



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGGC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) BspHI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTATCATGACCAAGCCGGTAGCAAGGGCGGGAACCTCCGCGA

1▶ M T K A G S K G G N L R D

601 CAAGCTGGACGGCAACGAACTGGACCTGAGCCTCAGCGACCTGAATGAGGTCCCGTGAAGGAGTTGGCTGCCCTTCAAAGGCCACCATCTGGATCTG

13▶ K L D G N E L D L S L S D L N E V P V K E L A A L P K A T I L D L

BstXI (683)

DraIII (748)
BstAPI (783)

701 TCTTGAATAAACTGACTACTCTACCGTCGATTTCTGTGGCCTCACACACCTGGTGAAGCTAGACCTGAGTAAGAACAAGCTGCAGCAGCTGCCAGCAG

47▶ S C N K L T T L P S D F C G L T H L V K L D L S K N K L Q Q L P A

BstEII (852)

801 ACTTTGGCCGTCTGGTCAACCTCCAGCACCTGGATCTCCTCAACAACAAGCTGGTCACTTGCCTGTGCTGAGCTTTGCTCAGCTCAAGAACCTGAAGTGTT

80▶ D F G R L V N L Q H L D L L N N K L V T L P V S F A Q L K N L K W L

BamHI (921) MscI (932)

901 GGACCTGAAGGATAACCCCTGGATCCTGTCTGGCCAAGGTGGCAGGTGACTGCTTGGATGAGAAGCAGTGAAGCAGTGTGCAAACAAGGTGTTACAG

113▶ D L K D N P L D P V L A K V A G D C L D E K Q C K Q C A N K V L Q

BsrBI (1027)

1001 CACATGAAGGCCGTGCAGGCAGATCAGGAGCGGAGAGGCAGCGGGCTGGAAGTAGAACGTGAGGCAGAGAAGAAGCGTGAGGCTAAGCAGCGAGCTA

147▶ H M K A V Q A D Q E R E R Q R R L E V E R E A E K K R E A K Q R A

BsrBI (1111)

1101 AGAAGCTCAGGAGCGGAACTGCGGAAGCGGAGAAGGCGGAAGAGAAGGAGCGCCGGAGAAGGAGTATGATGCCCTCAAAGCAGCCAAGCGGGAGCA

180▶ K E A Q E R E L R K R E K A E E K E R R R K E Y D A L K A A K R E Q

1201 GGAGAAGAAACCTAAGAAGGAAGCAAATCAGGCCCGAAATCTAAGTCTGGCTCCCGTCCCGCAAGCCACCACCCCGAAGCACACTCGTTCCTGGGCT

213▶ E K K P K K E A N Q A P K S K S G S R P R K P P P R K H T R S W A

1301 GTGCTGAAGCTGCTGCTGCTGCTGCTGCTATTTGGTGTGGCGGAGGGCTGGTTGCTTGTGCGGTGACAGAGCTGCAGCAGCAGCCCTCTGCACCAGCG

247▶ V L K L L L L L L L F G V A G G L V A C R V T E L Q Q Q P L C T S

MscI (1496)

NheI (1490)

1401 TGAACACCATCTATGACAATGCGGTCCAGGGTCTACGCCCATGAGATCCTCCAGTGGGTCTCCAGACCGACTCTCAGCAGTGAGCTTGCTAGCTGGC

280▶ V N T I Y D N A V Q G L R R H E I L Q W V L Q T D S Q Q • -

1501 CAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATT

HpaI (1628) MfeI (1639)

1601 TGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGGGAGTTTTTTAAAGCAAG

EcoRI (1724)

1701 TAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAA

1801 TAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTCCCAAGGTTT

SapI (1906)
SspI (1963)
SwaI (1977)

1901 GAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGA

2001 AAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGGACTTAGGGAACAAGGAACCTTTAATA

2101 GAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATC

141▶ • N R T Y K L P I L E E I T T K V L K G N M

SacI (2238)
BstXI (2267)

2201 TCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGT

118▶ E I L V 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

2301 AGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTTCAGCACAGACAGTACCCTGCCAAT

85▶ P H R 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

StuI (2402)
 2401 GTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTC
 52 Y A E 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

BbsI (2548)
XmnI (2544)
 2501 TCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATAC
 18 E T A V E V L E L D Q Q S I N F T K M

AseI (2610) **SacI (2667)**
 2601 TATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACAC

SpeI (2765)
 2701 GCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGG

SnaBI (2893)
 2801 GTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAG

NdeI (2998)
 2901 ATGTACTGCCAAGTAGGAAAGTCCATAAAGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCA
 3001 TATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATA

PacI (3184) **SdaI (3176)** **BspLUIII (3194)**
 3101 CGTCATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGT
 3201 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACG
 3301 CCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTT
 3401 ACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGC

ApaLI (3508)
 3501 TGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAAGTCCAACCCGGTAAGACACGACTTATCGCCACT
 3601 GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCCTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA
 3701 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTT
 3801 TTGTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCAGC

EagI (3944) **PacI (3924)** **Swal (3933)** **NotI (3943)**
 3901 TTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTG
 4001 AATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCT
 4101 CTATCGAA