

pExp-His-NusA-TEV

SpeI  
>=====

ATGAATCACCATCACCATCACCATCACCATTCTGGCACTAGTGGCAACAAAGAAATTTTG  
90 100 110 120 130 140  
M N H H H H H H H S G T S G N K E I L

GCTGTAGTTGAAGCCGTATCCAATGAAAAGGCGCTACCTCGCGAGAAGATTTTCGAAGCA  
150 160 170 180 190 200  
A V V E A V S N E K A L P R E K I F E A

TTGGAAAGCGCGCTGGCGACAGCAACAAAGAAAAAATATGAACAAGAGATCGACGTCGGC  
210 220 230 240 250 260  
L E S A L A T A T K K K Y E Q E I D V R

GTACAGATCGATCGCAAAAGCGGTGATTTTGACACTTTCCGTCGCTGGTTAGTTGTTGAT  
270 280 290 300 310 320  
V Q I D R K S G D F D T F R R W L V V D

GAAGTCACCCAGCCGACCAAGGAAATCACCTTGAAGCCGCACGTTATGAAGATGAAAGC  
330 340 350 360 370 380  
E V T Q P T K E I T L E A A R Y E D E S

CTGAACCTGGGCGATTACGTTGAAGATCAGATTGAGTCTGTTACCTTTGACCGTATCACT  
390 400 410 420 430 440  
L N L G D Y V E D Q I E S V T F D R I T

ACCCAGACGGCAAAACAGGTTATCGTGCAGAAAGTGCCTGAAGCCGAACGTGCGATGGTG  
450 460 470 480 490 500  
T Q T A K Q V I V Q K V R E A E R A M V

GTTGATCAGTTCCGTGAACACGAAGGTGAAATCATCACCGCGTGGTGAAGAAAGTAAAC  
510 520 530 540 550 560  
V D Q F R E H E G E I I T G V V K K V N

CGCGACAACATCTCTCTGGATCTGGGCAACAACGCTGAAGCCGTGATCCTGCGCGAAGAT  
570 580 590 600 610 620  
R D N I S L D L G N N A E A V I L R E D

ATGCTGCCGCGTGAAAACCTCCGCCCTGGCGACCGCGTTCGTGGCGTGCTCTATTCCGTT  
630 640 650 660 670 680  
M L P R E N F R P G D R V R G V L Y S V

CGCCCCGAAGCGCGTGGCGCGCAACTGTTCTGTCCTGTTCCAAGCCGGAATGCTGATC  
690 700 710 720 730 740  
R P E A R G A Q L F V T R S K P E M L I

GAAGTGTTCGTTATTGAAGTGCCAGAAATCGGCGAAGAAGTGATTGAAATTAAGCAGCG  
750 760 770 780 790 800  
E L F R I E V P E I G E E V I E I K A A

GCTCGGATCCGGGTTCTCGTGCGAAAATCGCGGTGAAAACCAACGATAAACGTATCGAT  
810 820 830 840 850 860  
A R D P G S R A K I A V K T N D K R I D

CCGGTAGGTGCTTGCCTAGGTATGCGTGGCGCGCGTGTTCAGGCGGTGTCTACTGAACTG  
870 880 890 900 910 920  
P V G A C V G M R G A R V Q A V S T E L

GGTGGCGAGCGTATCGATATCGTCCTGTGGGATGATAACCCGGCGCAGTTCGTGATTAAC  
930 940 950 960 970 980  
G G E R I D I V L W D D N P A Q F V I N

GCAATGGCACCGGCAGACGTTGCTTCTATCGTGGTGGATGAAGATAAACACACTATGGAC  
990 1000 1010 1020 1030 1040  
A M A P A D V A S I V V D E D K H T M D

ATCGCCGTTGAAGCCGTAATCTGGCGCAGGCGATTGGCCGTAACGGTCAGAACGTGCGT  
1050 1060 1070 1080 1090 1100  
I A V E A G N L A Q A I G R N G Q N V R

CTGGCTTCGCAACTGAGCGGTTGGGAACTCAACGTGATGACCGTTGACGACCTGCAAGCT  
1110 1120 1130 1140 1150 1160  
L A S Q L S G W E L N V M T V D D L Q A

AAGCATCAGGCGGAAGCGCACGCAGCGATCGACACCTTACCAAATATCTCGACATCGAC

