



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCGCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspHI (568)**
501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTAGGAGGCCATCATGAGTGATTCTAAGGAAATGGGGAAGAGG
1 M S D S K E M G K R
XcmI (671) **DraIII (698)**
601 CAGCTTCGCCCTCTGGATGAGGAACTGCTGACATCCAGCCACACCAGGCACTCCATCAAAGGCTTTGGCTTCCAAACAAATTCTGGATTCAGTAGCTTCA
11 Q L R P L D E E L L T S S H T R H S I K G F G F Q T N S G F S S F

PstI (735)
701 CAGGGTGCCTGGTCCACAGTCAAGTCCCTTGGCACTGACGGTCTTCTCTAGCTGTTTGTCTGTGCTGCTGGTTGTCATCCTTGTCAAAGTCTACAA
44 T G C L V H S Q V P L A L Q V L F L A V C S V L L V V I L V K V Y K

XcmI (854) **BsrBI (884)**
801 AATACCCAGTTCTCAGGAAGAAAACAATCAGATGAATGTCTACCAAGAACTGACCCAGTTGAAGGCTGGCGTAGATCGACTGTGCCGCTCCTGCCCTGG
77 I P S S Q E E N N Q M N V Y Q E L T Q L K A G V D R L C R S C P W

DraIII (978)
901 GACTGGACGCACTTCCAAGGAAGCTGTTACTTCTCTGTGGCCAGAAGTCTGGAATGATTCTGCCACTGCCTGCCACAATGTGGGGGCTCAACTTG
111 D W T H F Q G S C Y F F S V A Q K S W N D S A T A C H N V G A Q L
1001 TGGTCATCAAGAGTGATGAAGAGCAGAACCTTCTACAACAACTTCTAAGAAGAGAGGCTACACTTGGATGGGCTCATTGACATGAGCAAGGAGTCTAC
144 V V I K S D E E Q N F L Q Q T S K K R G Y T W M G L I D M S K E S T

BspHI (1138) **BbsI (1182)**
1101 ATGGTACTGGGTAGATGGTTACCTCTGACTCTCAGTTTCATGAAGTATTGGAGTAAAGGAGAACCTAACACCTGGGAGAGGAAGACTGTGCAGAGTTC
177 W Y W V D G S P L T L S F M K Y W S K G E P N N L G E E D C A E F

HindIII (1257) **MscI (1287)**
1201 AGAGATGACGGCTGGAATGACACCAAATGACTAACAAGAAATCTGGATCTGCAAAAAGCTTTCAACTTCTGCCCTAGCAAGTGATGGCCAACTCCCT
211 R D D G W N D T K C T N K K F W I C K K L S T S C P S K •

MscI (1331)
1301 CCACCATCTCCACAGTCCCAAAACCGTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGC

HpaI (1463) **MfeI (1474)**
1401 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCTTTTATGTTTCAGG

EcoRI (1559)
1501 TTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTCAAATACAGCATAGCAAACTTTAACCTCCAAT
1601 CAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCA

SspI (1798)
1701 TGGAGTTTAAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCAGTACCTCCACATTCCCTTTTATAGTAAAA

SwaI (1812) **EcoO109I (1873)**
1801 TATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTA
1901 GTAGTTGGACTTAGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTT
141 • N R T Y K L P I L E

SacI (2073)
2001 CCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAAGATGAGCTCTCTGCACATGCCACAGGGGCT
130 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 G C P S
BstXI (2102)
2101 GACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATG
97 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 A S G I

StuI (2237)
2201 GCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCCGACAT
63 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 A G V H

BbsI (2383) **XmnI (2379)**
2301 GGTGCTTGTTCCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCT
30 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 M

AseI (2445)
2401 CCTATAGTGAAGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAA

2501 ^{SacI (2502)} ACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCC GTTGATTT

2601 ^{SpeI (2600)} ACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACC
←

2701 ^{SnaBI (2728)} GCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA CTGCAAGTAGGAAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTT

2801 ^{NdeI (2833)} ACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGTACTGCAAGTGGGCAGTTTACC GTAAATACTCCACCCATTGACGTCAA

2901 TGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGT CATTATTGACGTCAATGGGGGGGGTCTTTGGCGGTTCAGCCAGGCGGGCCATTTACC GTAA

3001 ^{PacI (3019)} ^{PstI (3012)} ^{SdaI (3011)} ^{BspLU11I (3029)} GTTATGTAACGCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGG

3101 CTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCT

3201 CCCTCGTGCCTCTCTGTTCGACCCTGCCGCTTACCGGATACTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG

3301 ^{ApaLI (3343)} GTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTT CAGCCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT

3401 GAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGATTCTTGA

3501 AGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTTTGATC

3601 CGCAAACAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT

3701 ^{PacI (3759)} ^{Swal (3768)} ^{EagI (3779)} ^{NotI (3778)} ACGGGGTCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTT

3801 ATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCT

3901 GTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA