



PvuI (7)
SgfI (6)
MfeI (82) **EcoNI (96)**

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245) **Bsu36I (291)**

201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGGCCCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGTCTTTGTTTCGTTT

KasI (535)
AgeI (552)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCATCATGAATCACACTGTCCAAACCTTCTTCTCTCTGTCAA

1▶ M N H T V Q T F F S P V N

MscI (603)
DraIII (640)
KasI (660) **BsaBI (696)**

601 CAGTGGCCAGCCCCCAACTATGAGATGCTCAAGGAGGAGCACGAGGTGGCTGTGCTGGGGGCGCCCCACAACCTGTCCCCGACGTCCACCGTGATC

13▶ S G Q P P N Y E M L K E E H E V A V L G A P H N P A P P T S T V I

Tth111I (727)

701 CACATCCGACGAGACCTCCGTGCCGACCATGTCGTCTGGTCCCTGTTCAACACCCTTTCATGAACCCTGCTGCCTGGGCTTCATAGCATTGCGCT

47▶ H I R S E T S V P D H V V W S L F N T L F M N P C C L G F I A F A

Bsp120I (845)
Bsp120I (887)

801 ACTCCGTGAAGTCTAGGGACAGGAAGATGGTTGGCGACGTGACCGGGGCCAGGCTATGCCTCCACCCCAAGTGCCTGAACATCTGGGCCCTGATTCT

80▶ Y S V K S R D R K M V G D V T G A Q A Y A S T A K C L N I W A L I L

BstXI (948)
NheI (980)

901 GGGCATCCTCATGACCATTCTGCTCATGCTCATCCAGTGTGATCTTCCAGGCTATGATAGATCAGGAGGCATCACTGCTAGCTGGCCAGACATGAT

113▶ G I L M T I L L I V I P V L I F Q A Y G •

1001 AAGATACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATT

HpaI (1118)
MfeI (1129)

1101 ATAAGCTGAATAAACAAGTTAAACAACAACATTGCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGAGGTTTTTAAAGCAAGTAAACCTCT

EcoRI (1214)

1201 ACAAATGTGGTATGGAATTCTAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAG

SapI (1396)

1301 GCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGATTTTCCAAGGTTTGAAGTACTGCTC

SspI (1453)
SwaI (1467)

1401 TTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAAATTTACAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGT

1501 TTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTAAATAGAATTGGAC

1601 AGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCTCAATGAGCA

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

SacI (1728)
BstXI (1757)

1701 CAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCT

115▶ F C D P A 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

1801 GACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCCTCA

82▶ V A V I T 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

1901 ATGTGGACAGCAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCGACATGGTGTCTGTTGCTCCTCATAGAGCATGGTATCTTCTCAGTGGCGA

48▶ I H V A S 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

BbsI (2038)
XmnI (2034)

2001 CCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGTGATTATACTATGCCGATATACTATGCCGATG

15▶ E V L E L D Q Q S I N F T K M

AseI (2100)
SacI (2157)

2101 ATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCC

SpeI (2255)

2201 CATTTCGCTCAATGGGGCGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTT

SnaBI (2383)

2301 GGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTGCCTGCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTGC

NdeI (2488)

2401 AAGTAGGAAAGTCCATAAGGTCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACAC

2501 TTGATGTAAGTCCAAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATT

PacI (2674)
PstI (2667)
SdaI (2666) BspLU11I (2684)

2601 GACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCIGCAGGTTAAATAAGAACATGTGAGCAAAGG

2701 CCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAG

2801 AGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACC

ApaLI (2998)

2901 TGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGT

3001 GCACGAACCCCCGTTGAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC

3101 ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGGTCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTA

3201 TCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGGTAA

3301 GCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATT

EagI (3434)
PacI (3414) SmaI (3423) NotI (3433)

3401 TTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACT

3501 AACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA