



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

1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGGC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

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

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGCGGCGCTGCTGCTGGCGCTGGCCTTCAGCT

601 CTTGAGCGGCAAGGCGCTGCGCGGCGGGCACCATCAAACCTCTGTCCAGGAAGTCAACTCCTAACACAGCTTACCTGCTCTTTGAACAGCAGT

130 ▶ L S G Q G A C A A A G T I Q T S V Q E V N S K T Q L T C S L N S S

MscI (714) **PstI (745)**

701 GGC GTT GAC ATCG TTGGCCACCGCTGGATGAGAGGTGGCAAGTACTGCAGGAGGACACTCTGCCGACCTGCATACGAAGTACATAGTGGACGCAGATG

47 ▶ G V D I V G H R W M R G G K V L Q E D T L P D L H T K Y I V D A D

SspI (812)

801 ACCGCTCTGGGAATATTCCTGCATCTTCTTCTGAGCCTGTGGCAGAAGCGAGATCAATGTGGAAGGGCCACCCAGGATCAAGGTCGAAAGAAATC

80 ▶ D R S G E Y S C I F L P E P V G R S E I N V E G P P R I K V G K K S

NsiI (947)

901 AGAGCATTCCAGTGAGGGAGAGCTTGCAAACTGGTCTGCAAGTCCGATGCATCCTACCCTCTATTACAGATTGGTCTGGTTTAAACCTCTGACACT

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

PvuII (1075)

1001 GGGGAAGAAGAGGCAATACCAATAGCACTGAAGCCAATGGCAAGTATGTGGTGGTATCCACGCTGAGAAGTACAGCTGACCATCAGAACCTTGACG

147 ▶ G E E E A I T N S T E A N G K Y V V V S T P E K S Q L T I S N L D

DraIII (1169)

1101 TAAATGTTGACCCTGGCACCTACGTGTGTAATGCCACCAACGCCAGGGCACTACTCGGAAACCATCTCACTGCGTGTGCGGAGCCGCATGGCAGCCCT

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

AvrII (1209) **EcoO109I (1226)** **BstEII (1239)**

1201 CTGGCCCTTCTAGGCATCGTGGCTGAGGTCTGTTGTTGTTACCATCATCTTTATCTATGAGAAGAGGGGGAAGCCAGACCAGACCCTGGACGAGGAT

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

XcmI (1376)
BstXI (1376) **NheI (1399)**

1301 GACCTGGCGCCGCCCACTGAAGGGCAGTGGAACTCACATGAATGACAAGGACAAGAATGTACGCCAGAGGAACGCCACCTGAGTGGTGGGGCAGGCGG

247 ▶ D P G A A P L K G S G T H M N D K D K N V R Q R N A T •

MscI (1405)

1401 CTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTAT

HpaI (1537) **MfeI (1548)**

1501 TGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTT

EcoRI (1633)

1601 TAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTG

1701 AGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTGTATTTTC

SapI (1815) **SspI (1872)** **SwaI (1886)**

1801 CCAAGTTTGAAGTCTCTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCA

EcoO109I (1947)

1901 TTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAA

2001 CCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCTGGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTG

SacI (2147) **BstXI (2176)**

2101 CCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCT

121 ▶ G N M 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

2201 CATCAGATAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTCAC

88 ▶ D S Y 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

2301 **StuI (2311)**
CCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTCTTGTGTCCATAGAGCATG
55 R G I 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

2401 **BbsI (2457)**
XmnI (2453)
GTGATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCCTATAGTGAGTGTATTATACTATG
21 T I K E T A V E V L E L D Q Q S I N F T K M

2501 **AseI (2519)** **SacI (2576)**
CCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCC

2601 **SpeI (2674)**
ACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGAC
2701 GTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCAGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACT

2801 **SnaBI (2802)**
AATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCACTGACTGGGCATAATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCG

2901 **NdeI (2907)**
TACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTAT

3001 **PacI (3093)**
PstI (3086)
SdaI (3085)
GGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCTTGGGCGGTCAGCCAGCGGGCCATTTACCCTAAGTTATGTAACGCTGCAGGTTAAITTA

3101 **BspLU1II (3103)**
AGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAA

3201 AAATCGACGCTCAAGTCAAGTCAAGGTTGGCGAAACCCGACAGGACTATAAAGATACCAGGCTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACC

3301 CTGCCGTTACC GGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTT

3401 **ApaLI (3417)**
GCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGTGCCTTATCCGGTAACTATCGTCTTGTGAGTCCAACCCGGTAAGACACGACTT

3501 ATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACT

3601 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGTGGTAGCG

3701 GTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGA

3801 **EagI (3853)**
PacI (3833) **Swal (3842)** **NotI (3852)**
AAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTT

3901 TTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAG

4001 AACATTTCTCTATCGAA