



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCGCCGCCCTACCTGAGGCC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGTTGCTCAACTCTACGCTTTTGTTCGTTT

BspHI (560)
AgeI (552) 501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGGCGGCTACCTGAGATCACCGGTCATCATGAACCTCTTCCACAAGCGCCTTCGGTCCAGTTGC
XmnI (564) 1▶ M N S F S T S A F G P V A

601 CTTCTCCCTGGGGCTGCTCGGTGTTGCTGCTGCTGCTCCCTGCCCCAGTACCCCCAGGAGAAGATCCAAAGATGTAGCCGCCACACAGACAGCCA
13▶ F S L G L L L V L P A A F P A P V P G E D S K D V A A P H R Q P
701 CTCACCTCTTGAACGAATTGACAAACAAATTCGGTACATCTCAGCCCTGAGAAAGGAGACATGTAACAAGATAACATGTGTGAAA
47▶ L T S S E R I D K Q I R Y I L D G I S A L R K E T C N K S N M C E
801 GCAGCAAAGAGGCACTGGCAGAAAAACCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCAATCTGGATTAATGAGGAGACTGCCTGGT
80▶ S S K E A L A E N N L N L P K M A E K D G C F Q S G F N E E T C L V

Bst1107I (931)
901 GAAATCATCACTGGTCTTTTGGAGTTTGGAGTATACCTAGAGTACCTCCAGAACAGATTTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGT
113▶ K I I T G L L E F E V Y L E Y L Q N R F E S S E E Q A R A V Q M S

XbaI (1041)
1001 AAAAAAGTCTGATCCAGTTCCTGCAGAAAAAGCAAAGAATCTAGATGCAATAACCACCCCTGACCCAACCACAAATGCCAGCCTGCTGACGAAGCTGC
147▶ T K V L I Q F L Q K K A K N L D A I T T P D P T T N A S L L T K L

SapI (1183)
1101 AGGCACAGAACCAGTGGCTGCAGGACATGACAACCTCATCTCATTCTGCGCAGCTTTAAGGAGTTCCTGCAGTCCAGCCTGAGGGCTCTTCGGCAAATGTA
180▶ Q A Q N Q W L Q D M T T H L I L R S F K E F L Q S S L R A L R Q M •

MscI (1206)
NheI (1200) 1201 GCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTA
213▶

HpaI (1338) **MfeI (1349)**
1301 TTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTT

EcoRI (1434)
1401 TTAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTGAAATCCTTTTCT
1501 GAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGATTTTT

SapI (1616) **SspI (1673)** **Swal (1687)**
1601 CCCAAGTTTGAAGTCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATC

EcoO109I (1748)
1701 ATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGA
1801 ACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTT
141▶ • N R T Y K L P I L E E I T T K V L K

SacI (1948) **BstXI (1977)**
1901 GCCATTCTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACC
122▶ 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
2001 TCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGA
88▶ 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 V

StuI (2112)
2101 CCCTGCCAATGTAGGCCTCAATGTGACAGCAGAGATGATCTCCCGCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGCTCCATAGAGCAT
55▶ 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 M

BbsI (2258) **XmnI (2254)**
2201 GGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTAT
22▶ T I K E T A V E V L E L D Q Q S I N F T K M

AseI (2320) **SacI (2377)**
2301 GCCGATATACTATGCCGATGATTAATTGCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACTCC

SpeI (2475)
2401 CACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATGTA
2501 CGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGAC

SnaBI (2603)
2601 TAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGC

NdeI (2708)
2701 GTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAGTCCCTATTGGCGTTACTA

SdaI (2886) PacI (2894)
2801 TGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAATT

2901 AAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACA
←

3001 AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGAC

3101 CCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT

ApaLI (3218)
3201 CGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACT

3301 TATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACAC

3401 TAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGC

3501 GGTGGTTTTTTTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACG

EagI (3654)
PacI (3634) SmaI (3643) **NotI (3653)**
3601 AAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGT

3701 TTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAAGTGCAAGTGCAGGTGCCA
3801 GAACATTTCTCTATCGAA