



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGCTCAACTCTACGCTTTTGTTCGTTT

NgoMIV (441)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTTCATGATCTTCTCCTGCTAATGTTGAGCCTGGAATTGCA

1 M I F L L L M L S L E L Q

Bsu36I (637) **BsrGI (647)**
601 GCTTACCAGATAGCAGCTTTATTACAGTGACAGTCCCTAAGGAAGTGTACATAATAGAGCATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACT

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

DraIII (764) **BstXI (779)**
701 GGAAGTCATGTGAACCTTGAGCAATAACAGCCAGTTTAAAAAGGTGGAAAATGATACATCCCCACACCGTAAAGAGCCACTTTGCTGGAGGAGCAGC

47 G S H V N L G A I T A S L Q K V E N D T S P H R E R A T L L E E Q

AvrII (804) **NsiI (864)**
801 TGCCCTAGGGAAGGCTCGTTCCACATACCTCAAGTCCAAGTGAAGGACGAAGGACAGTACCAATGCATAATCATCTATGGGGTCGCTGGGACTACAA

80 L P L G K A S F H I P Q V Q V R D E G Q Y Q C I I I Y G V A W D Y K

HindIII (920)
901 GTACCTGACTCTGAAAGTCAAAGCTTCTACAGGAAAAATAAACTCACATCCTAAAGGTTCCAGAAAACAGATGAGGTAGAGCTCACCTGCCAGGCTACA

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

BstEII (1086)
1001 GGTATCCTCTGGCAGAAGTATCCTGGCCAAACGTGAGCGTTCTGCCAACACCAGCCACTCCAGGACCCCTGAAGGCTCTACCAAGTCCACAGTGTTCC

147 G Y P L A E V S W P N V S V P A N T S H S R T P E G L Y Q V T S V

BbrPI (1153)
1101 TCGCCTAAAGCCACCCCTGGCAGAACTTACAGTGTGTGTTCTGGAATACTCACGTGAGGGAACCTACTTTGGCCAGCATTGACCTCAAAGTCAGAT

180 L R L K P P P G R N F S C V F W N T H V R E L T L A S I D L Q S Q M

1201 GGAACCCAGGACCCATCAACTTGGCTGCTTACATTTTATCCCCTCTGTCATATTGCTTTTATTTTATAGCCACAGTATAGCCCTAAGAAAACAA

213 E P R T H P T W L L H I F I P S C I I A F I F I A T V I A L R K Q

NheI (1397)
1301 CTCTGTCAAAGCTGATTCTTCAAAGACACAACAAAAGACCTGTACCACAACAAAGAGGGAAGTGAACAGTGTATCTGAACTGTGGTCTTGGCT

247 L C Q K L Y S S K D T T K R P V T T T K R E V N S A I •

1401 AGCTGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTG

HpaI (1535) **MfeI (1546)**
1501 CTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAACCAATTGCATTCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGTTTTTTA

EcoRI (1631)
1601 AAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAG

1701 GGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCC

SapI (1813) **SspI (1870)** **SwaI (1884)**
1801 AAGGTTTGAACCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATCCCTTTTTAGTAAAATATTAGAAAATAATTTAAATACATCATT

1901 GCAATGAAAATAAATGTTTTTATTAGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACC

2001 TTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGGC

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

BstXI (2174)
2101 ATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCA

121 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 TCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCAGCAGACCCAATGGCAATGGCTTACGACAGACAGTGAACC

87 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 R

2301 TGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGCTCATAGAGCATGGT

54 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 T

BbsI (2455)
XmnI (2451)
2401 GATCTTCTCAGTGGGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCC

21 I K E T A V E V L E L D Q Q S I N F T K M

2501 **AseI (2517)**
GATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCAC

2601 **SpeI (2672)**
CGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCCATTGACGT

2701 CAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAA

SnaBI (2800)
2801 TACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTA

NdeI (2905)
2901 CTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGG

PacI (3091)
PstI (3084)
SdaI (3083)
3001 GAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGAGGTTAATTAAG

BspLU11I (3101)
3101 AACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAA

3201 ATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCT

3301 GCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCG

ApaLI (3415)
3401 TCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTAT

3501 CGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG

3601 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGT

3701 GGTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAA

EagI (3851)
PacI (3831) **SwaI (3840)** **NotI (3850)**
3801 ACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGTTTTT

3901 TTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAACAAACAAACAACTAGCAAATAGGCTGTCCCCAGTGCAGGTGCAGGTGCCAGAA

4001 CATTCTCTATCGAA