



PvuI (7)
SgfI (6) **MfeI (82)** **EcoNI (96)**
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **SphI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCAGCATGCCTACTGTGTGCTGAGCACCTTTTGTCTCTGCA
1 M H Y C V L S T F L L L H

FspI (659) **SacII (681)**
601 TCTGGTCCCGGTGGCGCTCAGTCTGTCTACCTGCAGCACCTCGCATGGATCAGTTTATGCGCAAGAGGATCGAGGCCATCCGCGGCAGATCCTGAGC
13 L V P V A L S L S T C S T L D M D Q F M R K R I E A I R G Q I L S

BspEI (732) **EcoO109I (746)** **BsaBI (762)**
701 AAGCTGAAGCTCACCAGCCCCCGAAGACTATCCGGAGCGGGATGAGGTCCCGCGGAGGTGATTTCCATCTACAACAGTACCAGGGACTTACTGCAGG
47 K L K L T S P P E D Y P E P D E V P P E V I S I Y N S T R D L L Q

BsrBI (835) **ScaI (851)**
801 AGAAGGCAAGCCGGAGGGCAGCCGCTGCGAGCGGAGCGAGCGAGGAGTACTACGCCAAGGAGTTTATAAAATCGCATGCCGTCCCACCTCCC
80 E K A S R R A A A C E R E R S D E E Y Y A K E V Y K I D M P S H L P

BstBI (984)
901 CTCGAAAATGCCATCCCGCCACTTTCTACAGACCCTACTTCAAGATCGTCCGCTTTGATGTCTCAACAATGGAGAAAAATGCTTGAATCTGGTGAAG
113 S E N A I P P T F Y R P Y F R I V R F D V S T M E K N A S N L V K

XcmI (1031)
1001 GCAGAGTTCAGGGTCTTCCGCTTGCAAAACCCAAAGCCAGAGTGCCGAGCAGCGGATTGAACTGTATCAGATCCTTAAATCCAAAGACTTAACATCTC
147 A E F R V F R L Q N P K A R V A E Q R I E L Y Q I L K S K D L T S

ClaI (1114) **BsrBI (1139)**
1101 CCACCCAGCGCTACATCGATAGCAAGTTGTGAAAACAGAGCGGAGGGTGAATGGCTCTCCTTCGACGTGACAGACGCTGTGCAGGAGTGGCTTACCA
180 P T Q R Y I D S K V V K T R A E G E W L S F D V T D A V Q E W L H H

XhoI (1297)
1201 CAAAGACAGGAACCTGGGGTTTAAATAAGTTTACACTGCCCTGCTGTACCTTCGTGCCGTCTAATAATTACATCATCCCGAATAAAAAGCGAAGAGCTC
213 K D R N L G F K I S L H C P C C T F V P S N N Y I I P N K S E E L

NdeI (1334)
1301 GAGGCGAGATTTGCAGGTATTGATGGCACCTACATATGCCAGTGGTATCAGAAAATAAAGTCCACTAGGAAAAAACAGTGGGAAGACCCAC
247 E A R F A G I D G T S T Y A S G D Q K T I K S T R K K T S G K T P

PshAI (1430) **NgoMIV (1451)** **BssHIII (1464)**
1401 ATCTCCTGTAATGTTGTTGCCCTCCTACAGACTGGAGTCACAACAGTCCAGCCGCGGGAAGAAGCGCGCTTTGGATGCTGCCTACTGCTTTAGAAATGT
280 H L L L M L L P S Y R L E S Q Q S S R R K K R A L D A A Y C F R N V

BamHI (1562)
1501 GCAGGATAATTGCTGCCTTCGCCCTTTTACATTGATTTTAAAGAGGATCTTGGATGGAAATGGATCCATGAACCCAAAGGTACAATGCTAATTCTGT
313 Q D N C C L R P L Y I D F K R D L G W K W I H E P K G Y N A N F C

BstXI (1612) **BsrGI (1658)** **HindIII (1679)**
1601 GCTGGGGCATGCCATATCTATGGAGTTCAGACACTCAACACACCAAAGTCTCAGCCTGTACAACACCATAAATCCCGAAGCTTCCGCTTCCCTTGTCT
347 A G A C P Y L W S S D T Q H T K V L S L Y N T I N P E A S A S P C

1701 GTGTGCCAGGATCTGGAACCACTGACATTCTATTACATTGAAATACGCCAAGATCGAACAGCTTCCAATATGATTGTCAAGTCTTTGAAATG
380 C V S Q D L E P L T I L Y Y I G N T P K I E Q L S N M I V K S C K C

MscI (1852)
1801 CAGCTAAAGTCTTGGGAAAGCCAGGACACGAAAATCACGGTGACAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGCAAAACCAACT
413 S •

HpaI (1984) **MfeI (1995)**
1901 AGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAATT

EcoRI (2080)
2001 GCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAATGTGGTATGGAATCTAAATACAGCATA
2101 GCAAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCAATGTGCATTAGCTGT
2201 TTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTGCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCC

SspI (2319) **Swal (2333)** **EcoO109I (2394)**
2301 CACATTCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCC
2401 TTCATAATATCCCCAGTTTAGTGTGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGG
1414 • N R T

2501 TGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTC
 137 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 E
 BstXI (2623)
 2601 TCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTGTGCCCG
 104 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 G
 StuI (2758)
 2701 TTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGG
 70 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 K T
 2801 TCCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGTGAGAGATGTT
 37 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 N
 XmnI (2900) AseI (2966)
 2901 GAAGGCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCA
 4 F T K M
 3001 GCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGGCGGAGTTGTTACGACAT
 SpeI (3121)
 3101 TTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCC
 SnaBI (3249)
 3201 CATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGC
 NdeI (3354)
 3301 ATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAA
 3401 TACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGC
 PacI (3540)
 3501 CAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCGCCG
 SdaI (3532) BspLU11I (3550)
 3601 TTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACC
 3701 AGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCT
 ApaLI (3864)
 3801 TTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCC
 3901 TTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAG
 4001 GCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAA
 4101 AAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAA
 PacI (4280) SmaI (4289) NotI (4299)
 4201 GAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTGGTCATGGCTAGTTAATTAACATTTAAATC AG
 EagI (4300)
 4301 CGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAA
 4401 AACAAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA