



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

MscI (563)

XcmI (560)

BstEII (555)

AgeI (552) **NcoI (560)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTACCATTGGCCACACTGGTGTCTTCCATGCCCTGCCACTG

1▶ M A T L V L S S M P C H W

SapI (618)
Acc65I (636)
BglII (695)

601 GCTGTTGTTCTGCTGCTCTTCTCAGTGAGCCGGTACCAGCAATGACAAGCAGTGACCTGCCACTGAATTTCCAAGGAAGCCCTGTTCCCGATC

13▶ L L F L L L L F S G E P V P A M T S S D L P L N F Q G S P C S Q I

NcoI (737)
ApaLI (773)

701 TGGCAGCACCCGAGGTTTGCAGCAAAAAGCGGAGCTCCATGGTGAAGTTTACTGCTACACAAACCCTCAGGTGCACTGACCTGGTCCGAAAGCGAG

47▶ W Q H P R F A A K K R S S M V K F H C Y T N H S G A L T W F R K R

801 GGAGCCAGCAGCCCAGGAAGTGGTCTCAGAAGAGGGACGCATTGTGCAGACCCAGAATGGCTCTGTCTACACCCTCACTATCCAAAACATCCAGTACGA

80▶ G S Q Q P Q E L V S E E G R I V Q T Q N G S V Y T L T I Q N I Q Y E

PvuII (960)

901 GGATAATGGTATCTACTTCTGCAAGCAGAAATGTGACAGCGCAACCATAATGTCACCAGCAGCTGTGGCACGGAACCTTAGTCTTAGGATTGACGACG

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

1001 TTGGACCAACTGAAGCGCGGAACACACTGAAAGATGGCATTATCTTGATCCAGACCCTCCTCATCATCTTTCATCATTGTGCCATCTTCTGCTAC

147▶ L D Q L K R R N T L K D G I I L I Q T L L I I L F I I V P I F L L

1101 TTGACAAGGATGACGGCAAGGCTGGGATGGAGGAAGATCACACCTATGAGGGCTTGAACATTGACCAGACAGCCACCTATGAAGACATAGTGACTCTTCG

180▶ L D K D D G K A G M E E D H T Y E G L N I D Q T A T Y E D I V T L R

MscI (1255)

NheI (1249)

1201 GACAGGGAGGTAAGTGGTCCGTAGGAGACATCCAGGCCAGGAATGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACA

213▶ T G E V K W S V G E H P G Q E •

HpaI (1387) **MfeI (1398)**

1301 ACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA

EcoRI (1483)

1401 ATTGCATTCATTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCAAAATGTGGTATGGAATCTAAAATACAGC

1501 ATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGC

SapI (1665)

1601 TGTTTGACGCTCACCTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTGAAGTCTCTTCAATTTCTTATGTTTTAAATGCACTGACC

SspI (1722)
SwaI (1736)
EcoO109I (1797)

1701 TCCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGG

1801 CCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCC

141◀ • N R

1901 TGGTGTACTTGTAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAG

138◀ 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 D S I L

BstXI (2026)

2001 CTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGC

105◀ 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 D K Q

StuI (2161)

2101 CCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCT

71◀ 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 E G T K

2201 TGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGAT

38◀ 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 Q Q S I

XmnI (2303)
AseI (2369)

2301 GTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCT

5◀ N F T K M

2401 CCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGA

2501 CTTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCAC

SpeI (2524)

2601 GCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTG

SnaBI (2652)

2701 GGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGCCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGT

NdeI (2757)

2801 AAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTC

2901 AGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC

PacI (2943)
PstI (2936)
SdaI (2935) BspLU11I (2953)

3001 GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGAT

3101 ACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGC

3201 GCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGC

ApaLI (3267)

3301 GCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG

3401 TAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGG

3501 AAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCT

3601 CAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAAT

PacI (3683) SmaI (3692)

3701 CAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAA

EagI (3703)
NotI (3702)

3801 CAAAACAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA