



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) *BspLU111 (560)*
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCTACCTGAGATCACCGGTCAACATGTGCTGTACCAAGAGTTTGCCTCGGCTGCTTTGAT

1 M C C T K S L L L A A L M
PshAI (652)
601 GTCAGTGTGCTACTCCACCTCTGCGGCGAATCAGAAGCAGCAAGCAACTTTGACTGTGTCTTGATACACAGACCGTATTCTTCATCCTAAATTTATT

13 S V L L L H L C G E S E A A S N F D C C L G Y T D R I L H P K F I
MscI (719)
PvuII (715) **FspI (781)** **XcmI (790)**
701 GTGGGCTTACACGCGCAGCTGGCCAATGAAAGCTGTGACATCAATGCTATCATCTTTACACAAAAGAAAAGTTGTCTGTGCGCAATCCAAAACAGA

47 V G F T R Q L A N E G C D I N A I I F H T K K K L S V C A N P K Q
MscI (871)
BspLU111 (845) **NheI (865)**
801 CTTGGGTGAAATATATTGTGCGTCTCCTCAGTAAAAAGTCAAGAACATGTAAAACTGTGGCTTGCTAGCTGGCCAGACATGATAAGATACATTGATGA

80 T W V K Y I V R L L S K K V K N M •
901 GTTTGGACAAACCACAACCTAGAATGCAGTGAIAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAA

HpaI (1003) **MfeI (1014)** **EcoRI (1099)**
1001 CAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGG

1101 AATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTT

SapI (1281)
1201 GCCAATGTGCATTAGCTGTTTGAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTGCTTTCATTTCTTTATGT

SspI (1338) **SwaI (1352)**
1301 TTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAATGTTTTTTATTAGGCAGA

EcoO109I (1413)
1401 ATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGC

1501 TTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTTCATCTCAATGAGCACAAGCAGTCAGGAG

141 • N R T Y K L P I L E E I T T K V L K G N M E I L V F C D P A
SacI (1613) **BstXI (1642)**
1601 CATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGT

110 Y D S I L E R C M G C P S V V R I S R D V E D S Y P H R V A V I T
StuI (1777)
1701 GTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCATATGTGGACAGCAGAG

77 D F D K Q G N S V A S G I A I A E A C V T V R G I Y A E I H V A S
1801 ATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTAGTGGCGACCTCCACAGCTCCA

43 I I E G T K T R I A A G V H H K N D E Y L M T I K E T A V E V L E L
BbsI (1923)
XmnI (1919) **AseI (1985)**
1901 GATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAC

10 D Q Q S I N F T K M
SacI (2042)
2001 AGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGG

SpeI (2140)
2101 GGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATGACGTCAATGGGGTGGAGACTTGAAAATCCCGTGGAG

SnaBI (2268)
2201 TCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAAGTCCC

NdeI (2373)

2301 ATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAA

2401 GTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGG

PacI (2559)

PstI (2552)
SdaI (2551) *BspLU11I (2569)*

2501 GGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAG

2601 GAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG

2701 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCC

ApaI (2883)

2801 CTTCCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGT

2901 TCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATT

3001 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGA

3101 AGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACCGG

PacI (3299)

3201 CAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGT

EagI (3319)
Swal (3308) **NotI (3318)**

3301 TAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCA

3401 TCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA