



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)**
PvuII (239) **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

BspHI (560)
AgeI (552) **SacII (584)** **SdaI (594)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCATCATGAAGTGAAGGCGCTTTTACCAGCGCCATCCTGCA
1 M K W K A L F T A A I L Q

BamHI (642)
601 GGCACAGTTGCCGATTACAGAGGCACAGAGCTTTGGCCTGCTGGATCCCAAACCTGCTACCTGCTGGATGGAATCCTTTCATCTATGGTGTATTCTC
13 A Q L P I T E A Q S F G L L D P K L C Y L L D G I L F I Y G V I L
701 ACTGCCTTGTTCCTGAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCGCGTACCAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAA
47 T A L F L R V K F S R S A D A P A Y Q Q G Q N Q L Y N E L N L G R

SmaI (836) **Bsu36I (877)** **BsrGI (890)**
801 GAGAGGAGTACGATGTTTTGACAAGAGACGTGGCCGGACCTGAGATGGGGGAAAGCCGACAGAGAAGGAAGAACCCTCAGGAAGGCGCTGTACAATGA
80 R E E Y D V L D K R R G R D P E M G G K P Q R R K N P Q E G L Y N E
901 ACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAAGTGGGATGAAAGGCGAGCGCCGGAGGGCAAGGGGCACGATGGCCTTACCAGGGTCTCAGT
113 L Q K D K M A E A Y S E I G M K G E R R R G K G H D G L Y Q G L S

BstAPI (1035) **NheI (1073)** **MscI (1079)**
1001 ACAGCCACCAAGGACACCTACGACGCCCTTACATGCAGGCCCTGCCCTCGCTAACAGCCAGGGGATTTTCAGCTAGCTGGCCAGACATGATAAGATAC
147 T A T K D T Y D A L H M Q A L P P R •
1101 ATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAGAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT

HpaI (1211) **MfeI (1222)**
1201 GCAATAAACAAAGTTAAACAACAACATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATG

EcoRI (1307)
1301 TGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAG

SapI (1489)
1401 GGGCTGTTGCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTCTCTTCATTT

SspI (1546) **SwaI (1560)**
1501 CTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAATGTTTTTTAT
1601 TAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGA
1701 AAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAGCA
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

BstXI (1850)
1801 GTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCCCTGATGGATCTGCCACCTCATCAGAGTAGGGGTGCCTGACAGCC
113 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 D S Y P H R V A
1901 ACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTGACCCTGCCAATGTAGGCTCAATGTGGA
79 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 G I Y A E I H V
2001 CAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCGACATGGTGTCTGTTGCTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCAC
46 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 I K E T A V E V

BbsI (2131) **XmnI (2127)** **AseI (2193)**
2101 CAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCTATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATT
13 L E L D Q Q S I N F T K M
2201 GTCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCTACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTGCG

SpeI (2348)
2301 GTCATGGGGCGGAGTTGTTACGACATTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAAACTCCCATGACGTCAATGGGGTGGAGACTGGAAATC

SnaBI (2476)
2401 CCCGTGAGTCAAACCGTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAGTAGG

NdeI (2581)
2501 AAAGTCCCATAAGGTCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGT
2601 ACTGCCAAGTGGGAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATATTGACGTCA

2701 ATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAA
SdaI (2759) PacI (2767) BspLU11I (2777)
2801 AAGGCCAGGAACCGTAAAAAGGCCGCTTGTGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGC
2901 GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGC
3001 CTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAA
ApaLI (3091)
3101 CCCCCGTTCCAGCCGACCCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTA
3201 ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCC
3301 TCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAG
3401 ATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGTCA
EagI (3527)
3501 TGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATAC
PacI (3507) SwaI (3516) NotI (3526)
3601 GCTCTCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAGGTGCCAGAACATTTCTCTATCGAA