



PvuI (7)
SgfI (6)

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
PvuII (239)
Bsu36I (291)
EcoNI (287)

201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATTGGCTGCCAGCGGCATCACCTCGTTCGCCACTGCC

1▶ M A A S G I T S L P A L P

FspI (680)
EagI (696)

601 GGAGGACGCGCGCCGCTTCCACCAGGCCACTTCAAGGACCCCAAGCGGCTCTACTGCAAGAACGGCGGCTTCTTCTCGCATCCATCCCGACGGC

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

SapI (720)

701 CGCGTGGATGGCGTCCGCGAGAAAGAGCGACCCACAGTCAAACACTCAACTCCAAGCAGAAGAGAGAGGAGTTGTGTCTATCAAGGGAGTGTGTCCAACC

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

Acc65I (800)

801 GGTACCTTGTATGAAGGAAGATGGACGGCTGCTGGCTTCTAAGTGTGTTACAGAAGAGTGTTCCTTCTTGAACGACTGGAATCTAATAACTACAATAC

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

XcmI (920)
BamHI (964)

901 TTACCGGTACGGAATACTCCAGTTGGTATGTGGCACTGAAACGAACTGGGAGTATAAACTCGGATCCAAAACGGGACCTGGACAGAAAGGCCATACTG

113▶ Y R S R K Y S S W Y V A L K R T G Q Y K L G S K T G P G Q K A I L

MscI (1033)
NheI (1027)

1001 TTTCTTCAATGTCTGCTAAGAGCTGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAAACCACAACCTAGAATGCAGTGAAAAAAT

147▶ F L P M S A K S •

HpaI (1165) MfeI (1176)

1101 GCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAAACAACAACATTGCATTCAATTTATGTTTCA

EcoRI (1261)

1201 GGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAA

1301 ATCAAGCCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTT

SapI (1443)

1401 CATGGAGTTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAATGCAGTACCTCCACATTCCTTTTATAGTAA

SspI (1500) SwaI (1514)

1501 AATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTT

1601 TAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAG

141▶ • N R T Y K L P I L

SacI (1775)

1701 TTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAAGGAGCATAGTCAAGATGAGCTCTGTCATGCCACAGGGG

131▶ 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 P

BstXI (1804)

1801 CTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAA

97▶ 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 G I

StuI (1939)

1901 TGGCAATGGCTTCAACAGACAGTACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCCGAC

64▶ 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

BbsI (2085)
XmnI (2081)

2001 ATGGTGCTTGTGCTCATAGAGCATGGTGTCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCC

31▶ 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 (2147)

2101 CTCCTATAGTGAGTCTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCT

SacI (2204)

2201 AAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGAT

SpeI (2302)

2301 TTAAGTACGCTCAAAACAACTCCCATTTGACGTCATGGGGTGGAGACTTGGAAATCCCGTGGTCAACCGCTATCCACGCCATTGATGTAAGTGCCTAA

2401 CCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAAGTCATGTACTGGGCATAATGCCAGGCGGGCCAT
SnaBI (2430)

2501 TTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTC
NdeI (2535)

2601 AATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGT

2701 AAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGGAAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTCCATA
PstI (2714) **SdaI (2713)** **BspLU11I (2731)** **PacI (2721)**

2801 GGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAG
←

2901 CTCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCAGCTGT

3001 AGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTC
ApaLI (3045)

3101 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTT

3201 GAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGATTGGTAGCTCTTGA

3301 TCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTCGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTT

3401 CTACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAATATCT
EagI (3481) **PacI (3461)** **SwaI (3470)** **NotI (3480)**

3501 TTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGG

3601 CTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA