



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552) NcoI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGCTAGGCTGTGCTTTCTGATGACCTGCTGGT

Bsu36I (654)

1 ▶ M A R L C A F L M T L L V

601 GATGAGCTACTGGTCAACCTGTCTAGGATGTGACCTGCCTCAGACTCATAACCTCAGGAACAAGAGACCTTGACACTTCTGGTAAAAATGAGGAGA

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

701 CTCTCCCCTCTCTCTGCCTGAAGGACCGGAAGACTTTGGATTCCCAGGAGAAGGTGGATGCCAGCAGATCAAGAAGGCTCAAGCCATCCCTGTCC

47▶ L S P L S C L K D R K D F G F P Q E K V D A Q Q I K K A Q A I P V

801 TGAGTGAGCTGACCCAGCAGATCCTGACCCTCTCACATCAAAGGACTCATCTGCTGTTGGGATGCAACCCTCTAGACTCCTTCTGCAATGACCTCAA

80▶ L S E L T Q Q I L T L F T S K D S S A A W D A T L L D S F C N D L N

XmnI (993)

901 CACTCAGCTCAATGACCTGCAAGGCTGTCTGATGCAGCAGGTAGAGATACAGGCACCTCCCCTGACCCAGGAAGACTCCCTGTGGCTGTGAGGAAATAC

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

1001 TTCCACAGGATCACTGTTTACCTGAGAGAGAAGAAACACAGCCCTGTGCCTGGGAGGTGGTCAGAGCAGAAATCTGGAGAGCCCTGTCTTCTCAGCCA

147▶ F H R I T V Y L R E K K H S P C A W E V V R A E I W R A L S S S A

MscI (1138)

NheI (1132)

1101 AGTTGCTGACCAGCCTGAAAGAAGAGAAGTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAA

180▶ K L L T S L K E E K •

HpaI (1270) MfeI (1281)

1201 AAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACCAATTGCATTCATTTTATG

EcoRI (1366)

1301 TTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACC

1401 TCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCT

SapI (1548)

1501 TCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAACCTAGCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCCACATCCCTTTTTT

SspI (1605)
SwaI (1619)
EcoO109I (1680)

1601 AGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCC

1701 CAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCTGGTGTACTTGAGGGGG

141 ◀ • N R T Y K L P

SacI (1880)

1801 ATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCAC

132◀ 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 E R C M G C

1901 AGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGA

99◀ 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 N S V A S

StuI (2044)

2001 CCCAATGGCAATGGCTTCAGCACAGACAGTACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCC

66◀ G I 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

XmnI (2186)

2101 CCGACATGGTGCTTGTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGG

32◀ G V H 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 (2252)

2201 TGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGT

SacI (2309)

2301 TCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCG

2401 **SpeI (2407)**
TTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGC

2501 **SnaBI (2535)**
CAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGG

2601 **NdeI (2640)**
GCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTG

2701
ACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTT

2801 **PstI (2819)** **SdaI (2818)** **PaeI (2826)** **BspLU11I (2836)**
ACCGTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAGGCCAGGAAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT

2901
CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCCT

3001
GGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAC

3101 **ApaLI (3150)**
GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCGACCGCTGCGCCTTATCCGGTAACTA

3201
TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG

3301
TTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAAGATTGGTAGCT

3401
CTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGAT

3501 **EagI (3586)** **PaeI (3566)** **SwaI (3575)** **NotI (3585)**
CTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAA

3601
TATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAA

3701
ATAGGCTGTCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA