



PvuI (7)
SgfI (6) MfeI (82) EcoNI (96)
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
PvuII (239) EcoNI (287)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

BspHI (560) MscI (596)
AgeI (552)
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCATCATGAGGCTCAGCACAGCAACGCTGTTCTCTCTCTGGC
1▶ M R L S T A T L L L L L A

PvuII (600)
601 CAGCTGCCTCTCTCCAGGCCACGGTATTCTGGAAGCCATTACACAACTTAAATGTAGGTGTTCTGGAGTGATTTCACTGTTGTGGTCTAAACATC
13▶ S C L S P G H G I L E A H Y T N L K C R C S G V I S T V V G L N I
701 ATAGATCGGATTCAGATTACGCCCTGGGAATGGCTGCCCAAACTGAAGTTGTGATCTGGACCAAGATGAAGAAAGTTATATGTGTAATCCTCGT
47▶ I D R I Q V T P P G N G C P K T E V V I W T K M K K V I C V N P R

BspLU11I (825) **BbsI (846)** **SapI (878)**
801 CCAATGGTTACAAAGATTATTAAGACATGTCCAAGCAAAGTCTGTCTTCAACTCCCAAGCTCCAGTGAGTAAGAGAAGAGCTGCCTGAAGCCACTA
80▶ A K W L Q R L L R H V Q S K S L S S T P Q A P V S K R R A A •

MscI (931)
NheI (925)
901 TCATCTCAAAGACACACCTGCACCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGC

HpaI (1063) MfeI (1074)
1001 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAACATTGCATTCATTTTATGTTTCAGG

EcoRI (1159)
1101 TTCAGGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAAT
1201 CAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCA

SapI (1341) **SspI (1398)**
1301 TGGAGTTAAGATATAGTGATTTTCCCAAGTTTGAAGTCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGTAATA

Swal (1412) **EcoO109I (1473)**
1401 TATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTA
1501 GTAGTTGGACTTAGGGAACAAAGGAACCTTTAATGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTT
141▶ • N R T Y K L P I L E

SacI (1673)
1601 CCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCT
130▶ E I 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

BstXI (1702)
1701 GACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATG
97▶ V V 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

StuI (1837)
1801 GCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGCGCTCAATGTGGACAGCAGAGATGATCTCCCGTCTTGGTCTGATGGCCGCCCGACAT
63▶ A I 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

BbsI (1983) **XmnI (1979)**
1901 GGTGCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTATGGTGGCCCT
30▶ H K 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

AseI (2045)
2001 CCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAA

SacI (2102)
2101 ACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTT

SpeI (2200)
2201 ACTAGTCAAACAAACTCCCATGACGTCATGGGGTGGAGACTTGGAAATCCCCTGAGTCAAACCGCTATCCACGCCATTGATGACTGCCAAAACC

SnaBI (2328)
2301 GCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTACCAAGTGGAAAGTCCCATAGGTCATGTAAGTGGCATAATGCCAGCGGGCCATTT

NdeI (2433)
2401 ACCGTCATTGACGTCATAGGGGGCTACTTGGCATATGATACACTTGTGACTGCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAA

2501 TGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAA

PacI (2619)

PstI (2612)

SdaI (2611)

BspLU11I (2629)

2601 GTTATGTAACGCTGCAGGTTAATTAAAGAACTGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG

2701 CTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCT

2801 CCCTCGTGCCTCTCTGTTCGACCCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCACGCTGTAG

ApaLI (2943)

2901 GTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT

3001 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGGTCTACAGAGTTCTTGA

3101 AGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATC

3201 CGGCAACAACACCACCGCTGGTAGCGGTGTTTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT

EagI (3379)

PacI (3359) SwaI (3368)

NotI (3378)

3301 ACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAATATCTTT

3401 ATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCT

3501 GTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA