



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGGCTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552)
BspHI (560)
Bsp120I (587)
XmaI (584)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGTCATCATGACTATGTTTGAGAATGTCACCCGGCCCTGGCTAG

PvuII (601)
SapI (690)

601 ACAGCTGAACCCCTCGAGGGGATCTGACACCCCTAGACAGCCTCATCGACTTCAAACGTTCCATCCCTTCTGCCTGGTGTGAGGAAGAGGAAGAGCACA

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

ApaLI (721)

701 CTGTTCTGGGAGCCCGTATGTGCACACCGACTACACTCTCCTGGATGTGCTGGAGCCGGGAGCTCCCCCTCAGATCCGACAGACAGTGGCAACTTTA

47▶ L F W G A R Y V H T D Y T L L D V L E P G S S P S D P T D S G N F

801 GCTTTAAGAAATATGCTGGATGCTCGAGTAGAGGGAGATGTGGATGTGCCAAAGACAGTGAAGTAAAGGGGACTGCGGGTCTGTCACGGAGCAGCACACT

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

BstXI (926)

901 GGAGGTGCAGACGCTCAGCGTGGCTCCACGGCTCTGGAGAATTGCACAAGGAGAGGAAACTGTGACGACACCACCCATTCTGAAGGAGATGCGGGAA

113▶ E V Q T L S V A P T A L E N L H K E R K L S A D H P F L K E M R E

NgoMIV (1066)

1001 CGCGGGGAGAACCTCTATGTGGTGTGAGGTGGTGGAAACCTACAGGAAGTCACTCTGGAGCGAGCCGGCAAGGCAGAGGGCTGCTTCTCTCCCT

147▶ R G E N L Y V V M E V V E T L Q E V T L E R A G K A E G C F S L P

BamHI (1123)

1101 TCTTTGCCCACTGGGACTACAGGGATCCGTGAACCACAAGGAGGCTGTAACCATCCCCAAGGGCTGTGTTCTGGCCTATCGAGTGAACAACCTGATGGT

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

SphI (1244)

1201 CAACGGCAAAGATGAGTGGGCAATCCACACATTTGCAATGACAGCATGCAAACTTCCCTCCTGGAGAAAAGCCAGGAGAAGGGAAGTTCATATTGATC

213▶ N G K D E W G I P H I C N D S M Q T F P P G E K P G E G K F I L I

BbsI (1327)

1301 CAGGCATCTGATGTTGGGAGATGCACGAAGACTTCAAGACATTAAGGAAGAGGTTGAGCGAGAGACTCAGGAAGTGGAGAAGTAAAGTCCAGTGGGGC

247▶ Q A S D V G E M H E D F K T L K E E V Q R E T Q E V E K L S P V G

AvrII (1431)
XbaI (1482)
DraIII (1495)

1401 GAAGTCACTACTCACTTCCCTCAGCCATCTCCTAGGAAAGAAAGAGCTCCAGGACCTTGAGCAGACGCTTGAAGGGGCTTAGACAAGGGACACGA

280▶ R S S L L T S L S H L L G K K K E L Q D L E Q T L E G A L D K G H E

1501 AGTGACCCTGGAAGCACTCCCCAAGATGCTCCTGCTGTCAAAGGACGCTATGGACCCATCCTTACTTCTCGGGGCTCTGACAGTGTAAAGTGAAGCC

313▶ V T L E A L P K D V L L S K D A M D A I L Y F L G A L T V L S E A

HindIII (1606)
AgeI (1641)
NcoI (1670)

1601 CAACAGAAGCTTCTAGTAAAATCCTTGGAGAAAAGATCCTACCGTGCAACTGAAGCTGGTGAAGCACCATTGGAGAAGAAGTCTCTGCAAGATAAAG

347▶ Q Q K L L V K S L E K K I L P V Q L K L V E S T M E K N F L Q D K

1701 AGGGTGTTCCTCCCTGCAACCTGATCTGCTCCTCCTCGGGGAGGAGAACTGATCCTAACAGAAGCACTGGTGGGACTAAGCGGCTGGAAGTCCA

380▶ E G V F P L Q P D L L S S L G E E E L I L T E A L V G L S G L E V Q

BspEI (1827)
BamHI (1824)
EcoRI (1893)

1801 GAGATCAGCCCCAGTACACGTTGGATCCGGACACGCTCCCCACCTTTGTGCCCTCTATGCTGGCCTCTCCCTCCTCAACTGCTAAGCAAGAATTCC

413▶ R S G P Q Y T W D P D T L P H L C A L Y A G L S L L Q L L S K N S

MscI (1925)
NheI (1919)

1901 TAATGCACCTTCTTTGCCTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATT

447▶ •

HpaI (2057)
MfeI (2068)

2001 TGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAATTGCATTCTTTATGTTTCAGGTTACGG

EcoRI (2153)

2101 GGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCC

2201 TCTACTGAAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTTTCATGGAGT

2301 TTAAGATATAGTGTATTTTCCCAAGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCA
SapI (2335) SspI (2392)

2401 GAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTT
SwaI (2406)

2501 GGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAA
141 • N R T Y K L P I L E E I BstXI (2696)

2601 TGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCAC
128 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 S V V
2701 CCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTTCTGCCGGTTCACAGCAGACCCCAATGGCAATG
95 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 A I

2801 GCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCT
61 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 H H K BbsI (2977)

2901 TGTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATA
28 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

3001 GTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGC
AseI (3039)

3101 TCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGT
SpeI (3194)

3201 CAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACCGCATCA
SnaBI (3322)

3301 TCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCT

3401 ATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAA
NdeI (3427)

3501 GTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATG

3601 TAACGCTGCAGGTTAAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGC
PacI (3613) PstI (3606) SdaI (3605) BspLU11I (3623)

3701 CCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCTTTCCCCTGGAAGCTCCCTCG

3801 TGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCT

3901 CAGTTCGGTGTAGGTCGTTGCTCCTCAAGCTGGGCTGTGTCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC
ApaLI (3937)

4001 AACCCGGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGT

4101 GGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA

4201 ACAAACCACCGCTGGTAGCGGTGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG

4301 TCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTC
EagI (4373) PacI (4353) SwaI (4362) NotI (4372)

4401 ATTACATCTGTGTGTTGGTTTTTGTGTTGAATCGTAACATAACGCTCTCCATCAAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCC

4501 AGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA