

pExp-His-MBP-TEV

SpeI  
>=====

ATGAATCACCATCACCATCACCATCACCATTCTGGCACTAGTGGCAAAATCGAAGAAGGT  
90 100 110 120 130 140  
M N H H H H H H H S G T S G K I E E G  
AAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGCCTCGCTGAAGTCGGTAAG  
150 160 170 180 190 200  
K L V I W I N G D K G Y N G L A E V G K  
AAATTCGAGAAAGATAACCGGAATTAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAG  
210 220 230 240 250 260  
K F E K D T G I K V T V E H P D K L E E  
AAATTCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGAC  
270 280 290 300 310 320  
K F P Q V A A T G D G P D I I F W A H D  
CGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTC  
330 340 350 360 370 380  
R F G G Y A Q S G L L A E I T P D K A F  
CAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCT  
390 400 410 420 430 440  
Q D K L Y P F T W D A V R Y N G K L I A

BglII  
>=====

TACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCG  
450 460 470 480 490 500  
Y P I A V E A L S L I Y N K D L L P N P  
CCAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGC  
510 520 530 540 550 560  
P K T W E E I P A L D K E L K A K G K S  
GCGCTGATGTTCAACCTGCAAGAACCGTACTTACCTGGCCGCTGATTGCTGCTGACGGG  
570 580 590 600 610 620  
A L M F N L Q E P Y F T W P L I A A D G  
GTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAAC  
630 640 650 660 670 680  
G Y A F K Y E N G K Y D I K D V G V D N  
GCTGGCGGAAAGCGGGTCTGACCTTCTGGTTGACCTGATTA AAAACAAACACATGAAT  
690 700 710 720 730 740  
A G A K A G L T F L V D L I K N K H M N  
GCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACC  
750 760 770 780 790 800  
A D T D Y S I A E A A F N K G E T A M T  
ATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACG  
810 820 830 840 850 860  
I N G P W A W S N I D T S K V N Y G V T  
GTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTTCGTTGGCGTGCTGAGCGCAGGT  
870 880 890 900 910 920  
V L P T F K G Q P S K P F V G V L S A G  
ATTGACGCCGCCAGTCCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACATCTGCTG  
930 940 950 960 970 980  
I D A A S P N K E L A K E F L E N Y L L  
ACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAG  
990 1000 1010 1020 1030 1040  
T D E G L E A V N K D K P L G A V A L K  
TCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACAATGGAAAACGCCCG  
1050 1060 1070 1080 1090 1100  
S Y E E E L A K D P R I A A T M E N A Q  
AAAGGTGAAATCATGCCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACT  
1110 1120 1130 1140 1150 1160  
K G E I M P N I P Q M S A F W Y A V R T

GCGGTGATCAACGCCGCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAG  
 1170 1180 1190 1200 1210 1220  
 A V I N A A S G R Q T V D E A L K D A Q

BsaI XhoI  
 >.....===== >=====

ACTAATAGCGGTACCGAAAACCTGTACTTCCAGTGAGACCTTAATTAACCTCGAGCGCATG  
 1230 1240 1250 1260 1270 1280  
 T N S G T E N L Y F Q \* - - - \* - - - -

HindIII  
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GAGCCACCCGCGAGTTCGAAAAATAAGCTTG  
 1290 1300 1310  
 - - - - - - - - - -

#	Enzymes that cut	Frequency	Isoschizomers
	BglII	1	
	BsaI	1	BsaI
	HindIII	1	
	SpeI	1	
	XhoI	1	