



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGTGCCTA
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

KasI (535) **NcoI (560)**
AgeI (552) **BstEII (555)**
XcmI (560)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATGGGGATGCTGGTGCCTACTGCTAGTCTGCTGGCT
1▶ M G M L V P T A L A R L

PvuII (619) **MscI (644)**
601 GCTGAGCCTGTTCCAGCAGCAGCTGGGTTCCCTCTGGAGTGGCTGGCCATCCTGTTCTGCTGGCTGAGAATAGCATTAGGGTGGCTAGATCCCGGGAAG
13▶ L S L F Q Q Q L G S L W S G L A I L F C W L R I A L G W L D P G K
XmaI (691)

BstXI (744)
701 GAACAGCCACAGGTCGGGGTGAAGTGGAGGAGACCCAGGAGACCAGGAAGATGGGAACAGCACTCAGCGCACACCCCGTGAGTGTCAACTACCACT
47▶ E Q P Q V R G E L E E T Q E T Q E D G N S T Q R T T P V S V N Y H
801 TCACTCGTCAGTCAACTACAAATGTGGCTTCTGCTTCCACACAGCCAAGACATCCTTCTGCTGCCCTGGAGGAGGCAAGCGAGGACTGCTTCTGCT
80▶ F T R Q C N Y K C G F C F H T A K T S F V L P L E E A K R G L L L L

HindIII (976)
901 CAAACAGGCTGGTTTGGAGAAGATCAACTTTTCTGGAGGAGAACCCTTCTTCCAGGACAGGGTGAATACTTGGCAAGCTTGTGAGATTCTGCAAGGAG
113▶ K Q A G L E K I N F S G G E P F L Q D R G E Y L G K L V R F C K E

NheI (1002)
1001 GAGCTAGCCCTGCCTCTGTGAGCATAGTGAAGCAATGGCAGCCTATCCAGGAGAGATGGTTCAAGGACTATGGGGAGTATTTGGACATTCTTGCTATCT
147▶ E L A L P S V S I V S N G S L I Q E R W F K D Y G E Y L D I L A I

BbrPI (1162)
1101 CCTGCGACAGCTTCGATGAGCAGGTTAATGCTCTGATTGGCCGTGGTCAAGGAAAAAAGAACACGTGGAAAACCTTCAAAGCTGAGGAGGTGGTGCAG
180▶ S C D S F D E Q V N A L I G R G Q G K K N H V E N L Q K L R R W C R

AseI (1234) **BbsI (1255)**
1201 GGATTACAAGGTGGCTTTCAAGATCAACTCTGTCTTAATCGCTTCAACGTGGACGAAGACATGAATGAACACATCAAGGCCCTGAGCCCTGTGCCTGG
213▶ D Y K V A F K I N S V I N R F N V D E D M N E H I K A L S P V R W

Bsu36I (1350)
1301 AAGTTTTCCAGTGCCTCCTAATTGAGGGTGAAGACTCAGGAGAAGATGCCCTGAGGGGAGCAGAAAGATTTCTTATAAGCAATGAAGAATTTGAAACAT
247▶ K V F Q C L L I E G E N S G E D A L R E A E R F L I S N E E F E T
1401 TCTTGGAGCGTCACAAAGAGGTGCTGTTGGTGCCTGAATCAACCAAGATGAAAGACTCCTACCTTATCTAGATGAATATATGCGCTTCTGAA
280▶ F L E R H K E V S C L V P E S N Q K M K D S Y L I L D E Y M R F L N

AgeI (1504) **XcmI (1526)**
1501 CTGTACCGGTGGCCGGAAGGACCTTCCAAGTCTATTCTGGATGTTGGCGTGAAGAAGCAATAAAGTTCAGTGGATTGATGAGAAGATGTTTCTGAAG
313▶ C T G G R K D P S K S I L D V G V E E A I K F S G F D E K M F L K

AvrII (1651)
PshAI (1649)
BstEII (1646) **MscI (1663)**
1601 CGTGGCGAAAGTATGTGTGGAGTAAAGCTGACCTGAAGCTGGACTGGTACCTAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGAC
347▶ R G G K Y V W S K A D L K L D W •

HpaI (1795)
1701 AAACCACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAA

MfeI (1806) **EcoRI (1891)**
1801 CAACAACAATTGCATTATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAA
1901 AATACAGCATAGCAAACTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGT

SapI (2073)
2001 GCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTTCTTCTTTATGTTTTAAATG

SspI (2130) **SwaI (2144)**
2101 CACTGACCTCCCACATTCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGAT
2201 GCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCT

2301 TTAGTTCCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCA
141▶ • 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

SacI (2405) **BstXI (2434)**
2401 GAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGT
107▶ S I 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

2501 CTTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTC
74 K 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
2601 CCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGC
41 G 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
BbsI (2715) AseI (2777)
2701 TGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGA
74 Q S I N F T K M
SacI (2834)
2801 TGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGT
SpeI (2932)
2901 TGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCG
SnaBI (3060)
3001 CTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTC
NdeI (3165)
3101 ATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAG
3201 TTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTGTT
PacI (3351)
PstI (3344)
SdaI (3343) BspLU11I (3361)
3301 GGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTA
3401 AAAAGGCCCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT
3501 ATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGA
ApaLI (3675)
3601 AGCGTGGCGCTTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCG
3701 ACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC
3801 GAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT
3901 ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAA
PacI (4091)
4001 AAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTACGTTAAGGGATTTGGTTCATGGCTAGTTAATTAAC
EagI (4111)
SwaI (4100) NotI (4110)
4101 ATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACA
4201 AAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA