



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

Psp1406I (203) **Bsu36I (291)**
HindIII (245) **EcoNI (287)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCATCATGAGCTCCCCGCCACCCGCCGCAAGGGCTTTTACCG
1▶ M S S P P P A R K G F Y R

BstEII (606) **BssHII (630)**
601 CCAGGAGGTGACCAAAACGCCTGGGAGGTGCGCGCTGTACCAAGACTGCAGCCCGTTGGCTCTGGTGCCTATGGTGCAGTGTGCTCTGCAGTAGAC
13▶ Q E V T K T A W E V R A V Y Q D L Q P V G S G A Y G A V C S A V D
701 AGCCGCACTGGCAACAAGGTGGCCATCAAGAAGTTGTACCGCCCTTCCAGTCGGAGCTGTTTGC AAGCGCGCTACAGAGAGTTGCGCCCTCTCAAAC
47▶ S R T G N K V A I K K L Y R P F Q S E L F A K R A Y R E L R L L K
801 ACATGCGCCACGAGAACGTCATTGGGCTACTGGATGTGTTACACCTGATGAGTCTTGACGACTTACAGACTTCTACCTGGTGTGATGCCATTCATGG
80▶ H M R H E N V I G L L D V F T P D E S L D D F T D F Y L V M P F M G
901 CACTGATCTGGGCAAACTCATGAAGCATGAGACCTGAGTGAAGACAGAATCCAGTTTCTGTGTATCAGATGTTGAAGGGGCTGAAGTATATCCATGCG
113▶ T D L G K L M K H E T L S E D R I Q F L V Y Q M L K G L K Y I H A
1001 GCTGGTGTATCCACAGAGACTTGAAGCCTGGCAACCTGGCTGGAATGAGGACTGTGAGCTGAAGATCCTAGACTTTGGCCTTGCCAGGCAGGCAGACA
147▶ A G V I H R D L K P G N L A V N E D C E L K I L D F G L A R Q A D
901 CACTGATCTGGGCAAACTCATGAAGCATGAGACCTGAGTGAAGACAGAATCCAGTTTCTGTGTATCAGATGTTGAAGGGGCTGAAGTATATCCATGCG
113▶ T D L G K L M K H E T L S E D R I Q F L V Y Q M L K G L K Y I H A
1001 GCTGGTGTATCCACAGAGACTTGAAGCCTGGCAACCTGGCTGGAATGAGGACTGTGAGCTGAAGATCCTAGACTTTGGCCTTGCCAGGCAGGCAGACA
147▶ A G V I H R D L K P G N L A V N E D C E L K I L D F G L A R Q A D
1101 GTGAGATGACAGGATATGTTGTAACCCGGTGGTATCGGGCACCAGAGGTGATCTTGAATTGGATGCGCTACACGCAGACAGTGGACATTTGGTCCGTTGG
180▶ S E M T G Y V V T R W Y R A P E V I L N W M R Y T Q T V D I W S V G
BspHI [m] (1272)

1201 CTGCATCATGGCGGAGATGATTACTGGGAAGATCTGTTCAAAGCAATGACCACCTGGACCAGCTGAAGGAGATCATGAAGATCACAGGGACGCCCCCT
213▶ C I M A E M I T G K I L F K G N D H L D Q L K E I M K I T G T P P
1301 CCTGAGTTTGTTCAGAAGCTACAGAGTGCAGAGGCAAGAACAATGGAAGGCTCCCTGAGTTAGAAAAGAAGGATTTTGCCTCTGCTGACCAACG
247▶ P E F V Q K L Q S A E A K N Y M E G L P E L E K K D F A S V L T N
1401 CAAGCCCTCAGGCTGTGAATCTCCTGGAAGGATGCTGGTGTGATGCGGAACAGCGGGTGACAGCAGCTGAGGCGTTAACCCTACTTTGAGTC
280▶ A S P Q A V N L L E R M L V L D A E Q R V T A A E A L T H P Y F E S
1501 CCTTCGGGACACTGAGGATGAACCAAGGCCGAGAAATATGACGACTCCTTTGATGATGTAGACCCGACCCCTTGAAGGATGGAAGCGTGTGACTTACAAG
313▶ L R D T E D E P K A Q K Y D D S F D D V D R T L E E W K R V T Y K
MscI (1689)

1601 GAAGTTCTCAGCTTCAAGCCTCCTAGGAGCCAGAGTTC A AAGGAGACGGCTCTGTGACGACCTCTGGTGGTTTCTAGCTGGCCAGACAT
347▶ E V L S F K P P R Q L G A R V P K E T A L •
1701 GATAAGATACATTGATGAGTTTGGACAAACCACAACACTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACC

HpaI (1821) **MfeI (1832)**
1801 ATTATAAGCTGCAATAAAACAAGTTAACAACAACAAATTGCATTTTATGTTTCAGGTTTCAGGGGGAGGTGGGAGGTTTTTAAAGCAAGTAAACC

EcoRI (1917)
1901 TCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCA
2001 TAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTATGAGGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTAC

SspI (2156) **SwaI (2170)**
2101 CTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAAATTTAAATACATCATTGCAATGAAAATAAA

EcoO109I (2231)
2201 TGTTTTTTATTAGGCAGAATCCAGATGTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGGACTTAGGGAACAAGGAACCTTTAATAGAAATTG
2301 GACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGGAGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGA
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
BstXI (2460)

2401 GCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTG
116▶ 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 H
2501 CCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTACGACAGACAGTGCCTGCCAATGTAGGCC
83▶ 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 A
StuI (2595)

2601 TCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGCTCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGG
 49 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 A
 BbsI (2741)
 2701 CGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCG
 16 V E V L E L D Q Q S I N F T K M
 XmnI (2737)
 2801 ATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGC T TATCTGACGGTTCACATAACAGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACC
 AseI (2803)
 2901 GCCCATTTCGCTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAG
 SpeI (2958)
 3000 ACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAC
 SnaBI (3086)
 3100 TGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGCCATATGAT
 NdeI (3191)
 3200 ACACCTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAT
 3300 TATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGC
 SdaI (3369) PacI (3377) BspLU11I (3387)
 3398 AAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAAATCGACGCTCA
 3498 AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCG
 3598 GATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGG
 3698 CTGTGTGCACGAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATGCCACTGGCA
 ApaLI (3701)
 3798 GCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTAT
 3898 TTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTGT
 3998 TTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAA
 EagI (4137)
 4098 GGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATC
 PacI (4117) SmaI (4126) NotI (4136)
 4198 GTAACAAACATACGCTCTCCATCAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTAT
 4298 CGAA