



PvuI (7)
SgfI (6)

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) **NcoI (560)**

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCAACCTGGACTGGCCTCACAACTGCTGTTTCTTCTTACCAT

13▶ M D W P H N L L F L L T I

Bsp120I (667)
DraIII (688)

601 TTCCATCTTCTGGGGCTGGCCAGCCAGGAGCCCCAAAAGCAAGAGGAAGGGGCAAGGGCGCCTGGGCCCTGGCCCTGGCCCTCACCAGGTGCCA

13▶ S I F L G L G Q P R S P K S K R K G Q G R P G P L A P G P H Q V P

701 CTGGACCTGGTGTACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGGCCAGCTGAGGAACAGCTCAGAGCTGG

47▶ L D L V S R M K P Y A R M E E Y E R N I E E M V A Q L R N S S E L

801 CCCAGAGAAAGTGTGAGTCAACTTGCAGCTGTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCCGTATCCC

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

XmnI (942)

901 CGTGGACCTGCCGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTACCATGACGAGGACCGCAGCATGGTGTGAGCGTGCCGGTGTTCAGCCAG

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

BssHIII (1056)

1001 GTTCTGTGCGCCGCGCCTCTGCCCGCCACCGCCCCGACAGGGCCTTGGCCAGCGCGCAGTCAATGGAGACCATCGCTGTGGGCTGCACCTGCATCT

147▶ V P V R R R L C P P P P R T G P C R Q R A V M E T I A V G C T C I

MscI (1166)
NheI (1160)

1101 TCTGAATCACCTGGCCAGAAGCCAGGCAGCAGCCGAGACCATCCTCCTTGACCTTTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTG

180▶ F •

HpaI (1298)

1201 GACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGT

MfeI (1309)
EcoRI (1394)

1301 TAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTC

1401 TAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAA

SapI (1576)

1501 TGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAAGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAA

SspI (1633)
Swal (1647)

1601 ATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCA

1701 GATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTA

SacI (1908)

1801 GCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAG

141▶ 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

SacI (1908)

1901 TCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAA

108▶ D S I 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

StuI (2072)

2001 AGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGAT

75▶ D K 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

2101 CTCCCAGTCTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGCTCCAGATCC

42▶ E G 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

BbsI (2218)
XmnI (2214)
AseI (2280)

2201 TGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGTGATCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGT

8▶ Q Q S I N F T K M

SacI (2337)

2301 GGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGG

2401 AGTTGTTACGACATTTTGGAAAGTCCC GTT GATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAA
SpeI (2435)

2501 CCGCTATCCACGCCCATTTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAG
SnaBI (2563)

2601 GTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGATGTACTGCCAAGTGGG
NdeI (2668)

2701 CAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGGTC

2801 GTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACC
PacI (2854)
PstI (2847)
SdaI (2846)
BspLU11I (2864)

2901 GTAAAAAGGCCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGG

3001 ACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCG

3101 GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGC
ApaLI (3178)

3201 CCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG

3301 AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA

3401 GTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAA

3501 AAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATT
PacI (3594)

3601 AACATTTAAATCAGCGGCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAA
EagI (3614)
SwaI (3603) NotI (3613)

3701 ACAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA