

10 20 30 40 50 60 70 80  
ATGCCAGTTACAATAAACCACTTCAACTATAACGATCCTATTGATAATAACAACATCATCATGTGGAACCTCCATTTGC  
TACGGTCAATGTTATTTGTTGAAGTTGATATTGCTAGGATAACTATTATTGTTGTAGTAGTACTACCTGGAGGTAAACG  
MetProValThrIleAsnAsnPheAsnTyrAsnAspProIleAspAsnAsnAsnIleIleMetMetGluProProPheAla

90 100 110 120 130 140 150 160  
AAGAGGTACTGGAAGATATTATAAGGCTTTCAAGATCACAGATAGAATTTGGATAATACCAGAAAGATATACTTTTGGTT  
TTCTCCATGACCTTCTATAATATCCGAAAGTTCTAGTGTCTATCTTAAACCTATTATGGTCTTCTATATGAAAACCAA  
ArgGlyThrGlyArgTyrLysAlaPheLysIleThrAspArgIleTrpIleIleProGluArgTyrThrPheGly

170 180 190 200 210 220 230 240  
ATAAACCTGAGGATTTCAATAAGAGTTCCGGTATTTTCAATAGAGATGTTTGTGAATATTATGATCCAGATTACTTAAAT  
TATTTGGACTCCTAAAGTTATTTCTCAAGGCCATAAAAGTTATCTCTACAAACACTTATAACTAGGTCTAATGAATTTA  
TyrLysProGluAspPheAsnLysSerSerGlyIlePheAsnArgAspValCysGluTyrTyrAspProAspTyrLeuAsn

250 260 270 280 290 300 310 320  
ACCAATGATAAGAAGATATCTTCTTACAAACAATGATCAAGTTATTCAATAGAATCAAATCAAACCATTTGGGTGAAA  
TGGTTACTATTCTTCTTATAGAAGAATGTTTGTACTAGTTCAATAAGTTATCTTAGTTTAGTTTGGTAAACCACTTTT  
ThrAsnAspLysLysAsnIlePheLeuGlnThrMetIleLysLeuPheAsnArgIleLysSerLysProLeuGlyGluLys

330 340 350 360 370 380 390 400  
GTTATTAGAGATGATTATCAATGGTATACCTTATCTTGGAGATAGAAGAGTTCCATTAGAAGAGTTTAAACCAAACATTG  
CAATAATCTCTACTAATAGTTACCATATGGAATAGAACCTCTATCTTCTCAAGGTAATCTTCTCAAATTTGTGTTTGTAA  
LeuLeuGluMetIleIleAsnGlyIleProTyrLeuGlyAspArgArgValProLeuGluGluPheAsnThrAsnIle

410 420 430 440 450 460 470 480  
CTAGTGTAACTGTTAATAAGTTAATCAGTAATCCAGTGAAGTGGAGAGAAAGAAAGGTATCTTCGCAAATCTAATAATC  
GATCACATTGACAATTATTCAATTAGTCATTAGGTCCACTTACCTCTCTTCTTCCATAGAAGCGTTTAGATTATTAG  
AlaSerValThrValAsnLysLeuIleSerAsnProGlyGluValGluArgLysLysGlyIlePheAlaAsnLeuIleIle

490 500 510 520 530 540 550 560  
TTTGGTCTGGACCAGTCTAAATGAAAATGAGACTATAGATATAGGTATACAGAATCACTTTGCATCAAGAGAAGGCTT  
AAACCAGGACCTGGTCAAGATTACTTTTACTCTGATATCTATATCCATATGTCTTAGTGAACGTAGTTCTCTCCGAA  
PheGlyProGlyProValLeuAsnGluAsnGluThrIleAspIleGlyIleGlnAsnHisPheAlaSerArgGluGlyPhe

570 580 590 600 610 620 630 640  
TGGAGGTATAATGCAAATGAAATCTGTCCAGAATATGTTAGTGTATTCAATAATGTTCAAGAAAACAAAGGTGCAAGTA  
ACCTCCATATTACGTTTACTTTAAGACAGGTCTTATACAATCACATAAGTTATTACAAGTTCTTTTGTTCACCGTTTAC  
GlyGlyIleMetGlnMetLysPheCysProGluTyrValSerValPheAsnAsnValGlnGluAsnLysGlyAlaSer

650 660 670 680 690 700 710 720  
TATTCAATAGAAGAGTTATTCTCAGATCCAGCCTTGATATTAATGCATGAACCTTATACATGTGTTGCATGGTTTTATAT  
ATAAGTTATCTTCTCCAATAAAGAGTCTAGGTCCGAACATATAATTACGTACTTGAATATGTACACAACGTACCAAATATA  
IlePheAsnArgArgGlyTyrPheSerAspProAlaLeuIleLeuMetHisGluLeuIleHisValLeuHisGlyLeuTyr

730 740 750 760 770 780 790 800  
GGTATCAAAGTCGACGATTTACCAATTTGTTCCAAATGAAAAGAAGTTCTTCATGCAATCTACAGATGCTATACAGGCAGA  
CCATAGTTTCAGCTGCTAAATGGTTAACAAGTTTACTTTTCTTCAAGAAGTACGTTAGATGTCTACGATATGCTCCGTCT  
GlyIleLysValAspAspLeuProIleValProAsnGluLysLysPhePheMetGlnSerThrAspAlaIleGlnAlaGlu

810 820 830 840 850 860 870 880  
AGAACTATATACATTTGGTGGTCAAGATCCAAGTATCATAACTCCTTCTACAGATAAGAGTATCTATGATAAAGTGTGTC  
TCTTGATATATGTAACCACCAAGTTCTAGGTTTCATAGTATTGAGGAAGATGTCTATTCTCATAGATACTATTTCAACAG  
GluLeuTyrThrPheGlyGlnAspProSerIleIleThrProSerThrAspLysSerIleTyrAspLysValLeu

890 900 910 920 930 940 950 960  
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TCTTAAAGTCTCCATATCAACTATCTGAATTTGTTCCAAGATCAAACATATAGTCTAGGATCATAATGTAGTTGTAGATA  
GlnAsnPheArgGlyIleValAspArgLeuAsnLysValLeuValCysIleSerAspProSerIleAsnIleAsnIleTyr

970 980 990 1000 1010 1020 1030 1040  
AAGAATAAGTTAAGGATAAGTACAAGTTCGTTGAAGATTCTGAAGTAAGTATAGTATAGATGTTGAAAGTTTCGATAA  
TTCTTATCAAATTCCTATTTCATGTTCAAGCAACTTCAAGACTTCCATTATCATATCTACAACCTTTCAAAGCTATT  
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1050 1060 1070 1080 1090 1100 1110 1120  
GTTATATAAGAGTTTAAATGTTTCGGTTTCACAGAACTAATATAGCAGAGAAGTATAAGATAAAGACTAGAGCTTCTTACT  
CAATATATTCTCAAATTAAGCCAAAGTGTCTTTGATTATATCGTCTCTTGATATTCTATTTCTGATCTCGAAGAATGA  
LeuTyrLysSerLeuMetPheGlyPheThrGluThrAsnIleAlaGluAsnTyrLysIleLysThrArgAlaSerTyr

1130 1140 1150 1160 1170 1180 1190 1200  
TCAGTGATTCCTTACCACAGTAAAGATCAAGAATCTATTAGATAATGAAATCTATACTATAAGAGGAAGGTTTCAACATA  
AGTCACTAAGGAATGGTGGTCAATTTCTAGTTCTTAGATAATCTATTACTTTAGATATGATATCTCCTTCCAAGTTGTAT  
PheSerAspSerLeuProProValLysIleLysAsnLeuLeuAspAsnGluIleTyrThrIleGluGluGlyPheAsnIle

1210 1220 1230 1240 1250 1260 1270 1280  
TCTGATAAAGATATGGGAAAGAATATAGAGGTCAGAATAAAGCTATCAATAAGCAAGCTTATGAAGAAATCAGCAAGGA  
AGACTATTCTATACCTCTTTCTTATATCTCAGTCTTATTTCGATAGTTATTCGTTTCAAGTACTTCTTTAGTCTGTTCT  
SerAspLysAspMetGluLysGluTyrArgGlyGlnAsnLysAlaIleAsnLysGlnAlaTyrGluGluIleSerLysGlu

1290 1300 1310 1320

GCATTTGGCTGTTTATAAGATACAAATGTGTAAAAGTGTAAATGA  
CGTAAACCGACAAATATTCTATGTTTACACATTTTCACAATTTACT  
HisLeuAlaValTyrLysIleGlnMetCysLysSerValLys\*\*\*