



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGGGGTAACGGAAAGTGTGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

KasI (535) **BspLU11I (560)**
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCAACATGTCTCTGGAAAAGATGTGGGAGGAGGTACCTGTTC
BstEII (588)
1▶ M S L E K M W E E V T C S

BamHI (609) **MscI (642)** **NsiI (663)**
601 TATCTGCCTGGATCCCATGGTGGAGCCTATGAGTATCGAATGTGGCCATTGCTTTTGAAGGAATGCATTTTTGAAGTTGGGAAGAATGGGGCAGTTCA
13▶ I C L D P M V E P M S I E C G H C F C K E C I F E V G K N G G S S
BstAPI (656)
701 TGTCGGAGTGGCGGCAACAGTTTCTGCTCCGAAACCTCAGGCCAATAGACATATGCCAACATGGTGGAAAACCTTAAACAGATAGCCAGAATACCA
47▶ C P E C R Q Q F L L R N L R P N R H I A N M V E N L K Q I A Q N T
BstXI (758)
801 AGAAGAGTACCCAGGAAACGCACTGCATGAAGCATGGAGAGAAGCTTCACTATTCTGTGAGGAAGATGGGCAGGCCCTTTGCTGGGTGTGTGCCAGTC
80▶ K K S T Q E T H C M K H G E K L H L F C E E D G Q A L C W V C A Q S
SandI (923) **Bst1107I (949)** **BbrPI (967)**
901 TGGGAAACACCGGGACCACACCAGGTCCTATTGAAGAGGCTGCTAAGGTATACCAGGAGAAGATCCACGTGGCTTTAGAAAACTGAGAAAGGGGAAA
113▶ G K H R D H T R V P I E E A A K V Y Q E K I H V A L E K L R K G K
1001 GAGTTGGCCGAGAAGATGAAAATGGATCTCAGCATGCAAGAAACAGACTGGAAGAGGAACATTGACACCCAGAAGTTCAGGATTACCGCAGAGTTGCGAC
147▶ E L A E K M E M D L T M Q R T D W K R N I D T Q K S R I H A E F A

PvuII (1135)
1101 TTCAGAATAGCTTGTGGCTCAGGAGGAGCAGAGGCTGCAGAGGCTGGAGAAGGATCAAAGGGAGTACCTGAGACTCCTGGGGAAGAAGGAGGCTGA
180▶ L Q N S L L A Q E E Q R Q L Q R L E K D Q R E Y L R L L G K K E A E
SdaI (1221)
1201 GCTGGCTGAGAAGAACCAGGCCCTGCAGGAGCTGATCTCAGAGCTGGAGAGGAGATTCTGGTTTTCAGAGCTGGAGTACTGCAGGAGGTGAGGATCATC
213▶ L A E K N Q A L Q E L I S E L E R R I R G S E L E L L Q E V R I I

BamHI (1312)
1301 CTGGAAAGGAGTGGATCCTGGAACCTGGACACGTTAGATATTGACGCCCCAGACCTAACAAAGCACATGCCCTGTGCCAGGGCGGAAGAAGATGCTGAGGA
247▶ L E R S G S W N L D T L D I D A P D L T S T C P V P G R K K M L R
1401 CGTGTGGGTTTCATATTACTCTGGATCGCAACACCCGCAACTCATGGCTCATCATCTCAAAGGATCGGAGACAAGTGAGGATGGGAGACACCCATCAGAA
280▶ T C W V H I T L D R N T A N S W L I I S K D R R Q V R M G D T H Q N
1501 CGTGTCTGACAATAGGAGAGGTTTGTAAATTACCCATGGTGTAGGTCGCCAGAGATTCTCCTCTGGGAAGATGACTGGGAGGTAGATGTGACTCAA
313▶ V S D N K E R F S N Y P M V L G A Q R F S S G K M Y W E V D V T Q

StuI (1604) **XmnI (1671)**
1601 AAGGAGGCTGGATCTGGGGTGGTTCAGAGATTCTGTTTCAGAGGAAAGGGCAGTTTTCACTCAGTCCCGAGAATGGCTTCTGGACCATTGGTTATGGC
347▶ K E A W D L G V C R D S V Q R K G Q F S L S P E N G F W T I W L W

Acc65I (1717)
1701 AAGACAGCTATGAGGCTGACAGTCCAGACCACCCTCCACATTCAAGTACCTCCATGCCAAATTGGGATCTTTGTGGACTATGAGGCTGGCGTTGT
380▶ Q D S Y E A G T S P Q T T L H I Q V P P C Q I G I F V D Y E A G V V
1801 CTCCTTCTACAACATAACTGACCATGGCTCCCTCATTTACACCTTCTCGGAGTGTGTTTTTGTGGACCTCTGCGACCTTTCTCAATGTTGGTTTCAAT
413▶ S F Y N I T D H G S L I Y T F S E C V F A G P L R P F F N V G F N

MscI (1992)
1901 TATAGTGGGGAAATGCAGCGCCTCTAAAGCTCTGTCCACTAAAGATGTGATGGTCAGGAGCCAGTGCCTACTGACGGTACTTCCCCTAGCTGGCCAGA
447▶ Y S G G N A A P L K L C P L K M •
2001 CATGATAAGATACATTGATGAGTTTGGACAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTA

HpaI (2124) **MfeI (2135)**
2101 ACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCTTTATGTTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAA

EcoRI (2220)
2201 ACCTTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAG
2301 GCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATAGTGTATTTTCCCAAGGTTTGAAC

SapI (2402) **SspI (2459)** **Swal (2473)**
2401 TAGCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAT
2501 AAATGTTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGGACTTAGGGAACAAAGGAACCTTTAATAGAAA

2601 TTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCACTCAA
141 • N R T Y K L P I L E E I T T K V L K G N M E I
SacI (2734) BstXI (2763)

2701 TGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGG
117 L V F C D P A Y 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
StuI (2898)

2801 GTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAG
84 H R V A V I T D 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
2901 GCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCTCATAGAGCATGGTGATCTTCTCAG
50 A E I H V A S I I 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
BbsI (3044)

3001 TGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATG
17 A V E V L E L D Q Q S I N F T K M
XmnI (3040)

3101 CCGATGATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCT
AseI (3106) SacI (3163)

3201 ACCGCCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGG
SpeI (3261)

3301 AGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGGACTAATACGTAGATGT
SnaBI (3389)

3401 ACTGCCAAGTAGGAAAGTCCCATAAAGTTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATG
NdeI (3494)

3501 ATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTC
SdaI (3672) PacI (3680) BspLU11I (3690)

3601 ATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGACCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGC
3701 AAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCA
3801 AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCG
3901 GATACCTGTCCGCTTTCTCCCTTGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGG
ApaLI (4004)

4001 CTGTGTGCACGAACCCCGTTTCAGCCGACCGCTGCGCTTATCCGTAACCTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCA
4101 GCAGCCACTGTTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGCCTAACTACGCTACACTAGAAGAACAGTAT
4201 TTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTGT
4301 TTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAA
EagI (4440)

4401 GGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTTGTGTAATC
PacI (4420) SwaI (4429) NotI (4439)

4501 GTAACATAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGCAAGTGACAGGTGCCAGAACATTTCTCTAT
4601 CGAA