



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

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC
EcoNI (287)
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

KasI (535) **AgeI (552)** **BspHI (560)** **BsrBI (595)**
501 TCTGTTCTGGCGCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCATCATGACAATGAGATATGAAAACCTCCAGAACTGGAGCG
1▶ M T M R Y E N F Q N L E R
601 GGAAGAGAAAAACAGGAGATGAGAAATGGTGACAAGAAAGGGAATGGAGTCTCCAAAGTTTGGCTTAATTCCTCCAGTCTTCTGTGGCGCATC
13▶ E E K N Q E M R N G D K K G G M E S P K F A L I P S Q S F L W R I

BamHI (772)
701 CTCTTTGGACCCACCTCCTCTGTTCTCCTGGGCTCAGCCTCCTGCTACTGGTGGTCATCTCCGTGATTGGATCCAAAATTCAGTTAAGGAGGG
47▶ L S W T H L L L F S L G L S L L L L V V I S V I G S Q N S Q L R R

AvrII (801) **BstBI (886)**
801 ACCTAGGCACCTAAGAGCCATTTTAGACAACACCACCTCCAAGATAAAGGCTGAATTCAGTCCCTGGACTCCAGGGCTGACAACTCGAAAAAGGAT
80▶ D L G T L R A I L D N T T S K I K A E F Q S L D S R A D N F E K G I

BstAPI (933)
901 CAGTTCTGAAAGTGGATGTGGAGGATCACAGGCAGGAACTGCAGGCAGCCGAGACTTGAGCCAGAAGTGACTTCTCTGGAGAGCACACTGGAGAAG
113▶ S S L K V D V E D H R Q E L Q A G R D L S Q K V T S L E S T L E K

BglIII (1020) **BsrGI (1044)** **StuI (1070)** **MscI (1088)**
1001 AGGGAGCAGGCTCTCAAAACAGATCTGTCTGATTTAACCGACCATGTACAACAGCTGGAGACAGACTTGAAGGCTTGACGTGCCAGCTGGCCAACTCA
147▶ R E Q A L K T D L S D L T D H V Q Q L E T D L K A L T C Q L A N L
1101 AGAACAATGGCTCGGAAGTGGCTGCTGCCCGTTCAGTGGACGGAGCATGAAGGCAGCTGCTATTGGTTCTCTGAGTCTGAGAAGTCGTGGCCTGAAGC
180▶ K N N G S E V A C C P L H W T E H E G S C Y W F S E S E K S W P E A

NgoMIV (1211)
1201 TGACAAGTACTGCCGGCTGGAGAATTCTCACCTGGTGGTCAACTCCCTGGAGGAGCAGAATTTTCTACAGAATCGTTAGCCAATGTGCTTAGCTGG
213▶ D K Y C R L E N S H L V V V N S L E E Q N F L Q N R L A N V L S W

ScaI (1205) **DraIII (1228)**
1301 ATGGCCCTAACGGACCAAAATGGCCCTGGCGATGGGTGGATGGGACCGACTTTGACAAAGTTTCAAGAATTGGAGGCCACTGCAGCCGGATAACTGCC
247▶ M G L T D Q N G P W R W V D G T D F D K G F K N W R P L Q P D N W

NdeI (1405) **Tth111I (1462)**
1401 ATGGACATATGCTAGGTGGAGGCGAGGACTGTGCCACTTTTCTACGATGGTGGTGAATGACGATGCTGCGCAGAGGCATTACCATTGGATCTGTGA
280▶ H G H M L G G G E D C A H F S Y D G R W N D D V C Q R H Y H W I C E

NheI (1561) **XcmI (1555)** **MscI (1567)**
1501 AACAGAGCTGGGCAAAGCCAGCTCAGCCCACTCCCACTTATAGCCTCAGTTCATAAGCTAGCTGGCCGACATGATAAGATACATTGATGAGTTT
313▶ T E L G K A S S A H S P Q L I A S V P •

HpaI (1699)
1601 GGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAG

MfeI (1710)
1701 TTAACAACAACAATTGCATTCTTTTATGTTTCAGGTTTCAGGGGAGGTGGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATT
1801 CTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTTTGCCA

SapI (1977)
1901 ATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTCTTCTTTATTTATGTTT

SspI (2034) **SwaI (2048)**
2001 AATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCC
2101 AGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAATTGGACAGCAAGAAAGCGAGCTTCT

SacI (2309) **BstXI (2338)**
2201 AGCTTTAGTTCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATA
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
2301 GTCAGAGATGAGCTCTCTGCACATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCA
109▶ D 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

StuI (2473)
2401 AAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGA
75▶ F D 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
2501 TCTCCCCAGTCTGGTCTGATGGCCGCCCGACATGGTGCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATC
42▶ E 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

BbsI (2619)
XmnI (2615) **AseI (2681)**
 2601 CTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCG
 9 Q Q S I N F T K M

SacI (2738)
 2701 TGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCG

SpeI (2836)
 2801 GAGTTGTTACGACATTTTGGAAAGTCCCCTGATTACTAGTCAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAA

SnaBI (2964)
 2901 ACCGCTATCCAGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAA

NdeI (3069)
 3001 GGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGG
 3101 GCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGT

PacI (3255)
SdaI (3247) **BspLU11I (3265)**
 3201 CGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC
 3301 CGTAAAAAGGCCGCTTGTGCGGTTTTCCATAGGCTCCGCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAG
 3401 GACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTC

ApaLI (3579)
 3501 GGGAAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTTCCAG
 3601 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA
 3701 GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGTGAAGCC
 3801 AGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGA

PacI (3995)
 3901 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTGGTCAATGGCTAGTTAAT

EagI (4015)
SwaI (4004) **NotI (4014)**
 4001 TAACATTTAAATCAGCGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAA
 4101 AACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA