn	att Ile	aag Lys	agg Arg	ttg Leu 920	ata Ile	aaa Lys	ttt Phe	agt Ser	gat Asp 925	3447
aat Asn	aac Asn	aag Lys	cta Leu	ata Ile 930	aca Thr	tca Ser	ttt Phe	gaa Glu	tta Leu 935	aag Lys	aat Asn	ata Ile	gag Glu	tca Ser 940	agc Ser	3495
agt Ser	gga Gly	gta Val	agt Ser 945	aca Thr	tta Leu	aat Asn	aca Thr	agt Ser 950	ttt Phe	tta Leu	att Ile	caa Gln	tct Ser 955	atg Met	att Ile	3543
gat Asp	tat Tyr	aaa Lys 960	gcg Ala	caa Gln	aac Asn	ttt Phe	gac Asp 965	ttc Phe	aat Asn	aaa Lys	tta Leu	agt Ser 970	aca Thr	tca Ser	gta Val	3591
aaa Lys 975	gta Val	cag Gln	att Ile	tat Tyr	tgt Cys 980	caa Gln	ata Ile	act Thr	aat Asn	ata Ile	agt Ser 985	tta Leu	tca Ser	gaa Glu	att Ile	3639
caa Gln 990	gat Asp	gct Ala	agt Ser	aat Asn	tta Leu 995	gta Val	aaa Lys	att Ile	ata Ile	gct Ala 1000	gaa Glu	gca Ala	aat Asn	gaa Glu 1005	att Ile	3687
gaa Glu	ata Ile	aat Asn	tta Leu	ata Ile 1010	cca Pro	aca Thr	tta Leu	gca Ala	aat Asn 1015	gct Ala	ata Ile	cca Pro	tta Leu	ata Ile 1020		3732
aca Thr	aca Thr	ata Ile	gtt Val	gat Asp 1025	gga Gly	ata Ile	aat Asn	ttg Leu	att Ile 1030	gca Ala	aat Asn	ata Ile	gat Asp	gaa Glu 1035		3777
tta Leu	ata Ile	aat Asn	act Thr	aaa Lys 1040	gat Asp	gaa Glu	tta Leu	cta Leu	aga Arg 1045	aag Lys	gaa Glu	tta Leu	gca Ala	gct Ala 1050		3822
aga Arg	att Ile	gga Gly	att Ile	att Ile 1055	tca Ser	tct Ser	aat Asn	atg Met	aca Thr 1060	gca Ala	gct Ala	att Ile	agt Ser	tct Ser 1065		3867
tat Tyr	att Ile	tta Leu	tat Tyr	ttt Phe 1070	act Thr	gaa Glu	ttt Phe	gga Gly	gaa Glu 1075	gta Val	ttt Phe	aat Asn	cct Pro	tta Leu 1080		3912
tta Leu	gtg Val	cca Pro	att Ile	gca Ala 1085	ggg Gly	ata Ile	tca Ser	agt Ser	ggg Gly 1090	att Ile	cct Pro	act Thr	tta Leu	gta Val 1095		3957
aat Asn	aat Asn	att Ile	tta Leu	att Ile 1100	tta Leu	gag Glu	gaa Glu	aaa Lys	tct Ser 1105	aaa Lys	gaa Glu	ata Ile	aca Thr	gaa Glu 1110		4002
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gtg Val	tct Ser	gat Asp	aat Asn	aac Asn 1130	agt Ser	ata Ile	ttg Leu	att Ile	cca Pro 1135	ctt Leu	gat Asp	gat Asp	att Ile	gca Ala 1140		4092
att Ile	tct Ser	aag Lys	att Ile	gat Asp 1145	ttt Phe	aat Asn	aaa Lys	aga Arg	gaa Glu 1150	gtt Val	atc Ile	tta Leu	gat Asp	aaa Lys 1155		4137

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tta gat ata tgg gca atg gaa gga gga tca gga tta agt ggt aaa Leu Asp Ile Trp Ala Met Glu Gly Gly Ser Gly Leu Ser Gly Lys 1160 1165 1170	4182
gaa act ttt ttt tct gct ccg tat ata aat gaa aat ctt cct aaa Glu Thr Phe Phe Ser Ala Pro Tyr Ile Asn Glu Asn Leu Pro Lys 1175 1180 1185	4227
tta tct att gat aat ttg ctt aag ata gat ata aat aaa ata gat Leu Ser Ile Asp Asn Leu Leu Lys Ile Asp Ile Asn Lys Ile Asp 1190 1195 1200	4272
ttt tca att aaa ggt atg atg cta cct aat ggc gtt agt aaa aca Phe Ser Ile Lys Gly Met Met Leu Pro Asn Gly Val Ser Lys Thr 1205 1210 1215	4317
tta ggt tat gag ttc aat aca gtt gcc aat ata tat gaa tta gaa Leu Gly Tyr Glu Phe Asn Thr Val Ala Asn Ile Tyr Glu Leu Glu 1220 1225 1230	4362
aat gat ggt gta aat tta tta aat aga att aga gat aat tat cca Asn Asp Gly Val Asn Leu Leu Asn Arg Ile Arg Asp Asn Tyr Pro 1235 1240 1245	4407
gga cag ttt tat tgg aga tat tat gct act cta ttt aat tat ggt Gly Gln Phe Tyr Trp Arg Tyr Tyr Ala Thr Leu Phe Asn Tyr Gly 1250 1255 1260	4452
atg gta aat tta aaa att aat tat cat gac aca gat gta aaa ata Met Val Asn Leu Lys Ile Asn Tyr His Asp Thr Asp Val Lys Ile 1265 1270 1275	4497
aat tta gat aat gtt gat cgt atg ttt ata gta ccg aca tta aca Asn Leu Asp Asn Val Asp Arg Met Phe Ile Val Pro Thr Leu Thr 1280 1285 1290	4542
ata gat caa gct aga gaa aaa ctt tca tat aat ttt aat gga gca Ile Asp Gln Ala Arg Glu Lys Leu Ser Tyr Asn Phe Asn Gly Ala 1295 1300 1305	4587
gga gct aat tat tat ata tac ctt tcg tct caa cca ata aaa ata Gly Ala Asn Tyr Tyr Ile Tyr Leu Ser Ser Gln Pro Ile Lys Ile 1310 1315 1320	4632
ttt att aat ggg act aaa gaa gat aat tgg att ctt aat ata gat Phe Ile Asn Gly Thr Lys Glu Asp Asn Trp Ile Leu Asn Ile Asp 1325 1330 1335	4677
gat att gtt aaa gaa gtt aca att gtt aat aat agt ata gta aga Asp Ile Val Lys Glu Val Thr Ile Val Asn Asn Ser Ile Val Arg 1340 1345 1350	4722
gga aag ttt att gaa aat ata ttt aaa aaa tta act att gag gat Gly Lys Phe Ile Glu Asn Ile Phe Lys Lys Leu Thr Ile Glu Asp 1355 1360 1365	4767
aat aaa ata att ata gga aat caa aaa ata tat tta aaa aat aac Asn Lys Ile Ile Ile Gly Asn Gln Lys Ile Tyr Leu Lys Asn Asn 1370 1375 1380	4812
aaa aca aat ata cat ttt tct gta tct att tta gat gga gtg aat Lys Thr Asn Ile His Phe Ser Val Ser Ile Leu Asp Gly Val Asn 1385 1390 1395	4857
tta atg gta gaa gta gac ttt aat aat aaa atg tat cat tta tca Leu Met Val Glu Val Asp Phe Asn Asn Lys Met Tyr His Leu Ser 1400 1405 1410	4902

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caa Gln	aat Asn	aac Asn	ata Ile	aat Asn 1430	aaa Lys	tta Leu	ttt Phe	ggc Gly	tct Ser 1435	tca Ser	aat Asn	ata Ile	aaa Lys	tca Ser 1440	4992
ata Ile	cca Pro	tat Tyr	ttc Phe	tat Tyr 1445	aaa Lys	aat Asn	aat Asn	gga Gly	tta Leu 1450	gag Glu	aat Asn	tgt Cys	att Ile	gga Gly 1455	5037
gta Val	ttc Phe	tca Ser	ata Ile	aaa Lys 1460	aac Asn	aat Asn	gaa Glu	ttt Phe	att Ile 1465	tat Tyr	atg Met	tta Leu	aaa Lys	tat Tyr 1470	5082
gat Asp	gat Asp	aaa Lys	aat Asn	aaa Lys 1475	ata Ile	tat Tyr	aaa Lys	tat Tyr	aaa Lys 1480	gat Asp	aat Asn	aat Asn	tta Leu	gta Val 1485	5127
tgt Cys	ggg Gly	ttt Phe	aat Asn	tta Leu 1490	ttt Phe	gat Asp	ata Ile	tct Ser	tat Tyr 1495	gta Val	gat Asp	ata Ile	att Ile	tct Ser 1500	5172
aat Asn	gga Gly	gat Asp	aag Lys	aat Asn 1505	tat Tyr	ttg Leu	aaa Lys	gga Gly	att Ile 1510	tgg Trp	aat Asn	aca Thr	tca Ser	gtt Val 1515	5217
aat Asn	aat Asn	tca Ser	gaa Glu	tat Tyr 1520	aaa Lys	att Ile	gaa Glu	ttt Phe	tta Leu 1525	gtt Val	gaa Glu	tta Leu	ata Ile	gac Asp 1530	5262
caa Gln	aat Asn	act Thr	att Ile	gaa Glu 1535	atc Ile	att Ile	aaa Lys	ttg Leu	aat Asn 1540	tta Leu	agt Ser	gat Asp	gga Gly	tta Leu 1545	5307
ata Ile	aaa Lys	tca Ser	ttt Phe	tta Leu 1550	act Thr	ata Ile	tta Leu	gat Asp	aat Asn 1555	tta Leu	gaa Glu	agt Ser	tta Leu	gat Asp 1560	5352
gta Val	aaa Lys	att Ile	tca Ser	aca Thr 1565	ata Ile	tat Tyr	gat Asp	ttt Phe	tta Leu 1570	aaa Lys	aat Asn	att Ile	ctt Leu	ttt Phe 1575	5397
agg Arg	gat Asp	gta Val	ttt Phe	tta Leu 1580	gaa Glu	aat Asn	gag Glu	tca Ser	tta Leu 1585	aat Asn	ttt Phe	att Ile	gta Val	agt Ser 1590	5442
aaa Lys	ggc Gly	ttt Phe	gtt Val	ttg Leu 1595	aca Thr	ggg Gly	aat Asn	aat Asn	tca Ser 1600	aaa Lys	aat Asn	aaa Lys	tac Tyr	gag Glu 1605	5487
ttt Phe	ata Ile	tgt Cys	aat Asn	agt Ser 1610	gaa Glu	aat Asn	ata Ile	caa Gln	tta Leu 1615	tat Tyr	att Ile	act Thr	gaa Glu	ctt Leu 1620	5532
tac Tyr	act Thr	aat Asn	ggg Gly	act Thr 1625	aaa Lys	ttt Phe	agg Arg	aat Asn	tgg Trp 1630	ctt Leu	gac Asp	aat Asn	ggg Gly	aag Lys 1635	5577
ata Ile	tta Leu	gta Val	tca Ser	tca Ser 1640	aca Thr	ggg Gly	gaa Glu	agt Ser	tca Ser 1645	aat Asn	aat Asn	tta Leu	att Ile	gac Asp 1650	5622
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Ser Pro Lys Glu Gly Glu Tyr Lys Lys Ile Leu Glu Leu Leu Asp Glu
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 35 40 45

Leu Lys Leu Asn Glu Leu Ser Lys Ser Ile Asp Ile Tyr Leu Lys Lys
 50 55 60

Tyr Lys Asn Ser Lys Arg Asn Asn Ala Leu Tyr Gln Leu Lys Ser Asp
 65 70 75 80

Leu Thr Lys Glu Val Ile Glu Ile Lys Asp Thr Asn Leu Lys Pro Leu
 85 90 95

Glu Lys Asn Ile His Phe Val Trp Val Gly Gly Met Ile Asn Asn Ile
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Ser Ile Asp Tyr Ile Asn Gln Trp Lys Asp Ile Asn Ser Asp Tyr Glu
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Thr Ile Ile Trp Tyr Asp Ser Glu Ala Leu Leu Val Asn Ile Leu Lys
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Lys Ala Ile Ile Asp Ser Ser Asn Lys Glu Val Leu Thr Lys Tyr Glu
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Ser Val Leu Asn Asp Asn Ser Phe Asp Ser Asn Lys Phe Tyr Arg Glu
 165 170 175

Arg Met Glu Val Ile Phe Arg Lys Gln Lys Glu Phe Asn Asn Tyr Tyr
 180 185 190

Asn Thr Asn Asp Asn Tyr Thr Lys Ser Leu Asn Asp Val Ile Lys Val
 195 200 205

Tyr Leu Ile Glu Lys Tyr Leu Lys Thr Asp Glu Glu Leu Glu Lys Tyr
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Ile Asn Glu Ser Lys Glu Val Phe Lys Ala Asn Gly Ala Lys Asp Ile
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Arg Glu Tyr Asp Ile Leu Asp Asp Val Glu Leu Lys Ser Ile Tyr Glu
245 250 255

Gln Glu Leu Leu Met Arg Phe Asn Leu Ala Ser Ala Ser Asp Ile Ile
260 265 270

Arg Val Ile Val Leu Asn Lys Leu Gly Gly Ile Tyr Leu Asp Val Asp
275 280 285

Val Leu Pro Gly Ile Lys Lys His Ile Phe Lys Asp Ile Asn Lys Pro
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Thr Asn Ile Ser Glu Asn Lys Trp Gln Met Ile Gln Leu Glu Thr Ile
305 310 315 320

Met Lys Tyr Lys Gln Tyr Ile Lys Gly Tyr Thr Glu Asn Ser Phe Lys
325 330 335

Asn Leu Pro Ser Asp Leu Gln Glu Met Leu Gln Glu Lys Val Val Glu
340 345 350

Lys Asn Leu Lys Ser Asp Ile Phe Gln Arg Leu Gly Asp Ile Phe Ile
355 360 365

Ser Glu Leu Asp Thr Lys Ile Ala Phe Met Phe Gly Lys Ile Ala Asn
370 375 380

Gln Val Leu Ile Ser Lys Lys Asn Ser Tyr Ser Leu Asn Leu Ile Ile
385 390 395 400

Asn Gln Ile Lys Asn Arg Tyr Asn Ile Ile Asn Lys Cys Leu Ser Ser
405 410 415

Ala Ile Glu Lys Gly Ser Asn Phe Asn Asn Thr Val Asp Ile Phe Ile
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Gln Gln Leu Asn Glu Phe Tyr Val Asn Glu Gly Phe Phe Val Ser Lys
435 440 445

Val Met Gly Tyr Leu Gly Asp Gly Tyr Met Pro Asp Met Arg Ala Thr
450 455 460

Leu Asn Ile Ser Gly Pro Gly Ile Tyr Thr Ala Ala Tyr Tyr Asp Leu
465 470 475 480

Leu Tyr Phe Asn Glu Arg Ser Leu Asn Pro Gln Ile Leu Gln Glu Asp
485 490 495

Leu Lys Tyr Phe Glu Val Pro Gln Ala Leu Ile Ser Gln Gln Thr Glu
500 505 510

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Gln Glu Ile Asn Ser Ser Trp Thr Phe Asn Gln Val Lys Ser Gln Ile
515 520 525

Glu Tyr Lys Lys Leu Val Glu Lys Tyr Thr Asn Lys Ser Leu Ser Glu
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Asn Asp Lys Leu Asn Phe Asn Glu Asn Lys Ile Ile Asp Lys Val Glu
545 550 555 560

Leu Leu Asn Arg Ile Asn Ser Asn Asn Leu Ile Asn Phe Asp Asp Lys
565 570 575

Glu Tyr Leu Arg Tyr Ile Ile Gln Leu Gln Gly Asp Lys Val Ser Tyr
580 585 590

Glu Ala Ala Ile Asn Leu Phe Ile Lys Asn Pro Ser Asn Ser Ile Leu
595 600 605

Val Gln Glu Ile Asn Asn Ile Ser Tyr Tyr Phe Asn Ser Glu Tyr Lys
610 615 620

Ser Ile Asp Ser Ile Gln Phe Asp Asn Ile Pro Glu Ile Leu Lys Gly
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Lys Asn Lys Ile Lys Leu Thr Phe Ile Gly His Gly Glu Glu Glu Phe
645 650 655

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

Ile Tyr Lys Val Leu Asp Met Ile Lys Ser Asn Thr Asn Val Lys Glu
675 680 685

Ile Gln Ile Asp Leu Leu Gly Cys Asn Met Phe Ser Tyr Asn Ile Asn
690 695 700

Val Glu Glu Thr Tyr Pro Gly Lys Leu Leu Lys Val Val Leu Asp Tyr
705 710 715 720

Val Asp Lys Ile Tyr Asn Ala Asp Ile Lys Pro Glu Ile Lys Ile Ser
725 730 735

Ala Asn Gln Tyr Glu Val Arg Ile Asn Lys Asp Gly Lys Lys Glu Leu
740 745 750

Leu Ser His Ser Gly Glu Trp Leu Ser Lys Glu Glu Ala Ile Ile Lys
755 760 765

Asp Ile Ala Ser Lys Glu Ile Ile Tyr Phe Asp Thr Arg Glu Asn Thr
770 775 780

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

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Ile	Ile	Ser	Ser	Asn	Met	Thr	Ala	Ala	Ile	Ser	Ser	Tyr	Ile	Leu
	1055					1060					1065			
Tyr	Phe	Thr	Glu	Phe	Gly	Glu	Val	Phe	Asn	Pro	Leu	Leu	Val	Pro
	1070					1075					1080			
Ile	Ala	Gly	Ile	Ser	Ser	Gly	Ile	Pro	Thr	Leu	Val	Asn	Asn	Ile
	1085					1090					1095			
Leu	Ile	Leu	Glu	Glu	Lys	Ser	Lys	Glu	Ile	Thr	Glu	Tyr	Phe	Ser
	1100					1105					1110			
His	Ile	Ser	Lys	Val	Glu	Ser	Asp	Gly	Leu	Phe	Lys	Val	Ser	Asp
	1115					1120					1125			
Asn	Asn	Ser	Ile	Leu	Ile	Pro	Leu	Asp	Asp	Ile	Ala	Ile	Ser	Lys
	1130					1135					1140			
Ile	Asp	Phe	Asn	Lys	Arg	Glu	Val	Ile	Leu	Asp	Lys	Leu	Asp	Ile
	1145					1150					1155			
Trp	Ala	Met	Glu	Gly	Gly	Ser	Gly	Leu	Ser	Gly	Lys	Glu	Thr	Phe
	1160					1165					1170			
Phe	Ser	Ala	Pro	Tyr	Ile	Asn	Glu	Asn	Leu	Pro	Lys	Leu	Ser	Ile
	1175					1180					1185			
Asp	Asn	Leu	Leu	Lys	Ile	Asp	Ile	Asn	Lys	Ile	Asp	Phe	Ser	Ile
	1190					1195					1200			
Lys	Gly	Met	Met	Leu	Pro	Asn	Gly	Val	Ser	Lys	Thr	Leu	Gly	Tyr
	1205					1210					1215			
Glu	Phe	Asn	Thr	Val	Ala	Asn	Ile	Tyr	Glu	Leu	Glu	Asn	Asp	Gly
	1220					1225					1230			
Val	Asn	Leu	Leu	Asn	Arg	Ile	Arg	Asp	Asn	Tyr	Pro	Gly	Gln	Phe
	1235					1240					1245			
Tyr	Trp	Arg	Tyr	Tyr	Ala	Thr	Leu	Phe	Asn	Tyr	Gly	Met	Val	Asn
	1250					1255					1260			
Leu	Lys	Ile	Asn	Tyr	His	Asp	Thr	Asp	Val	Lys	Ile	Asn	Leu	Asp
	1265					1270					1275			
Asn	Val	Asp	Arg	Met	Phe	Ile	Val	Pro	Thr	Leu	Thr	Ile	Asp	Gln
	1280					1285					1290			
Ala	Arg	Glu	Lys	Leu	Ser	Tyr	Asn	Phe	Asn	Gly	Ala	Gly	Ala	Asn
	1295					1300					1305			

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Tyr	Tyr	Ile	Tyr	Leu	Ser	Ser	Gln	Pro	Ile	Lys	Ile	Phe	Ile	Asn
1310						1315					1320			
Gly	Thr	Lys	Glu	Asp	Asn	Trp	Ile	Leu	Asn	Ile	Asp	Asp	Ile	Val
1325						1330					1335			
Lys	Glu	Val	Thr	Ile	Val	Asn	Asn	Ser	Ile	Val	Arg	Gly	Lys	Phe
1340						1345					1350			
Ile	Glu	Asn	Ile	Phe	Lys	Lys	Leu	Thr	Ile	Glu	Asp	Asn	Lys	Ile
1355						1360					1365			
Ile	Ile	Gly	Asn	Gln	Lys	Ile	Tyr	Leu	Lys	Asn	Asn	Lys	Thr	Asn
1370						1375					1380			
Ile	His	Phe	Ser	Val	Ser	Ile	Leu	Asp	Gly	Val	Asn	Leu	Met	Val
1385						1390					1395			
Glu	Val	Asp	Phe	Asn	Asn	Lys	Met	Tyr	His	Leu	Ser	Leu	Gln	Gly
1400						1405					1410			
Asn	Glu	Lys	Thr	Ile	Cys	Asn	Asn	Met	Asn	Ile	Ile	Gln	Asn	Asn
1415						1420					1425			
Ile	Asn	Lys	Leu	Phe	Gly	Ser	Ser	Asn	Ile	Lys	Ser	Ile	Pro	Tyr
1430						1435					1440			
Phe	Tyr	Lys	Asn	Asn	Gly	Leu	Glu	Asn	Cys	Ile	Gly	Val	Phe	Ser
1445						1450					1455			
Ile	Lys	Asn	Asn	Glu	Phe	Ile	Tyr	Met	Leu	Lys	Tyr	Asp	Asp	Lys
1460						1465					1470			
Asn	Lys	Ile	Tyr	Lys	Tyr	Lys	Asp	Asn	Asn	Leu	Val	Cys	Gly	Phe
1475						1480					1485			
Asn	Leu	Phe	Asp	Ile	Ser	Tyr	Val	Asp	Ile	Ile	Ser	Asn	Gly	Asp
1490						1495					1500			
Lys	Asn	Tyr	Leu	Lys	Gly	Ile	Trp	Asn	Thr	Ser	Val	Asn	Asn	Ser
1505						1510					1515			
Glu	Tyr	Lys	Ile	Glu	Phe	Leu	Val	Glu	Leu	Ile	Asp	Gln	Asn	Thr
1520						1525					1530			
Ile	Glu	Ile	Ile	Lys	Leu	Asn	Leu	Ser	Asp	Gly	Leu	Ile	Lys	Ser
1535						1540					1545			
Phe	Leu	Thr	Ile	Leu	Asp	Asn	Leu	Glu	Ser	Leu	Asp	Val	Lys	Ile
1550						1555					1560			

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Ser	Thr	Ile	Tyr	Asp	Phe	Leu	Lys	Asn	Ile	Leu	Phe	Arg	Asp	Val
1565						1570					1575			
Phe	Leu	Glu	Asn	Glu	Ser	Leu	Asn	Phe	Ile	Val	Ser	Lys	Gly	Phe
1580						1585					1590			
Val	Leu	Thr	Gly	Asn	Asn	Ser	Lys	Asn	Lys	Tyr	Glu	Phe	Ile	Cys
1595						1600					1605			
Asn	Ser	Glu	Asn	Ile	Gln	Leu	Tyr	Ile	Thr	Glu	Leu	Tyr	Thr	Asn
1610						1615					1620			
Gly	Thr	Lys	Phe	Arg	Asn	Trp	Leu	Asp	Asn	Gly	Lys	Ile	Leu	Val
1625						1630					1635			
Ser	Ser	Thr	Gly	Glu	Ser	Ser	Asn	Asn	Leu	Ile	Asp	Ile		
1640						1645					1650			

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