



PvuI (7)
SgfI (6)
MfeI (82) **EcoNI (96)**

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245) **Bsu36I (291)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTACCATTGGACGCCAAGTTCGTCGCCGTGCTGGCCCTGGTGC

601 GGCCGCGCTCGCATCAGTGACGGTAAACCAGTACGCTGAGCTACCGATGCCCTGCCGTTCTTCGAGAGCCACATCGCCAGGCCAACGTCGAAGCAT

13▶ A A L C I S D G K P V S L S Y R C P C R F F E S H I A R A N V K H

701 CTGAAAATCCTCAACTCCAACTGTGCCCTTCAAGTGTGACGGCTGAAGAACAACAACAGACAAGTGTGCATTGACCCGAAATTAAGTGGATCC

47▶ L K I L N T P N C A L Q I V A R L K N N N R Q V C I D P K L K W I

BamHI (794)

HindIII (815)
NheI (853)

801 AAGAGTACCTGGAGAAAGCTTTAAACAAGTAAGCAACAACAGCCAAAGGACTTGTCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAAC

80▶ Q E Y L E K A L N K •

MscI (859)

901 CACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAAACAAC

MfeI (1002)
EcoRI (1087)

1001 AACAAATGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTTACAAATGTGGTATGGAAATTTAAAATA

1101 CAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCAT

SapI (1269)

1201 TAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTAGCTCTTCATTCTTTATGTTTAAATGCACT

SspI (1326)
SwaI (1340)

1301 GACCTCCACATTCCTTTTTAGTAAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTC

EcoO109I (1401)

1401 AAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAG

141▶ •

1501 TTCCTGGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGA

139▶ 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 D P A Y D S I

SacI (1601)
BstXI (1630)

1601 TGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTT

106▶ 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 V I T D F D K

StuI (1765)

1701 CTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCA

73▶ 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 A S I I E G

1801 GTCTTGGTCTGATGGCCGCCCCGACATGGTGTCTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAG

39▶ 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 L E L D Q Q S

BbsI (1911)

XmnI (1907)
AseI (1973)

1901 AGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGCC

6▶ I N F T K M

SacI (2030)

2001 GTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGTTATATAGACTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTT

SpeI (2128)

2101 ACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTAT

SnaBI (2256)

2201 CCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAGTAGGAAAGTCCATAAGGTCATGT

NdeI (2361)

2301 ACTGGCATAATGCCAGCGGGCCATTTACCGTATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTAAGTGGGAGTTTAA

2401 CCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATATTGACGTCAATGGGGGGGCTGTTGGCC

PacI (2547)

PstI (2540)
SdaI (2539) BspLU11I (2557)

2501 GGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTTGCAGGTTAA**TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAA**
←

2601 GGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA

2701 AGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCG

ApaLI (2871)

2801 TGGCGCTTCTCATAGCTCAGCTGAGGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCGACCG

2901 CTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGG

3001 TATGTAGGCGGTGTACAGATTCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT

3101 TCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGG

PacI (3287) SmaI (3296)

3201 ATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTT

EagI (3307)
NotI (3306)

3301 AAATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAAC

3401 GAAACAAAACAACTAGCAAAATAGGCTGTCCCGAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA