



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCCGCCCTACCTGAGGCC

HindIII (245) 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

Bsu36I (291) 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATTGGGCGTCCCACGGCCCTGGAGGCCGGCAGCTGGCG

SfiI (576) 1▶ M G V P T A L E A G S W R

SapI (612)
BamHI (604) 601 CTGGGATCCCTGCTCTTCTGCTCTTCTGGTGGTCCCTAGTCCGGTGGCAGCCTTCAAGGTCGCCACGCCGATTCCCTGTATGTCTGTCCCGAG

AvrII (639) 13▶ W G S L L F A L F L A A S L G P V A A F K V A T P Y S L Y V C P E

SdaI (719) 701 GGCAGAACGTCACCCTACCTGCAGGCTCTTGGCCCTGTGGACAAAGGGCAGCATGTGACCTTCTACAAGAGCTGGTACCGCAGCTCGAGGGCGAGG

Bsp120I (732) 47▶ G Q N V T L T C R L L G P V D K G H D V T F Y K T W Y R S S R G E

DraIII (751) 801 TGCAGACCTGCTCAGAGCGCCGCCATCCGCAACCTCACGTTCCAGGACCTCACCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCAGCACCT

Acc65I (776) 80▶ V Q T C S E R R P I R N L T F Q D L H L H H G G H Q A A N T S H D L

XhoI (786)

XcmI (887)

FspI (959) 901 GGCTCAGCGCCACGGGCTGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTGGATAGCGGCCCTCTACTGCTGC

113▶ A Q R H G L E S A S D H H G N F S I T M R N L T L L D S G L Y C C

1001 CTGGTGGTGGAGATCAGGCACCACTCGGAGCACAGGTCATGGTGCATGGAGTGCAGGTGCAGAGCAGGCAAAGATGCACCATCCAACCTGTGTGG

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

1101 TGTACCCATCCTCTCCAGGAAGTAAAACATCACGGTGCAGCCCTGGTACGGGTGCATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCT

180▶ V Y P S S S Q D S E N I T A A A L A T G A C I V G I L C L P L I L L

1201 CCTGGTCTACAAGCAAAGGCAGGCGACCTCAACCGCCGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAACCCCGCTTTGAA

213▶ L V Y K Q R Q A A S N R R A Q E L V R M D S N I Q G I E N P G F E

1301 GCCTCACACCTGCCAGGGGATACCGAGGCCAAAGTCAGGCACCCCTGTCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGCGGCATCTGCTTT

247▶ A S P P A Q G I P E A K V R H P L S Y V A Q R Q P S E S G R H L L

BbsI (1441) 1401 CGGAGCCAGCACCCCTGTCTCTCCAGGCCCGGAGAGCTCTTCTCCATCCCTGGACCCTGCTCCTGACTCTCAAACCTTTGAGGTATCATAGCC

Tth111I (1459) 280▶ S E P S T P L S P P G P G D V F F P S L D P V P D S P N F E V I •

MscI (1512)
NheI (1506) 1501 CAGCTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTG

HpaI (1644) 1601 ATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAACAAATGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGA

MfeI (1655)

EcoRI (1740) 1701 GGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACCTTAACTCCAAATCAAGCCTCTACTGATCC

1801 TTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTG

SapI (1922) 1901 TATTTTCCAAGGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTAGTAAAATATTCAGAAAATAATTTAAA

SspI (1979) 2001 TACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAAC

Swal (1993) 2101 AAAGAACCTTTAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGAC

141▶ • N R T Y K L P I L E E I T T K V

SacI (2254) 2201 CAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTG

124▶ 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 R I S R

2301 TCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGA

90▶ 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 A E A C V

StuI (2418) 2401 CAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCCGACATGGTGCTTGTGCTCATA

57▶ 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 N D E Y

BbsI (2564)
XmnI (2560)
2501 GAGCATGGTGATCTTCTCAGTGGCGACCTCCACGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTA
24 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 (2626) **SacI (2683)**
2601 TACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAG
←

SpeI (2781)
2701 ACCTCCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTGATTTACTAGICAAAACAACTCC
←

2801 CATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGC
←

SnaBI (2909)
2901 GATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGGTCATGTAAGTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATA
←

NdeI (3014)
3001 GGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCG
←

SdaI (3192)
3101 TTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCTGCAGG
←

PacI (3200) **BspLU11I (3210)**
3201 TTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGC
←

3301 ATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGT
←

3401 TCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAG
←

ApaLI (3524)
3501 GTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGAC
←

3601 ACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGG
←

3701 CTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCT
←

3801 GGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGT
←

EagI (3960)
PacI (3940) **SwaI (3949)** **NotI (3959)**
3901 GGAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGT
←

4001 GTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGAAGTGCAG
4101 GTGCCAGAACATTTCTCTATCGAA