



PvuI (7) SgfI (6) MfeI (82)
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) Psp1406I (203) PvuII (239) Bsu36I (291)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555) AgeI (552) NcoI (560) BbsI (574)
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACTCTGAGATCACCGGTACCATGGCTACAGATGTCTTCAATTCAAAAACCTGGCCGT
1▶ M A T D V F N S K N L A V BstEII (699)

BsrGI (692)
601 TCAGGCACAAAAGAAGATCCTGGGCAAAATGGTATCCAATCCATCGCCACCACGCTGATCGACGACACCAGCAGCGAGGTGCTAGATGAGCTGTACAGG
13▶ Q A Q K K I L G K M V S K S I A T T L I D D T S S E V L D E L Y R
701 GTGACCAAGGAGTACACCAGAACAAGAAGGAGCGGAGAGGGTCATCAAGAACCTCATCAAGACGGTCATCAAGCTGGCCGTCTCCACAGGAACAATC
47▶ V T K E Y T Q N K K E A E R V I K N L I K T V I K L A V L H R N N

ApaLI (847) PshAI (864)
801 AGTTCAATCAAGACGAGCTGGCGCTCATGGAGAAGTTCAAGAAGAAGTGCACCAGCTTGCCATGACGGTCTGTCAGCTTCCACCAGGTAGAGTACACCTT
80▶ Q F N Q D E L A L M E K F K K K V H Q L A M T V V S F H Q V E Y T F
901 CGACCGCAATGTGCTGTCCAGGCTGCTGAACGAGTGCAGAGCTCTACAGGAGATCATTACGCGCCACCTACCGCCAAGTCTCACGGACGGGTTAAT
113▶ D R N V L S R L L N E C R E L L H E I I Q R H L T A K S H G R V N

BsrGI (1043) PmeI (1062)
1001 AATGTCTTTGACCATTTTTAGATTGTGATTTTTGGTGCCTTGTAACCTCCCTTTGAAAGTTTAAACCTCACTTACAGAACTTTGCGACGGCATCA
147▶ N V F D H F S D C D F L A A L Y N P F G K F K P H L Q K L C D G I

MscI (1159)
1101 AAAAAATGTTGGATGAAGAGAACATAGCTTGCGAAGTAAGATTGTGACCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAAC
180▶ N K M L D E E N I •

HpaI (1291)
1201 CACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAACAAAC

MfeI (1302) EcoRI (1387)
1301 AACAAATGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATTTAAAAATA
1401 CAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCAT

SapI (1569)
1501 TAGCTGTTTCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGTATTTCCCAAGGTTTGAAGTCTTCTTCTTTATGTTTTAAATGCACT

SspI (1626) SvaI (1640)
1601 GACCTCCACATTCCTTTTTAGTAAAAATATTCAGAAAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTC

EcoO109I (1701)
1701 AAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTAAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAG
1801 TTCCTGGTACTTTGAGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGA
139▶ N R T Y K L P I L E E I T T K V L K G N M E I L V F C D P A Y D S I
1901 TGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAAGTGGTGTCAAAGSCTT
106▶ L E R C M G C P S V V R I S R D V E D S Y P H R V A V I T D F D K

StuI (2065)
2001 CTGCCCCTTGCACAGCAGACCAATGGCAATGGCTTTCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCA
73▶ Q G N S V A S G I A I A E A C V T V R G I Y A E I H V A S I I E G
2101 GTCTTGGTCTGATGGCCGCCCCGACATGGTGTGCTTGTGCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAG
39▶ T K T R I A A G V H H K N D E Y L M T I K E T A V E V L E L D Q Q S

BbsI (2211) XmnI (2207) AseI (2273)
2201 AGATGTTGAAGGTCCTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGC
6▶ I N F T K M
2301 GTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTT

2401 ACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTAT
SpeI (2428)
←

2501 CCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGT
SnaBI (2556)

2601 ACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTAAGTGGGCAGTTTA
NdeI (2661)

2701 CCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGC

2801 GGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAA
PacI (2847)
PstI (2840)
SdaI (2839)
BspLU11I (2857)
←

2901 GGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA

3001 AGATACCAGGCGTTTCCCCCTGGAAGTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCG

3101 TGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCG
ApaLI (3171)

3201 CTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGG

3301 TATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT

3401 TCGGAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGGCAGAAAAAAGG

3501 ATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATT
PacI (3587) SwaI (3596)

3601 AAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAC
EagI (3607)
NotI (3606)

3701 GAAACAAAACAACTAGCAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA