



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCCTGTTGCTCAACTCTACGCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **BspHI (568)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTAGGAGGGCCATCATGAGTACTCCAAGGAACCAAGACTGCAG
1 M S D S K E P R L Q

StuI (632) **XhoI (652)** **NeoI (686)** **MscI (683)**
601 CAGCTGGCCTCCTGGAGGAGAACAGCTGAGAGGCCTTGGATTCCGACAGACTCGAGGATACAAGAGCTTAGCAGGGTGTCTTGGCCATGGTCCCCTGG
11 Q L G L L E E E Q L R G L G F R Q T R G Y K S L A G C L G H G P L
701 TGCTGCAACTCCTCTCCTCAGCCTCTGGCTGGGCTCCTTGTCCAAGTGTCCAAGGTCCCAAGCTCCAGCTCCATAAGTCAGGAACAATCCAGGCAAGACGCGAT
44 V L Q L L S F T L L A G L L V Q V S K V P S S I S Q E Q S R Q D A I
801 CTACCAGAACCTGACCCAGCTTAAAGCTGCAGTGGGTGAGCTCTCAGAGAAATCCAAGCTGCAGGAGATCTACCAGGAGCTGACCCAGCTGAAGGCTGCA
77 Y Q N L T Q L K A A V G E L S E K S K L Q E I Y Q E L T Q L K A A
901 GTGGTGAGCTTCCAGGAAATCTAAGCTGCAGGAGACTACCAGGAGCTGACCCGGTGAAGGCTGCAGTGGTGAGCTTCCAGGAAATCTAAGCTGC
111 V G E L P E K S K L Q E I Y Q E L T R L K A A V G E L P E K S K L
1001 AGGAGATCTACCAGGAGCTGACCTGGCTGAAGGCTGCAGTGGGTGAGCTTCCAGAGAAATCTAAGATGCAGGAGATCTACCAGGAGCTGACTCGGCTGAA
144 Q E I Y Q E L T W L K A A V G E L P E K S K M Q E I Y Q E L T R L K
1101 GGCTGAGTGGGTGAGCTTCCAGAGAAATCTAAGCAGCAGGAGATCTACCAGGAGCTGACCCGGCTGAAGGCTGCAGTGGGTGAGCTTCCAGAGAAATCT
177 A A V G E L P E K S K Q Q E I Y Q E L T R L K A A V G E L P E K S
1201 AAGCAGCAGGAGATCTACCAGGAGCTGACCCGACTGAAGGCTGCAGTGGGTGAGCTTCCAGAGAAATCTAAGCAGCAGGAGATCTACCAGGAGCTGACCC
211 K Q Q E I Y Q E L T R L K A A V G E L P E K S K Q Q E I Y Q E L T
1301 AGCTGAAGGCTGCAGTGAACGCCTGTGCCACCCTGTCCCTGGGAATGGACATTTCTCAAGGAAACTGTTACTTCATGTCTAACTCCAGCGGAAGTGC
244 Q L K A A V E R L C H P C P W E W T F F Q G N C Y F M S N S Q R N W

Bsp120I (1432)
1401 GCACGACTCCATCACCGCTGCAAAGAAGTGGGGGCCAGCTCGTAATCAAAAGTGTGAGGAGCAGAACTTCTACAGCTGCAGTCTTCCAGAAGT
277 H D S I T A C K E V G A Q L V V I K S A E E Q N F L Q L Q S S R S

BsaBI (1527) **BbrPI (1544)**
1501 AACCGCTTACCTGGATGGGACTTTCAGATCTAAATCAGGAAGGCACGTGGCAATGGGTGGACGGCTCACCTCTGTTGCCAGCTTCAAGCAGTATTGGA
311 N R F T W M G L S D L N Q E G T W Q W V D G S P L L P S F K Q Y W

Psp1406I (1617)
1601 ACAGAGGAGAGCCCAACAACGTTGGGGAGGAAGACTGC GCGGAATTTAGTGGCAATGGCTGGAACGACGACAAATGTAATCTTGCCAAATTTGGATCTG
344 N R G E P N N V G E E D C A E F S G N G W N D D K C N L A K F W I C

XmnI (1734)
1701 CAAAAAGTCCGACGCTCCTGCTCCAGGATGAAGACAGTTTCTTCTCCAGCCCTGCCACCCCAAACCCCTCCTGCGTAGCAGAACTTCAACCCC
377 K K S A A S C S R D E E Q F L S P A P A T P N P P P A •

MscI (1856) **NheI (1850)**
1801 TTTAAGTACAGTTCCTCTCTCCATCCTTCGACCTTCAAAAATCTCTGCTAGCTGGCAGACATGATAAGATACATTGATGAGTTTGGACAAACCAC

HpaI (1988) **MfeI (1999)**
1901 AACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAAC

EcoRI (2084)
2001 AATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAG
2101 CATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAG

SapI (2266)
2201 CTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCACTGAC

SspI (2323) **SwaI (2337)**
2301 CTCCACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAG
2401 GCCCTTCATAATATCCCCAGTTTGTAGTGTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTC
141 • N

BstXI (2627)
2501 CTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAAGGAGCAGATGTCAGAGATGA
138 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 L
2601 GCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTG
105 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 Q

StuI (2762)
2701 CCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGT
72 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 T

2801 TTGGTCTGATGGCCGCCCCGACATGGTGCTTGTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGA
38 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 I
XmnI (2904) AseI (2970)

2901 TGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTC
5 N F T K M

3001 TCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACG

3101 ACATTTTGGAAAGTCCCCTTGATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCA
SpeI (3125)

3201 CGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACT
SnaBI (3253)

3301 GGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCGAGTTTACCG
NdeI (3358)

3401 TAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTTGGGCGGT

3501 CAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACCGCTGCAGGTTAATAAGAACTGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGC
PacI (3544) SdaI (3536) BspLU11I (3554)

3601 CGCGTTGTGCGGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCAAACCCGACAGGACTATAAGA

3701 TACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGGACCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGG

3801 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTG
ApaLI (3868)

3901 CGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT

4001 GTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG

4101 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATC

4201 TCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAA
PacI (4284) SmaI (4293)

EagI (4304)
NotI (4303)

4301 TCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAA
4401 ACAAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA