



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

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

KasI (535) **AgeI (552)** **BspHI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCATCATGACTTCTGGCAGAGGCTCTGCTGGCACTATCGCCT
▶ ▶ ▶
M T S W Q R L C W H Y R L

BstXI (677)
601 GTGGACCCTGGGTTGCTACATGCTACTGCCATCCTTGCCTGAAACTGTCCCTCAGACTGAAGTGTGACTTCGATGCCATGGATCTGGACTCTGAGGAA
13▶ W T L G C Y M L L A I L A L K L S L R L K C D F D A M D L D S E E

PstI (714) **ScaI (710)** **BsrGI (728)**
701 TTTCAAAGCCAGTACTGCAGGGATCTCCTGTACAAGACCTGAAGCTGCCAGCCAAGAGTTCCATCAACTGCTCAGGGGTCATTCGAGGGGAGCAGAAG
47▶ F Q S Q Y C R D L L Y K T L K L P A K S S I N C S G V I R G E Q K

BstEII (801) **Bsu36I (870)**
801 CGGTGACCCAGGCTCTGCTGAATAACCTGGAAATTAAGAAGAAGCAGCAGCTCTTACAGAGGCCGACTACCTTAGGATGACAGCAGACTGTGAGCACTT
80▶ A V T Q A L L N N L E I K K K Q Q L F T E A D Y L R M T A D C E H F

BstBI (997)
901 CAAGACCAAGAGGAGTTTATACAGGTCCCACTGAGCAAGGAAGAGGCCAGCTTCCCCATTGCGTACTCCATGGTGGTGCATGAGAAGATTGAGAAGTTT
113▶ K T K R K F I Q V P L S K E E A S F P I A Y S M V V H E K I E N F

BsrGI (1019) **Bst1107I (1036)**
1001 GAAAGTTGCTGCGAGCTGTGTACACCCTCAGAATGTATACTGTGCCACATGGATCAGAAGTCTTTCAGAACCTTTAAGCAGGCAGTCAGGGCCATCG
147▶ E R L L R A V Y T P Q N V Y C V H M D Q K S S E P F K Q A V R A I
1101 TGTCATGCTTCCCAATGTCTTCATAGCTAGTAAGTTGGTGTGCTGCTATGCTTCTGGTCCAGGGTGCAGGCTGACCTAACTGCATGGAAGACTT
180▶ V S C F P N V F I A S K L V S V V Y A S W S R V Q A D L N C M E D L

XcmI (1265)
1201 GCTTCAGAGCCCCGTGCCATGGAATACCTCCTGAACCTGTGGACAGACTTCCCATCAAACCAATGCTGAGAGGTGCAAGGCCCTCAAGCTATTG
213▶ L Q S P V P W K Y L L N T C G T D F P I K T N A E M V K A L K L L

Acc65I (1326)
1301 AAAGGGCAGAACAGTATGGAGTCAGAGGTACCACCTCCACATAAAAAATCCCGCTGGAATATCACTATGAGGTGACAGACACATTGCACATGACCAGCA
247▶ K G Q N S M E S E V P P P H K K S R W K Y H Y E V T D T L H M T S

XhoI (1463) **BbrPI (1480)**
1401 AGAGGAAGACGCCCCACCTAATAACCTAACCATGTTCACTGGGAATGCCTACATGGTGGCTTCTCGAGACTTCATTGAACACGTGTTTCAGTAACTCAA
280▶ K R K K T P P N N L T M F T G N A Y M V A S R D F I E H V F S N S K
1501 AGCCCCGCAACTGATCGAGTGGGTAAGACACCTATAGTCCCGATGAGCAGCTTTGGGCCACCTCCAGCGTGCCTCGTGGATGCCTGGATCAGATCCC
313▶ A R Q Q L I E W V K D T Y S P D E H L W A T L Q R A S W M P G S D P
1601 TTGCATCGAAAATTTGACCTGTGACACATGAGAGCCATTGCGAGACTAACCAAGTGGTACGACCATGAGGGAGACATTGAGAWCCGGGACCTTACACGT
347▶ L H R K F D L S D M R A I A R L T K W Y D H E G D I E N G A P Y T
1701 CTTGCTCAGGAATCCACAGCGGCTGTCTGTGTTTATGGGTGAGGGGACCTGACTGGATACTTCAGAACCATCACCTTTGGCCAACAAGTTTGACCC
380▶ S C S G I H Q R A V C V Y G S G D L H W I L Q N H H L L A N K F D P

SspI (1835)
1801 AAAGGTGGATGATAATGTTCTTCACTGTTTGAAGAATATTTACGTCAAAAAGCCATCTATGGGACTGAACTATGAGACACTGTAAGACTATTGTTACCT
413▶ K V D D N V L Q C L E E Y L R H K A I Y G T E L •

NheI (1909)
1901 GTGTGGCAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAAACCACAACCTAGAAATGCAGTGAAAAAATGCTTTATTTGTGAAATTT

HpaI (2047) **MfeI (2058)**
2001 GTGATGCTATTGCTTTATTTGTAACATTATAAGCTGCAATAAAACAAGTTAAACAACAACCTGATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTG

EcoRI (2143)
2101 GGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAA
▶ ▶
2201 TCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATA

SspI (2382) **SwaI (2396)**
2301 GTGTATTTTCCCAAGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTGAGAAATAATTT
2401 AAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTATGAGTTGGACTTAGGG
2501 AACAAAGGAACCTTTAATAGAAATTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTT
▶ ▶ ▶
N R T Y K L P I L E E I T T K

2601 GACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTTGCACATGCCACAGGGGCTGACCACCTGATGGAT
 125 V L K G N M E I 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
 2701 CTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCAC
 91 R D V E D S Y P 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
 StuI (2821)
 2801 AGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCCTGATGGCCGCCCCGACATGGTGCTTGTGTCCTC
 58 V T V R G I Y 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
 BspHI (2971)
 2901 ATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTTCATGATGGCCCTCTATAGTGAGTCGTA
 25 Y L M T I K E T A V E V L E L D Q Q S I N F T K M
 XmnI (2963)
 3001 TTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATA
 AseI (3029) SacI (3086)
 3101 TAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAA
 SpeI (3184)
 3200 CTCCATTGACGTCATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAA
 SnaBI (3312)
 3300 TAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGGTCACTGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTC
 NdeI (3417)
 3400 AATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATT
 PstI (3596)
 3500 GCGGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTG
 SdaI (3595)
 3600 C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G A A A A G G C C A G G A A C C G T A A A A A G G C C G T T G C T G G C G T T T T T C C A T A G G C T C C G C C C C T G A
 PacI (3603) BspLU11I (3613)
 3699 C G A G C A T C A C A A A A T C G A C G C T C A A G T C A G A G G T G G C G A A A C C G A C A G G A C T A T A A G A T A C C A G G C G T T T C C C C T G G A A G C T C C C T C G T G C G C T C T
 3799 C C T G T T C C G A C C C T G C C G C T T A C C G G A T A C C T G T C C G C T T T C C C T T C G G G A A G C G T G G C G T T T C T C A T A G C T C A C G C T G T A G G T A T C T C A G T T C G G
 ApaLI (3927)
 3899 T G T A G G T C G T T C G C T C C A A G C T G G G C T G T G C A C G A A C C C C C G T T C A G C C C G A C C G C T G C G C T T A T C C G G T A A C T A T C G T C T T G A G T C C A A C C C G G T
 3999 A A G A C A C G A C T T A T C G C C A C T G G C A G C A G C C A C T G G T A A C A G G A T T A G C A G A G C G A G G T A T G T A G G C G G T G C T A C A G A G T T C T T G A A G T G G T G G C C T A A C
 4099 T A C G G C T A C A C T A G A A G A A C A G T A T T T G T A T C T G C G C T C T G C T G A A G C C A G T T A C C T T C G G A A A A A G A G T T G G T A G C T C T T G A T C C G G C A A A C A A A C C A
 4199 C C G C T G G T A G C G G T G G T T T T T T G T T T G C A A G C A G C A G A T T A C G C G C A G A A A A A A A G G A T C T C A A G A A G A T C C T T T G A T C T T T T C T A C G G G T C T G A C G C
 EagI (4363)
 4299 T C A G T G G A A C G A A A A C T C A C G T T A A G G G A T T T T G G T C A T G G C T A G T T A A T T A A C A T T T A A A T C A G C G G C C G C A A T A A A A T A T C T T T A T T T T C A T T A C A T C
 PacI (4343) SmaI (4352) NotI (4362)
 4399 T G T G T T G G T T T T T T G T G T G A A T C G T A A C A T A C A C T C T C C A T C A A A A C A A A C G A A A C A A A C A A A C T A G C A A A T A G G C T G T C C C C A G T G C A A G
 4499 T G C A G G T G C C A G A A C A T T T C T A T C G A A