



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGAGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

AgeI (552)
BspHI (568)

501 TCTGTTTGTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTAGGAGGGCCATCATGAACCAAGTGTGCCGTCAATTTCTGC

1▶ M N P S A A V I F C

BamHI (631)
RsrII (649)
ClaI (672)

601 CTCATCCTGCTGGGTCTGAGTGGGACTCAAGGGATCCCTCTCGCAAGGACGGTCCGCTGCAACTGCATCCATATCGATGACGGCCAGTGAGAATGAGGG

11▶ L I L L G L S G T Q G I P L A R T V R C N C I H I D D G P V R M R

HindIII (708)
BbrPI (742)
BspEI (797)

701 CCATAGGGAAGCTTGAATCATCCCTGCGAGCCTATCTCGCCACGTTGAGATCATTGCCACGATGAAAAAGAATGATGAGCAGAGATGTCTGAATCC

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

801 GGAATCTAAGACCATCAAGAATTAATGAAAGCGTTTAGCCAAAAAGGTCTAAAAGGCTCCTTAAGTGGAGTGAAGCCACGCACACACCCCGGTGCTG

77▶ E S K T I K N L M K A F S Q K R S K R A P •

MscI (931)
NheI (925)

901 CGATGGATGGACAGCAGAGACCTCGTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGC

HpaI (1063)
MfeI (1074)

1001 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCAATTTATGTTTCAGG

EcoRI (1159)

1101 TTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCATAGCAAACTTTAACCTCCAAT

1201 CAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCA

SapI (1341)
SspI (1398)

1301 TGGAGTTAAGATATAGTGTATTTTCCCAAGGTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAA

SwaI (1412)
EcoO109I (1473)

1401 TATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTA

1501 GTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTT

141▶ • N R T Y K L P I L E

SacI (1673)

1601 CCTCAATGGTGGTTTTGACCAGCTTGCCATTCACTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCATGCCACAGGGGCT

130▶ 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 P S

BstXI (1702)

1701 GACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATG

97▶ 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 G I

StuI (1837)

1801 GCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACAT

63▶ 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 G V H

BbsI (1983)
XmnI (1979)

1901 GGTGCTTGTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCT

30▶ 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 (2045)

2001 CCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAA

SacI (2102)

2101 ACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTT

SpeI (2200)

2201 ACTAGTCAAAAACAACTCCCATTGACGTCATGGGGTGGAGACTTGGAAATCCCCTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACC

2301 GCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTT
SnaBI (2328)

2401 ACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAA
NdeI (2433)

2501 TGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAA
PacI (2619)

PstI (2612)
SdaI (2611) **BspLU11I (2629)**

2601 GTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG
2701 CTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCT
2801 CCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG
ApaI (2943)

2901 GTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT
3001 GAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGA
3101 AGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATC
3201 CGGCAAACAACACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT

3301 ACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTT
EagI (3379)
PacI (3359) **Swal (3368)** **NotI (3378)**

3401 ATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCT
3501 GTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA