



PvuI (7)
SgfI (6) MfeI (82) EcoNI (96)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) HindIII (245) **Bsu36I (291)**
PvuII (239) EcoNI (287)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

KasI (535) **AgeI (552)**
SgrAI (551)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTGAGGATCATGATCGAAACATACAACCAAACCTTCTCCCGATC
1 M I E T Y N Q T S P R S

BstAPI (682)
601 TGCGGCCACTGGACTGCCATCAGCATGAAAATTTTTATGATTTACTTACTGTTTTTCTTATCACCCAGATGATTGGGTGAGCACTTTTTGCTGTGTAT
12 A A T G L P I S M K I F M Y L L T V F L I T Q M I G S A L F A V Y
701 CTTATAGAAGGTTGGACAAGATAGAAGATGAAAGGAATCTTCATGAAGATTTGTATTCATGAAAACGATACAGAGATGCAACACAGGAGAAGATCCT
46 L H R R L D K I E D E R N L H E D F V F M K T I Q R C N T G E R S
801 TATCCTTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAGAGGAGACGAAGAAAGAAAACAGCTTTGA
79 L S L L N C E E I K S Q F E G F V K D I M L N K E E T K K E N S F E

BspLU11I (936)
901 AATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATAC
112 M Q K G D Q N P Q I A A H V I S E A S S K T T S V L Q W A E K G Y

BstEII (1020) PvuII (1042)
1001 TACACCATGAGCAACAACCTGGTAACCTGGAAAATGGGAAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTT
146 Y T M S N N L V T L E N G K Q L T V K R Q G L Y Y I Y A Q V T F C

HindIII (1109)
1101 CCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGATTCGAGAGAATCTTACTCAGAGCTGCAAATACCCA
179 S N R E A S S Q A P F I A S L C L K S P G R F E R I L L R A A N T H

XcmI (1299)
1201 CAGTTCGCCAAAACCTTGCGGGCAACAATCCATTCACCTGGGAGGAGTATTTGAATTGCAACCAGGTGCTTCGGTGTGTTGCAATGTGACTGATCCAAGC
212 S S A K P C G Q Q S I H L G G V F E L Q P G A S V F V N V T D P S

NcoI (1308) **NheI (1351)**
MscI (1357)
1301 CAAGTGAGCCATGGCACTGGCTTACGTCCTTTGGCTTACTCAAACCTGAGCTAGTGGCCAGACATGATAAGATACATTGATGAGTTGGACAACCA
246 Q V S H G T G F T S F G L L K L •

HpaI (1489)
1401 CAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAAACAACAA

MfeI (1500) **EcoRI (1585)**
1501 CAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGATGGAATTTCAAATACA
1601 GCATAGCAAAACTTTAACCTCCAATCAAGCCTCTACTGAACTCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTA

SapI (1767)
1701 GCTGTTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTCTTCTTCTTTATGTTTTAAATGCACTGA

SspI (1824) SwaI (1838) **EcoO10**
1801 CCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAA
1901 GGCCCTTCATAATATCCCCAGTTTAGTAGTTGGAAGTGGGAAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTT
141 • N

StuI (2263) **SacI (2099)**
2001 CCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATG
139 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
2101 AGCTCTGCACATGCCACAGGGGTGACCACCCTGATGGATCTGCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCT
105 L 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

BbsI (2409)
2201 GCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGT
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
2301 CTTGGTCTGATGGCCCGCCGACATGGTCTTGTCTCATAGACATGGTGTATCTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAG
39 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

XmnI (2405) **AseI (2471)**
2401 ATGTTGAAGTCTTCACTGGCCCTCCTATAGTGAAGTCTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGT
5 I N F T K M

SacI (2528)
2501 CTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTAC

2601 GACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTATCC
SpeI (2626)
←

2701 ACGCCATTGATGTACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTAC
SnaBI (2754)

2801 TGGGCATAATGCCAGGCGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACC
NdeI (2859)

2901 GTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGCGGGGGTCTGTTGGCGG

3001 TCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGG
PstI (3038)
SdaI (3037)
PacI (3045)
BspLU11I (3055)
←

3101 CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCAAACCCGACAGGACTATAAAG
 3201 ATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG

3301 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCT
ApaLI (3369)

3401 GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA
 3501 TGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC
 3601 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGAT

3701 CTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAA
PacI (3785) SwaI (3794)

EagI (3805)
NotI (3804)

3801 ATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGA
 3901 AACAAAACAACTAGCAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA