



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552) **NcoI (560)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGCTATGTTCCGACGCTGGTGGCCTCGGCTCAGCA

1▶ M A M F R S L V A S A Q Q

EagI (611)

601 GCGGCAGCCGCCGCGGGCGGGCGGGCGGCGACAGCGGCCTGGAGGCGCAGTACACCTGCCCATCTGCCTGGAGGTCTATCACGGCCCGTGGCCATC

13▶ R Q P P A G P A G G D S G L E A Q Y T C P I C L E V Y H R P V A I

PvuII (702) **SdaI (744)**

701 GGCAGTGCGGCCACACGTTCTGCGGGGAGTGTCTCCAGCCCTGCCTGCAGGTGCCATCCCCGCTGTGCCACTCTGCCCGCTGCCCTTCGACCCCAAGA

47▶ G S C G H T F C G E C L Q P C L Q V P S P L C P L C R L P F D P K

BbrPI (817) **BstEII (873)** **ApaLI (895)**

801 AGGTGGACAAGGCCACCCACGTGGAGAAGCAGCTCTCATCCTACAAGCGCCCTGTCGAGGCTGCAACAAAAAGGTGACCCTGGCAAAGATGAGAGTGCA

80▶ K V D K A T H V E K Q L S S Y K A P C R G C N K K V T L A K M R V H

901 CATTTCGTCTGCCTGAAGTCCAGGAGCAGATGGCCAACTGCCCAAGTTCGTCGCCGTGGTGGCCACATCACAGCCTATCCCAGCAACATCCCCAAC

113▶ I S S C L K V Q E Q M A N C P K F V P V V P T S Q P I P S N I P N

DraIII (1063)

1001 AGGTCCACCTTCGCTGCCGTAAGTGTGGTGCAGCAGGAGTGGTGAAGCACTGTGTGGAAAGCCACCGCAGCGACCCCAACCGCG

147▶ R S T F A C P Y C G A R N L D Q Q E L V K H C V E S H R S D P N R

SmaI (1133) **EcoO109I (1133)** **BstAPI (1164)**

1101 TGGTGTGCCCCATCTGCTCGGCAATGCCTGGGGGACCCAGCTACAAGAGCGCCAACTTCTGCAGCACCTGCTTACCAGCACAAAGTTCCTCTACGA

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

NheI (1287)

1201 CACCTTTGTGGACTACAGTATTGACGAGGAGCGCCCTCCAGGCTGCTGTGCCCTGTCTCTCTGAGAAGTGAAGGGAAGCGCAGCTAGCTGGCCAG

213▶ T F V D Y S I D E E A A F Q A A L A L S L S E N •

1301 ACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGT

HpaI (1425) **MfeI (1436)**

1401 AACCATATAAGCTGCAATAAAACAAGTTAACAACAACAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAA

EcoRI (1521)

1501 AACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAA

1601 GGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAA

SapI (1703)
SspI (1760)
SwaI (1774)

1701 CTAGCTCTTCATTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATATTAGAAATAATTTAAATACATCATTGCAATGAAAA

EcoO109I (1835)

1801 TAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAA

1901 ATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGCTGACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCA

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

SacI (2035)

2001 ATGAGCACAAAGCAGTCAAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGG

117▶ 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 D S Y P

StuI (2199)

2101 GGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTACGACAGACAGTACCTGCCAATGTA

84▶ 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 G I Y

2201 GGCCTCAATGTGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCGACATGGTGTGTTGTCCTCATAGAGCATGGTATCTTCTCA

51▶ 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 I K E

BbsI (2345)

XmnI (2341)

2301 GTGGCGACCTCCACGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTAT

17▶ T A V E V L E L D Q Q S I N F T K M ◀

2401 **AseI (2407)** **SacI (2464)**
GCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCC

2501 **SpeI (2562)**
TACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTG

2601 **SnaBI (2690)**
GAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATG

2701 **NdeI (2795)**
TACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATAT

2801
GATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGT

2901 **SdaI (2973)PaeI (2981) BspLU11I (2991)**
CATTATTGACGTCAATGGGCGGGGTCTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAAITAAAGAACATGTGAG

3001
CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTC

3101
AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGTCCCTCGTGCGCTCTCTGTTCCGACCTGCCGCTTACC

3201
GGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGG

3301 **ApaLI (3305)**
GCTGTGTGCACGAACCCCGTTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGC

3401
AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA

3501
TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGGTTTTTTTG

3601
TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTA

3701 **EagI (3741)**
PaeI (3721) SwaI (3730) NotI (3740)
AGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGTGTGGTTTTTTGTGTGAAT

3801
CGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTA

3901
TCGAA