



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) **Bsu36I (291)**
Psp1406I (203) **PvuII (239)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCTCAACTCTACGCTTTGTTTCGTTT

BstEII (555)
AgeI (552) NcoI (560)
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCCCCGTGTGACCCACTCCTGGCCTTCAGCCT
601 GCTGGTCTCTGGACCTCCAGCCCCAACTCTGGGGGTGCTAATGATGCGGAAGACTGTGCTGTCTGTGACCCAGCGCCCCATCCTGGGAACATC
13▶ L V L W T F P A P T L G G A N D A E D C C L S V T Q R P I P G N I

XmnI (702) **PstI (735)** **XcmI (793)**
701 GTGAAAGCCTCCGCTACCTTCTAATGAAGATGCGCTGCAGGTGCCTGCTGTTGTGTTCCACACACTAAGGGGCTATCAGCTCTGTGCACCTCCAGACC
47▶ V K A F R Y L L N E D G C R V P A V V F T T L R G Y Q L C A P P D
ApaLI (785)

BsaBI (896)
801 AGCCCTGGTGGATCGCATCATCCGAAGACTGAAGAAGTCTTCTGCCAAGAACAAGGCAACAGCACCAGAAGGAGCCTGTGTCTTGTAGTAAAGAGATG
80▶ Q P W V D R I I R R L K K S S A K N K G N S T R R S P V S •

NheI (925)
BstXI (922) MscI (931)
901 TGAATCACTCTGCCCCAGGAAACAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGC

HpaI (1063) **MfeI (1074)**
1001 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAAATTCATTCTTTATGTTTCAGG

EcoRI (1159)
1101 TTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAT
1201 CAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTCTTTCA

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

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

SacI (1673)
1601 CCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCT
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 GCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCGACAT
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

XmnI (1979)
1901 GGTGCTTGTGCTCATAGAGCATGGTGTCTTCTAGTGGCAGCTCCACCAGCTCCAGATCTGTGAGAGATGTTGAAGTCTTCATGGTGGCCCT
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 CCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAA

SacI (2102)
2101 ACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTT

SpeI (2200)
2201 ACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACC

2301 GCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTT
SnaBI (2328)

2401 ACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAA
NdeI (2433)

2501 TGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAA
PacI (2619)

PstI (2612)
SdaI (2611) **BspLU11I (2629)**

2601 GTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGG
2701 CTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCT
2801 CCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG
ApaLI (2943)

2901 GTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT
3001 GAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGA
3101 AGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATC
3201 CGGCAAACAACCCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT

3301 ACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTT
EagI (3379)
PacI (3359) SmaI (3368) **NotI (3378)**

3401 ATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCT
3501 GTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA