



PvuI (7)
SgfI (6)
MfeI (82)

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552) NcoI (560)

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGGGTTTTGGATCTTAGCAATTCTCACAAATTCTCAT

601 GTATCCACAGCAGCAAAGTTTAGTAAACAATCATGGGCTGGAAAAATGAGGCTTTAATTGTAAGATGTCTAGACAAGGAAAACCTAGTTACACCGTG

13▶ Y S T A A K F S K Q S W G L E N E A L I V R C P R Q G K P S Y T V

Bsu36I (761)
PvuII (788)

701 GATTGGTATTACTCACAACAACAAAAGTATCCCACTCAGGAAAGAATCGTGTGTTTGCCTCAGGCCAACTTCTGAAGTTTCTACCAGCTGCAGTTG

47▶ D W Y Y S Q T N K S I P T Q E R N R V F A S G Q L L K F L P A A V

801 CTGATTCTGGTATTTATACCTGTATTGTGAGAAGTCCACATTTCAATAGGACTGGATATGCGAATGTACCATATATAAAAAACAATCAGATTGCAATGT

80▶ A D S G I Y T C I V R S P T F N R T G Y A N V T I Y K K Q S D C N V

901 TCCAGATTATTTGATGTATTCAACAGTATCTGGATCAGAAAAAATTCAAAATTTATTGTCTACCATTGACCTCTACAACCTGGACAGCACCTCTTGAG

113▶ P D Y L M Y S T V S G S E K N S K I Y C P T I D L Y N W T A P L E

SapI (1018)

1001 TGGTTTAAAGAATTGTCAAGGATCAAGGTACAGGGCGCACAAAGTCATTTTTGGTCATTGATAATGTGATGACTGAGGACGCGAGGTGATTACA

147▶ W F K N C Q A L Q G S R Y R A H K S F L V I D N V M T E D A G D Y

Tth111I (1149)

1101 CCTGTAATTTATACACAATGAAATGGAGCCAATTATAGTGTGACGGCGACCAGGTCCTTACGGTCAAGGATGAGCAAGGCTTTTCTGTGTTCCAGT

180▶ T C K F I H N E N G A N Y S V T A T R S F T V K D E Q G F S L F P V

1201 AATCGAGCCCTGCACAAAATGAAATAAAGGAAGTGGAAATTGGAAAAAACGAAACCTAATTGCTGCTGTTTGGAAAAAGGCACTCAGTTCTTG

213▶ I G A P A Q N E I K E V E I G K N A N L T C S A C F G K G T Q F L

EcoRI (1355)

1301 GCTGCCGTCTGTGGCAGCTTAATGAAACAAAATTACAGACTTTGGTGAACCAAGAATTCAACAAGAGGAAGGGCAAAATCAAAGTTTCAGCAATGGGC

247▶ A A V L W Q L N G T K I T D F G E P R I Q Q E E G Q N Q S F S N G

XbaI (1407)

1401 TGGCTTGTCTAGACATGTTTTAAGAATAGCTGACGTGAAGGAAGAGGATTTATTGCTGCAGTACGACTGTCTGGCCCTGAATTTGCATGGCTTGAGAAG

280▶ L A C L D M V L R I A D V K E E D L L L Q Y D C L A L N L H G L R R

MscI (1566)

NheI (1560)

1501 GCACACCGTAAGACTAAGTAGGAAAAATCCAAGTAAGGAGTGTCTGAGACTATGATCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTG

313▶ H T V R L S R K N P S K E C F •

HpaI (1698)

1601 GACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGT

MfeI (1709)
EcoRI (1794)

1701 TAACAACAACAATTGCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTC

1801 TAAATACAGCATAGCAAACCTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAA

SapI (1976)

1901 TGTGATTAGCTGTTGAGCCTCACCTCTTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGGTTTGAAGTACTGCTTCTTCTTTATGTTTTAA

SspI (2033)
SwaI (2047)

2001 ATGCACTGACCTCCACATTCCTTTTTAGTAAATATTCAGAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCA

2101 GATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTA

2201 GCTTTAGTTCCTGGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAG

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 Y

SacI (2308)
BstXI (2337)

2301 TCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAA

108▶ 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 D F

2401 AGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTACGACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGAT
75 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 I I
2501 CTCGCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCC
42 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 D

BbsI (2618)
XmnI (2614) **AseI (2680)**

2601 TGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGT
8 Q Q S I N F T K M

SacI (2737)

2701 GGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGG

SpeI (2835)

2801 AGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGAGACTTGGAAATCCCGTGAGTCAAA

SnaBI (2963)

2901 CCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAG

NdeI (3068)

3001 GTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGG
3101 CAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCT

PacI (3254)
SdaI (3246) **BspLU11I (3264)**

3201 GTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACC
3301 GTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGG
3401 ACTATAAAGATACCAGGCTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCG

ApaLI (3578)

3501 GGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGTTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGC
3601 CCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
3701 AGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA
3801 GTTACCTTCGAAAAAGAGTTGGTAGCTCTTATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAA

PacI (3994)

3901 AAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATT

EagI (4014)
Swal (4003) **NotI (4013)**

4001 AACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAA
4101 ACAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA