



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGGC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552)
SphI (560)
BstXI (575)
NheI (597)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTGAGCATGCAGATCATCACCACAGCCCTGGTGTGCTTGTGCT

1► M Q I I T T A L V C L L L

Acc65I (642)

SphI (635)

Bsu36I (690)

601 AGCTGGGATGTGGCCGGAAGATGTGGACAGCAAGACATGCAGGTACCCCTTCTCCAGATGTTGCTTCTCATTGCGGAGCAAGAGATTCGCCCTGAGGGCA

13► A G M W P E D V D S K S M Q V P F S R C C F S F A E Q E I P L R A

SspI (747)

StuI (773)

701 ATCCTGTGTACAGAAATACCAGCTCCATCTGCTCCAATGAGGGCTTAATATTCAAGCTGAAGAGAGGCAAAGAGCCCTGCGCCTTGACACAGTTGGAT

47► I L C Y R N T S S I C S N E G L I F K L K R G K E A C A L D T V G

AvrII (854)

MscI (866)

801 GGGTTCAGAGGCACAGAAAAATGCTGAGGCACTGCCCGTCAAAAAGAAAAATGAGCCTAGGACTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTG

80► W V Q R H R K M L R H C P S K R K •

HpaI (998)

901 GACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGT

MfeI (1009)
EcoRI (1094)

1001 TAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTC

1101 TAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAA

SapI (1276)

1201 TGTGCATTAGCTGTTTGAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGATTTTTCCCAAGTTTGAAGTACTGCTTCTTCTTTATGTTTTAA

SspI (1333)
SwaI (1347)

1301 ATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCA

EcoO109I (1408)

1401 GATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTA

1501 GCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAG

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 (1608)

BstXI (1637)

1601 TCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAA

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 (1772)

1701 AGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCATATGTGGACAGCAGAGATGAT

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

1801 CTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTAGTGGCGACCTCCACAGCTCCAGATCC

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 (1918)

XmnI (1914)

AseI (1980)

1901 TGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGT

8◄ Q Q S I N F T K M

SacI (2037)

2001 GGATGGCGTCTCCAGCTTATCTGACGGTTCATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGG

SpeI (2135)

2101 AGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAA

SnaBI (2263)

2201 CCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAGTAGGAAAAGTCCATAAG

2301 **NdeI (2368)**
GTCATG TACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGG

2401 CAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTC

PacI (2554)
PstI (2547)
SdaI (2546) **BspLU11I (2564)**

2501 GTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACC

2601 GTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGG

2701 ACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCCG

ApaI (2878)

2801 GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCCAGC

2901 CCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAG

3001 AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA

3101 GTTACCTTCGAAAAAGATTGGTAGCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAA

PacI (3294)

3201 AAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATT

EagI (3314)
Swal (3303) **NotI (3313)**

3301 AACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAA

3401 ACAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA