



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

1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552) **NcoI (560)**
Bsp120I (589)

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCCGCCGACATCAGCCAGTGGGCCGGCCCTTGTG

1 ▶ M A A D I S Q W A G P L C

BstAPI (627) **SalI (640)**

601 CTTGACGAGGTGGACGAGCCGCCCCAGCACGCCCTGCGGGTGCAGTACGCCGGGTGACGGTGGACGAGCTGGGCAAAGTGCTAACGCCACCCAGGTT

13 ▶ L Q E V D E P P Q H A L R V D Y A G V T V D E L G K V L T P T Q V

BamHI (792)

701 ATGAACAGGCCAGCAGCATTTTCATGGACGGCCTTGTCTGGGAACTCTACACCTGGTCTCACAGACCCGATGCTCCAGCAGGAAGATCCCA

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

801 AATTCAGGGAGTGGCACCCTTCTGGTGGTCAACATGAAGGGTAATGACATTAGCAGTGGCACTGCTCTCAGATTATGTGGGCTCCGGGCTCCAG

80 ▶ K F R E W H H F L V V N M K G N D I S S G T V L S D Y V G S G P P S

901 TGGCACAGGTCTCCACCGCTATGCTGGCTGGTGTACGAGCAGGAACAGCCGCTGAGCTGCGACGAGCCATTCTCAGCAACAAGTCTGGAGACAATCGC

113 ▶ G T G L H R Y V W L V Y E Q E Q P L S C D E P I L S N K S G D N R

BbrPI (1059)

1001 GGCAAGTCAAGTGGAGACCTTCCGCAAGAAGTATAAAGTGGGAGCCCGGTGGCGGGCACGTGCTACCAAGCCGAGTGGGATGACTATGTCCCAAGC

147 ▶ G K F K V E T F R K K Y N L G A P V A G T C Y Q A E W D D Y V P K

MscI (1143)

PvuII (1108)
NheI (1137)

1101 TGTACGAGCAGCTGTGAGGAAGTAGGGTGTGCACGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAG

180 ▶ L Y E Q L S G K •

HpaI (1275) **MfeI (1286)**

1201 TGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACCTGCAATTCATT

EcoRI (1371)

1301 TTATGTTTCAGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTT

1401 TAACCTCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCT

SapI (1553)

1501 CACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAACCTAGCTCTTCATTCTTTATGTTTAAATGCACTGACCTCCCACATCCC

SspI (1610)
SwaI (1624)

1601 TTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATA

1701 TCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTACTTGA

141 ▶ • N R T Y K L

SacI (1885)

1801 GGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAAGGATAGTCAAGATGAGCTCTCTGCACAT

134 ▶ 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 E R C M

BstXI (1914)

1901 GCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTACA

101 ▶ 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 G N S V

StuI (2049)

2001 GCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGG

67 ▶ 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 T R I A

BbsI (2195)

XmnI (2191)

2101 CCGCCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTT

34 ▶ 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 N F T K

AseI (2257)

2201 CATGGTGGCCCTCCTATAGTGTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTG

1 ▶ M

2301 **SacI (2314)**
 ACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAG

2401 **SpeI (2412)**
 TCCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGT

2501 **SnaBI (2540)**
 ACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCA

2601 **NdeI (2645)**
 GGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTACCGTAAATACTCCACC

2701 CATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGAAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGC

2801 **PstI (2824)** **SdaI (2823)** **PaeI (2831)** **BspLU11I (2841)**
 CATTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCG

2901 TTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTC

3001 CCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAG

3101 **ApaLI (3155)**
 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGT

3201 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA

3301 CAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGG

3401 TAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCT

3501 **EagI (3591)** **PaeI (3571)** **SwaI (3580)** **NotI (3590)**
 TTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAA

3601 TAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTA

3701 GCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA