



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCGATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245)
Bsu36I (291)
PvuII (239)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGGC
301 GCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspHI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTATCATGAGGTCACCTTCAGATGCTGCTCCTGGCTGCTCTGCT
1▶ M R S L Q M L L L A A L L

SphI (618)
PstI (613) **XhoI (632)**
601 TCTGGGACTTTTTCTGCAGCATGCCAGAGCTGCTCGAGCCACCAATGTAGGCCGAGAGTGTGCTGCTGGATTACTTCAAAGGGGCCATTCTATCAGGAAG
13▶ L G T F L Q H A R A A R A T N V G R E C C L D Y F K G A I P I R K
BspLU11I
701 TTGGTGAGCTGGTATAAGACCTCAGTGGAGTGTCCAGGGATGCCATCGTGTCTGACTGTCCAGGGCAAGCTCATCTGTGCAGACCCAAAGACAAC
47▶ L V S W Y K T S V E C S R D A I V F L T V Q G K L I C A D P K D K

BstXI (812) **NheI (863)**
801 ATGTGAAGAAGCCATCAGATTGGTAAAAACCAAGGCCATGACCTTCCCGTGAAGCATTGCTAGCTGGCCAGACATGATAAGATAACATTGATGAGT
80▶ H V K K A I R L V K N P R P •
901 TTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACA

HpaI (1001) **MfeI (1012)** **EcoRI (1097)**
1001 AGTTAACAAACAATTCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAA
1101 TTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGC

SapI (1279)
1201 CAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGAGTAAAGATATAGTGTATTTCCCAAGGTTTGAAGTAGCTTTCATTCTTTATGTTT

SspI (1336) **SwaI (1350)**
1301 TAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAAT

EcoO109I (1411)
1401 CCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTT
1501 CTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCA
—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

SacI (1611) **BstXI (1640)**
1601 TAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGT
109▶ 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 P H R V A V I T D

StuI (1775)
1701 CAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGAT
76▶ F 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
1801 GATCTCCCGAGTCTGGTCTGATGGCCGCCCCGACATGGTGTCTGTTGTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACTCCACCAGCTCCAGA
43▶ I 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

BbsI (1921)
XmnI (1917) **AseI (1983)**
1901 TCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAG
9▶ D Q Q S I N F T K M

SacI (2040)
2001 CGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGG

SpeI (2138)
2101 CGGAGTTGTTACGACATTTTGGAAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTC

SnaBI (2266)
2201 AAACCGCTATCCACGCCATTGATGACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCAT

NdeI (2371)

2301 AAGGTCATGTA CTGGCATAATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTA CTGCCAAGT

2401 GGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGG

PacI (2557)
PstI (2550)
SdaI (2549) BspLU11I (2567)

2501 GTCGTTGGGCGGT CAGCCAGCGGGCCATTTACCGTAAGTTATGTAACG CTGCAGGTTAAT TAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGA

2601 ACCGTA AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGAC

2701 AGGACTATAAAGATAACCAGGCGTTTCCCCTGGAAAGCTCCCTCGTGGCTCTCTGTTCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCT

ApaLI (2881)

2801 TCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCC

2901 AGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG

3001 CAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAG

3101 CCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCA

PacI (3297)

3201 GAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTA

EagI (3317)
SwaI (3306) **NotI (3316)**

3301 ATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATC

3401 AAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA