



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGCTAGGTAAGTTAAAGCTCAGGTCGAGACC

NgoMI (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **SphI (560)**
501 TCTGTTCTGCGCGGTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTGACGATGCCCTCAACGTGAACCTCACCAACAGGAACATGA 1 M P L N V N F T N R N Y D

601 CCTCGACTACGACTCCGTACAGCCCTATTTTCATCTGCGACGAGGAAGAGAATTTTCATCACAGCAACAGCAGAGCGAGCTGCAGCCGCCCGCCAGT 13 L D Y D S V Q P Y F I C D E E E N F Y H Q Q Q Q S E L Q P P A P S

EcoRV (703)
701 GAGGATATCTGGAAGAAATTCGAGCTGCTTCCACCCCGCCCTGTCCCGAGCCGCGCTCCGGGCTGCTCTCCATCCTATGTTGCGGTGCGTACGT 47 E D I W K K F E L L P T P P L S P S R R S G L C S P S Y V A V A T

801 CCTTCTCCCAAGGAAGACGATGACGGCGGGTGGCAACTTCCACCGCGATCAGCTGGAGATGATGACCGAGTTACTTGGAGGAGACGGTGA 80 S F S P R E D D D G G G G N F S T A D Q L E M M T E L L G G D M V N

901 CCAGAGCTTCATCTGCGATCCTGACGACGAGACCTTCAAGAACATCATCATCCAGACTGTATGTGGAGCGGTTTCTCAGCCGCTGCCAAGCTGGTC 113 Q S F I C D P D D E T F I K N I I I Q D C M W S G F S A A A K L V

BssHII (1027) **SacII (1059)** **SdaI (1095)**
1001 TCGGAGAAGCTGGCCTCCTACCAGGCTGCGCGCAAAGACAGCACCAGCCTGAGCCCGCCGCGGGCACAGCTGCTCCACCTCCAGCCTGTACTGC 147 S E K L A S Y Q A A R K D S T S L S P A R G H S V C S T S S L Y L

1101 AGGACCTCACCGCCGCGCTCCGAGTGCATTGACCCCTCAGTGGTCTTTCCCTACCCGCTCAACGACAGCAGCTCGCCAAATCCTGTACTCTGTCGGA 180 Q D L T A A A S E C I D P S V V F P Y P L N D S S S P K S C T S S D

1201 TTCCACGGCTTCTCTCCTTCTCGACTCGCTGCTGTCTCCGAGTCTCCACAGGCGCCAGCCTGAGCCCTAGTGTGATGAGGAGACACCGCC 213 S T A F S P S D S L S L S E S S P R A S P E P L V L H E T P P

1301 ACCACAGCAGCGACTCTGAAGAAGAGCAAGAAGATGAGGAAGAATTTGATGTGTGTCTGTGGAGAAGAGGCAAAACCTGCCAAGAGGTCGGAGTCGG 247 T T S S D S E E E Q E D E E E I D V V S V E K R Q T P A K R S E S

1401 GCTCATCTCCATCCGAGGCCACAGCAAACCTCCGACAGCCACTGGTCTCAAGAGGTGCCAGTCTCCACTCACCAGCACAACCTACGCCGACCCCC 280 G S S P S R G H S K P P H S P L V L K R C H V S T H Q H N Y A A P P

1501 CTCACAAGGAAGACTATCCAGTCCCAAGAGGGCCAAAGTTGGACAGTGGCAGGCTCTGAAGCAGATCAGCAACAACCGCAAGTGTCCAGCCAG 313 S T R K D Y P A A K R A K L D S G R V L K Q I S N N R K A C S S P R

1601 TCCTCAGACACGGAGGAAAACGACAAGAGGCGGACACACAACGTCTTGAACGTGAGAGGAGAACGAGCTGAAGCGCAGCTTTTTTGCCTGCGTGACC 347 S S D T E E N D K R R T H N V L E R Q R R N E L K R S F F A L R D

1701 AGATCCCTGAATTGAAAACAACGAAAAGGCCCCCAAGGTAGTGATCCTCAAAAAAGCCACCGCTACATCCTGTCCATTCAAGCAGACGAGCACAAGCT 380 Q I P E L E N N E K A P K V V I L K K A T A Y I L S I Q A D E H K L

BstBI (1862) **BspEI (1882)**
1801 CACCTCTGAAAAGGACTTATTGAGGAAACGACGAGAACAGTTGAAACACAAAACCTCGAACAGTTCGAAACTCTGGTGCAGAGTCCGGAGGGGGTGGCTCT 413 T S E K D L L R K R R E Q L K H K L E Q L R N S G A E S G G G G S

Tth111I (1907) **KasI (1928)** **BamHI (1939)** **NheI (1948)** **MscI (1954)**
1901 CCTGGCAGACGTCGTCGCGCAGACGCAGGCGCCGCGCGGATCCTGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACACAA 447 P G R R R R R R R R R R R R G S •

HpaI (2086) **MfeI (2097)**
2001 CTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACA

EcoRI (2182)
2101 TTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCA

2201 TAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTCATTAGCT

2301 GTTTCAGCCTCACCTTCTTTCATGAGTTAAGATATAGTGATTTTCCCAAGGTTGAACTAGCTCTTCATTTCTTATGTTTTAAATGCACTGACCT

SspI (2421) **SwaI (2435)**
2401 CCCACATTCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGC

2501 CCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAAATTTGACAGCAAGAAGCGAGCTTCTAGCTTTAGTTCCT 141 • N R

BstXI (2725) **SacI (2696)**
2601 GGTGACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAGAGATGAGC 138 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 Y D S I L

2701 TCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCC 104 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 F D K Q G

