



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

101 GAGAAGGTGGCGCGGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
EcoNI (287)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560)
BstEII (555)
KasI (535) **AgeI (552)** **XmaI (590)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATGGCCGAAAACCTGTACCGAGCCCGTCCCGGGTTTA

PstI (679)
601 CAGCCCATCTGTGCTGTTTCTGCACCCAGACATGGGTATAGGCGGAGCCGAGCGCCTAGTGTGGACGCGCGCTGGCGCTGCAGGAGTACGGCTGTGAT
13▶ S P S V L F L H P D M G I G G A E R L V L D A A L A L Q E Y G C D
FspI (769)
701 GTGAAGATATGGACCGGCACTACGACCCGAACCACTGCTTCATCGAGACCCGCGAGCTCTCGGTGCAATGCGCAGGGGACTGGCTGCCTCGAGCCTGG
47▶ V K I W T A H Y D P N H C F I E T R E L S V Q C A G D W L P R S L

SacII (810)
EagI (807)
NotI (806) **KasI (814)** **FspI (836)**
801 GCTGGGCGGCGCGCGCGCCATCTGCTCCTACGTGCGCATGGTCTTTCTGGCGCTCTACGTGCTGTTTCTCTCCGGCGAGGAGTTCGACGTGGTGGT
80▶ G W G G R G A A I C S Y V R M V F L A L Y V L F L S G E E F D V V V
MscI (938) **BglII (981)**
901 GTGCGACCAAGTGTCTGCCTGTATCCCGGTGTTCAAACCTGGCCAGCGGTAAGAGGGTCTATTTTACTGTCACTTCCAGATCTGCTGCTTACTCAG
113▶ C D Q V S A C I P V F K L A R R R K R V L F Y C H F P D L L L T Q
Bsp120I (1028) **BstXI (1058)**
1001 AGAAATTCAGCTCTGAAGAAGTTCTACAGGGCCCATCGACTGGATCGAGGAATACACCACAGGCATGGCAGACCGCATCTTGGTCAACAGCCAGTACA
147▶ R N S A L K K F Y R A P I D W I E E Y T T G M A D R I L V N S Q Y
Tth11I (1128)
1101 CTGCTCCGTCCTTAAAGAAACCTCAAGACCTGTCTCACAGAAATCCTGATGTGCTCTACCATCTCTGAATATCGGCAGCTTTGACTTGGCTATTCC
180▶ T A S V F K E T F K T L S H R N P D V L Y P S L N I G S F D L A I P
Tth11I (1213)
1201 TGAAAAGATAGATGACCTCGTCCCAAGGGGAAGCAATTCCTGTTCTCTATCAACCGATACGAAAGGAAGAAAAAATCTGCCCTTGGCACTGAGATCC
213▶ E K I D D L V P K G K Q F L F L S I N R Y E R K K N L P L A L R S

XcmI (1324)
BstEII (1319) **BamHI (1379)**
1301 TTGGTGCAGTTCGGAATCGGTTACCATCTCAAGAGTGGGATAAGGTTTCATCTTTCATGCGCGGTGGTTATGACGATAGGATCCCGGAGAAGTGGAGC
247▶ L V Q L R N R L P S Q E W D K V H L F M A G G Y D D R I P E N V E
BglII (1484)
1401 ACTATAAGGAGTTGAAGAAAATGGTCCAAGAGTCAAGACCTGAGCGTCATGTGACCTTCTGCGGTCTTCTCGGACAGACAGAGATCTCACTCCTCCA
280▶ H Y K E L K K M V Q E S D L E R H V T F L R S F S D R Q K I S L L H
BsrGI (1565)
1501 CGGCTGCTTGTGTGCTCTACACTCCGAGCAACGAGCACTTTGGCATCGTCCCTCTGGAGGCCATGTACATGCAGTGCCAGTCATCGCTGTTAATAAC
313▶ G C L C V L Y T P S N E H F G I V P L E A M Y M Q C P V I A V N N
Bsp120I (1603) **ApaLI (1660)** **NcoI (1676)**
1601 GGTGGGCCCTGGAGTCCATTGTCCACAAGGTCACGGGTTCTGTGTGAGCCAGACCCAGTCTCAGAAGCCATGGAGAAGTTCATCCACAAC
347▶ G G P L E S I V H K V T G F L C E P D P V H F S E A M E K F I H K

Ppu10I (1763)
NsiI (1763)
1701 CATCCTAAAAGCCAGATGGGCTCGCTGAAAAGCCAGGGTGGCGGAGAAGTTTTAGCTGATGCATTTGCAGACCAGCTGTACCAGTATGTCACGAA
380▶ P S L K A T M G L A G K A R V A E K F S A D A F A D Q L Y Q Y V T K

MscI (1822)
NheI (1816)
1801 GCTGGTGTAGTCAGGAGCTAGCTGGCCAGACATGATAAGATCATTGATGAGTTTGGACAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTGT
413▶ L V •

HpaI (1954) **MfeI (1965)**
1901 GAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGTGAATAAACAAGTTAAACAACAATTCATTCTTTATGTTTCAGGTTTCAGGGGG

EcoRI (2050)
2001 AGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCT

2101 ACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTA

SspI (2289)
2201 AGATATAGTATTTTTCCAAGTTTGAAGTACCTCTTCAATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAA

Swal (2303)
2301 ATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTAGTAGTTGGA
2401 CTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGG
141 • N R T Y K L P I L E E I T
BstXI (2593)
2501 TGGTTTTGACCAGCTTGCCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCT
127 T K 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
2601 GATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCT
94 I S 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
StuI (2728)
2701 TCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGCTTGT
60 E A C 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
BspHI (2878)
2801 TGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCCTATAGTG
27 D E 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
AseI (2936)
2901 AGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCT
SpeI (3091)
3001 GCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTTACTAGTCA
3100 AAACAAACTCCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATC
SnaBI (3219)
3200 ATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCAT
NdeI (3324)
3300 TGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGT
3400 CCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGTCCAGCCAGGCGGGCCATTTACCGTAAGTTATGTA
PstI (3503)
SdaI (3502) PacI (3510) BspLU11I (3520)
3500 ACGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTCCATAGGCTCCGC
3598 CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCG
3698 TGGCTCTCCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCT
ApaLI (3834)
3798 CAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC
3898 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGT
3998 GGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA
4098 ACAAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG
EagI (4270)
PacI (4250) Swal (4259) NotI (4269)
4198 TCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCCAATAAAATATCTTTATTTTC
4298 ATTACATCTGTGTGTTGTTTTTTGTTGTAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCC
4398 AGTGCAAGTGCAGGTGCCAGAACATTTCTATCGAA