



PvuI (7)
SgfI (6) MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) PvuII (239) **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) BspHI (560) StuI (570) **FspI (599)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAATGAAGTCAGGCCTCTGGTATTTCTTCTCTCTCTGCTT
1▶ M K S G L W Y F F L F C L
BsrGI (672) **Tth111I (697)**
601 GGCATTAAAGTTTTAACAGGAGAAATCAATGGTTCGCCAATTATGAGATGTTTATATTTTACAACGGAGGTGTACAAATTTTATGCAAATATCCTGAC
13▶ R I K V L T G E I N G S A N Y E M F I F H N G G V Q I L C K Y P D
701 ATTGTCCAGCAATTTAAATGCAAGTGTGAAAGGGGGCAAATACTCTGCGATCTCACTAAGACAAAAGGAAAGTGGAAACACAGTGTCCATTAAGAGTC
47▶ I V Q Q F K M Q L L K G G Q I L C D L T K T K G S G N T V S I K S
801 TGAAATTCGCCATTCTCAGTTATCCAACAACAGTGTCTCTTTTTTCTATACAACTTGACCATTCTCATGCAACTATTACTTCTGCAACCTATCAAT
80▶ L K F C H S Q L S N N S V S F F L Y N L D H S H A N Y Y F C C N L S I

PvuII (973) **BstEII (986)**
901 TTTTGATCCTCCTCTTTTAAAGTAACCTTACAGGAGATATTTGCATATTTATGAATCACAACCTTTGTTGCCAGCTGAAGTCTGGTTACCCATAGGA
113▶ F D P P P F K V T L T G G Y L H I Y E S Q L C C Q L K F W L P I G

NsiI (1032) ApaLI (1078)
1001 TGTGCAGCCTTTGTTGTAGTCTGCATTTTGGGATGCATACTTATTTGTTGGCTTACAAAAAAGAAAGTATTCATCCAGTGTGCACGACCCTAACGGTGAAT
147▶ C A A F V V V C I L G C I L I C W L T K K K Y S S S V H D P N G E

BspHI (1106) **MscI (1188)**
BspLU11I (1100) **XbaI (1135)** **NheI (1182)**
1101 ACATGTTTCATGAGAGCAGTGAACACAGCCAAAAAATCTAGACTCACAGATGTGACCCCTATAATATGGAACCTCTGGCACCCAGGCTAGCTGGCCAGACATG
180▶ Y M F M R A V N T A K K S R L T D V T L •
1201 ATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCA

HpaI (1320) MfeI (1331)
1301 TTATAAGCTGCAATAAACAGTTAAACAACAACATTCATTCTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCT

EcoRI (1416)
1401 CTACAAATGTGGTATGAATTCTAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCAT

SapI (1598)
1501 AGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAACCTAGC

SspI (1655) SwaI (1669)
1601 TCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAAT

EcoO109I (1730)
1701 GTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGG
1801 ACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAG
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

SacI (1930) **BstXI (1959)**
1901 CACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGC
116▶ 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 D S Y P H

StuI (2094)
2001 CTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGCCTGCCAATGTAGGCCT
82▶ 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 G I Y A E
2101 CAATGTGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCGACATGGTGTCTGTTGCTCCTCATAGAGCATGGTGTCTTCTCAGTGGC
49▶ 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 I K E T A

BbsI (2240) **XmnI (2236)**
2201 GACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGA
16▶ V E V L E L D Q Q S I N F T K M

AseI (2302) SacI (2359)
2301 TGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCG

2401 CCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGAC
SpeI (2457)

2501 TTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTIONGCAAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTG
SnaBI (2585)

2601 CCAAGTAGGAAAGTCCCATAAGGTCATGTACTIONGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATAC
NdeI (2690)

2701 ACTTGATGTACTIONGCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTA

2801 TTGACGTCAATGGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAA
PstI (2869) Pacl (2876)
SdaI (2868) BspLU11I (2886)

2901 GGCCAGCAAAAAGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTC

3001 AGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTGCCGTTACCGGATA

3101 CCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGT

3201 GTGCACGAACCCCGTTGACCCGACCCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAG
ApaLI (3200)

3301 CCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGG

3401 TATCTGGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTC

3501 AAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGA

3601 TTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAATATCTTTATTTTCATTACATCTGTGTGGTTTTTTTGTGTAATCGTAA
EagI (3636)
Pacl (3616) SwaI (3625) NotI (3635)

3701 CTAACATACGCTCTCCATCAAAAACAAACGAAACAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA