



PvuI (7)
SgfI (6)
EcoNI (96)

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552)
BspHI (560)

501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCATCATGACACCCACAGACTTACAAGCCCTATTCCTAACAT

▶

1▶ M T P T D F T S P I P N M

NcoI (632)
HpaI (646)

601 GGCTGATGACTATGGCTCTGAATCCACATCTTCCATGGAAAGACTACGTTAACTTCAACTTCACTGACTTCTACTGTGAGAAAAACAATGTCAGGCAGTTT

13▶ A D D Y G S E S T S S M E D Y V N F N F T D F Y C E K N N V R Q F

701 GCGAGCCATTTCTCCACCTTGTACTGGCTCGTGTTCATCGTGGTGCCTTGGCAACAGTCTTGTATCCTTGTCTACTGGTACTGCACAAGAGTGA

47▶ A S H F L P P L Y W L V F I V G A L G N S L V I L V Y W Y C T R V

801 AGACCATGACCGACATGTTCTTTTGAATTTGGCAATTGCTGACCTCCTCTTTTGTACTTCTCCCTTCTGGGCCATTGCTGCTGCTGACCAAGTGGAA

80▶ K T M T D M F L L N L A I A D L L F L V T L P F W A I A A A D Q W K

BsrGI (935)

901 GTTCCAGACCTTCATGTGCAAGGTGGTCAACAGCATGTACAAGATGAACTTACAGCTGTGTGTTGCTGATCATGTGCATCAGCGTGGACAGGTACATT

113▶ F Q T F M C K V V N S M Y K M N F Y S C V L L I M C I S V D R Y I

BsrGI (1049)

1001 GCCATTGCCAGGCCATGAGAGCACATACTTGGAGGGAGAAAAGGCTTTGTACAGCAAATGGTTTGTCTTACCATCTGGGTATTGGCAGCTGCTCTCT

147▶ A I A Q A M R A H T W R E K R L L Y S K M V C F T I W V L A A A L

NcoI (1157)

1101 GCATCCCAGAAATCTTATACAGCCAAATCAAGGAGGAATCCGGCATTGCTATCTGCACCATGGTTTACCCTAGCGATGAGAGCACAAACTGAAGTCAGC

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

1201 TGTCTTGACCTGAAGGTCAATTCTGGGGTCTTCTTCCCTTCTGGTTCATGGCTTGTGCTATACCATCATTTACACCCTGATACAAGCCAAGAAG

213▶ V L T L K V I L G F F L P F V V M A C C Y T I I I H T L I Q A K K

1301 TCTTCAAAGCACAAAGCCCTAAAAGTGACCATCACTGTCTGACCGTCTTTGTCTTGTCTCAGTTTCCCTACAACCTGCATTTTGTGGTGCAGACCATTG

247▶ S S K H K A L K V T I T V L T V F V L S Q F P Y N C I L L V Q T I

BstEII (1461)

1401 ACGCTATGCCATGTTCACTCCAACCTGTGCCGTTTCCACCAACATTGACATCTGCTTCCAGGTCACCCAGACCATCGCCTTCTTCCACAGTTGCCTGAA

280▶ D A Y A M F I S N C A V S T N I D I C F Q V T Q T I A F F H S C L N

1501 CCCTGTTCTATGTTTTGTGGGTGAGAGATTCGCCGGGATCTCGTGAACACCTGAAGAAGTGGGTTGCATCAGCCAGGCCAGTGGGTTTCATTT

313▶ P V L Y V F V G E R F R R D L V K T L K N L G C I S Q A Q W V S F

HindIII (1614)
Bsu36I (1649)

1601 ACAAGGAGAGAGGGAAGCTTGAAGCTGTCGTCTATGTTGCTGGAGACAACCTCAGGAGCACTTCCCTCTGAGGGTCTTCTCTGAGGTGCATGGTTCTT

347▶ T R R E G S L K L S S M L L E T T S G A L S L •

MscI (1708)

NheI (1702)

1701 TTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGAAATTTGTGATGC

HpaI (1840)

1801 TATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACCAATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTT

EcoRI (1936)

1901 TTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTT

2001 CTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATT

SapI (2118)
SspI (2175)
SwaI (2189)

2101 TTCCAAGGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACA

EcoO109I (2250)

2201 TCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAG

2301 GAACCTTTAATAGAAATTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGC

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

SacI (2450)
BstXI (2479)

2401 TTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCA

122▶ 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 D V

2501 CCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTTCAGCACAGACAGT

89▶ 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 T

StuI (2614)
 2601 GACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGC
 56 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 L

XmnI (2756)
 2701 ATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACT
 22 M T I K E T A V E V L E L D Q Q S I N F T K M

AseI (2822) **SacI (2879)**
 2801 ATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCT

SpeI (2977)
 2901 CCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATT
 3001 GACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATG

SnaBI (3105)
 3101 ACTAATACGTAGATGTAAGTAGGAAAGTCCATAAGGTCACTGTAAGTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGG

NdeI (3210)
 3201 GCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTAC

PacI (3396)
PstI (3389)
SdaI (3388)
 3301 TATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAA

BspLU11I (3406)
 3401 ITAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCA
 3501 CAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCG
 3601 ACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCG

ApaLI (3720)
 3701 TTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGA
 3801 CTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC
 3901 ACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTA
 4001 GCGGTGGTTTTTTTGGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAA

EagI (4156)
PacI (4136) **SwaI (4145)** **NotI (4155)**
 4101 CGAAAACACGTTAAGGGATTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTG
 4201 GTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGC
 4301 CAGAACATTTCTCTATCGAA