



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGTTGCTCAACTCTACGTCTTTGTTTCGTTT

BspLU111 (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACT

601 CTCTCTTTCTGGCCTGGAGGCTATCCAGCGTACTCCAAGATTCAAGTTTACTCAGTCATCCAGCAGAGAATGGAAAGTCAAATTTCTGAATTGCTAT

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

701 GTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTGAGACTTGTCTTTTCAGCAAGACT

47▶ V S G F H P S D I E V D L L K N G E R I E K V E H S D L S F S K D

801 GGTCTTTCTATCTTGTACTACACTGAATTCACCCCACTGAAAAAGATGAGTATGCCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGT

80▶ W S F Y L L Y Y T E F T P T E K D E Y A C R V N H V T L S Q P K I V

EcoRI (826)
Tth111I (876)

901 TAAGTGGGATCGAGACATGTAAGCAGCATCATGGAGGTTTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGA

113▶ K W D R D M •

BspLU111 (914)
MscI (949)

1001 ATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACACAACAATTGCA

HpaI (1081) **MfeI (1092)**

1101 TTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCCTAAATACAGCATAGCA

1201 AAACTTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTG

EcoRI (1177)

1301 CAGCCTCACCTTCTTTCATGAGGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTAAATGCACTGACCTCCAC

SspI (1416) **SwaI (1430)**
EcoO109I (1491)

1401 ATTCCCTTTTATGATAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTC

1501 ATAATATCCCCAGTTTATGATGTTGACTTAGGGAACAAAGAACCTTAAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGT

141▶ • N R T Y

SacI (1691)

1601 ACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCT

136▶ 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 L E R

BstXI (1720)

1701 GCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTG

103▶ 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 Q G N

StuI (1855)

1801 CTCACAGCAGACCAATGGCAATGGCTTCAGCAGACAGTACCCTGCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCC

69▶ 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 T K T R

XmnI (1997)

1901 TGATGGCCGCCCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAA

36▶ 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 I N F

BbsI (2001)
AseI (2063)

2001 GGTCTTATGGTGGCCCTCTATAGTGTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCT

3▶ T K M

SacI (2120)

2101 IATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTTT

SpeI (2218)

2201 GGAAAGTCCCCTGATTACTAGTCAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCAT

SnaBI (2346)

2301 TGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTGCCTGCAAGTAGGAAAGTCCCATAAGGTCATGTAAGTGGCATA

NdeI (2451)

2401 ATGCCAGGCGGGCATTACCGTCAATGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCGGTTTACCGTAAATAC

2501 TCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGAAACATACGTCAATATTGACGTCAATGGGCGGGGCTGTTGGGCGGTCAGCCAG

PacI (2637)

PstI (2630)

SdaI (2629)

BspLU111 (2647)

2601 GCGGGCCATTTACCGTAAGTTATGTAACGCTTGCAGGTTAA**TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTG**
2701 **CTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGTACCAGG**
2801 **CGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTTC**

ApaLI (2961)

2901 **TCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACAGCCGACCGCTGCGCCTTA**
3001 **TCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCG**
3101 **GTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG**
3201 **AGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAA**

EagI (3397)

PacI (3377) SmaI (3386) **NotI (3396)**

3301 **GATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGG**
3401 **CCGCAATAAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAAC**
3501 **AACTAGCAAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA**