



PvuI (7)
SgfI (6)
 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) **NcoI (560)**
 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGTCCCATGGCATTCAACACAGATGAATCAAGACTGTGGTTGA
 1▶ M A F N T D E I K T V V E

HindIII (600) **DraIII (638)**
 601 AAGCTTTGAGACCACCCCTATGAATATGAGTGGGCACCACCTGTGAAAAAGTCAGAATCAAGAGCTGGGGTCATGGCTCCTGCCCTCACTGTACTCC
 13▶ S F E T T P Y E Y E W A P P C E K V R I K E L G S W L L P P L Y S
 701 CTGGTGTTCATCATCGGCCTCCTGGGCAACATΔAATGGTTGTGTGATCCTCATAAAGTACAGGAAGCTACAAATTATGGCTAATATCTACCTGTTCAACT
 47▶ L V F I I G L L G N I M V V L I L I K Y R K L Q I M A N I Y L F N

BspLU11I (884)
 801 TGGAATTTCTGACCTGCTCTTTCTCTTCACTGTCCATTCTGGATTCACTATGTTCTGTGGAATGAGTGGGGTTTTGGCCACTACATGTGCAAAATGCT
 80▶ L A I S D L L F L F T V P F W I H Y V L W N E W G F G H Y M C K M L

BsrGI (923) **BglIII (932)**
 901 GTCTGGGTTTTATTACCTGGCCTTGACAGCGAGATCTTTTTCATCATICTGCTGACAATTGACAGATACCTGGCTATCGTCCATGCTGTGTTGCCCTT
 113▶ S G F Y Y L A L Y S E I F F I I L L T I D R Y L A I V H A V F A L

EcoO109I (1046)
 1001 CGAGCCCGAACTGTGACTTTTGCTACTATCACCAGTATCATTACCTGGGGCCTTGCAGGACTGGCAGCATTGCTGAATTTATCTTCCATGAGTCTCAAG
 147▶ R A R T V T F A T I T S I I T W G L A G L A A L P E F I F H E S Q

PstI (1119) **BbsI (1147)** **XmnI (1158)** **SapI (1198)**
 1101 ACAGCTTTGGAGAGTTTTCTGCAGTCTCGTATCCAGAGGGTGAAGAAGACAGCTGGAAACGTTTCCATGCTCTAAGAATGAATATCTTTGGTCTAGC
 180▶ D S F G E F S C S P R Y P E G E E D S W K R F H A L R M N I F G L A
 1201 TCTTCTCTCCTCATTATGGTTATCTGCTACTCAGGAATCATTAAAACTCTCTGAGATGTCCCAATAAAAAAACACAAGGCCATCCGCTTATTTTT
 213▶ L P L L I M V I C Y S G I I K T L L R C P N K K K H K A I R L I F
 1301 GTTGTATGATAGTCTTTTTATTTTTGGACCCGTAACAACCTGGTCTCCTTTTTCTGCTTTTACAGCACATTTTTAGAGACCAGCTGTCAGCAGA
 247▶ V V M I V F F I F W T P Y N L V L L F S A F H S T F L E T S C Q Q

AseI (1459) **BspEI (1496)**
 1401 GTAACATCTGGACCTGGCCATGCAGGTGACTGAGGTGATTGCCTACACCCACTGCTGATTAATCCAGTAATCTACGCCTTTGTTGGTGGAGAGGTTCCG
 280▶ S K H L D L A M Q V T E V I A Y T H C C I N P V I Y A F V G E R F R
 1501 GAAACACCTTCGGCTCTTTTTCCACAGAAATGTGGCAGTTTACCTGGGAAAATATATTCGTTTCTTCTGGTGGAGAAAATGGAAAGAACAGCTCTGTC
 313▶ K H L R L F F H R N V A V Y L G K Y I P F L P G E K M E R T S S V

NheI (1649)
 1601 TCCCATCAACTGGGAGCAAGAAATCTCTGTGGTGTGTTAGTTGGGCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCA
 347▶ S P S T G E Q E I S V V F •

HpaI (1787)
 1701 ACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA

EcoRI (1883)
 1801 ATTGCATTCATTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTTACAATGTGGTATGGAATCTAAAATACAGC
 1901 ATAGCAAACTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGC

SapI (2065)
 2001 TGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATAGTGTATTTTCCCAAGGTTTGAAGTCTTCTTCTTTATGTTTTAAATGCACTGACC

SspI (2122) **SwaI (2136)** **EcoO109I (2197)**
 2101 TCCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGG
 2201 CCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCC
 141▶ • N R

SacI (2397)
 2301 TGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAG
 138▶ 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 L

BstXI (2426)
 2401 CTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGC
 105 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

StuI (2561)
 2501 CCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCT
 71 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 K

2601 TGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGAT
 38 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 I

BbsI (2707)
XmnI (2703)
 2701 GTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCTGGATGGCGTCT
 5 N F T K M

AseI (2769)
 2701 GTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCTGGATGGCGTCT

SacI (2826)
 2801 CCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGA

SpeI (2924)
 2901 CATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCAC

SnaBI (3052)
 3001 GCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTG

NdeI (3157)
 3101 GGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGT
 3201 AAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTC

PacI (3343)
PstI (3336)
SdaI (3335)
 3301 AGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAITAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC
 3401 GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGAT
 3501 ACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGC

BspLU11I (3353)
 3301 AGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAITAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC

ApaLI (3667)
 3601 GCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGC
 3701 GCCTTATCCGGTAACTATCGTCTTGTGCTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG
 3801 TAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGG
 3901 AAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCT

PacI (4083) **Swal (4092)**
 4001 CAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGATTTTGGTCATGGCTAGTTAATTAACATTTAAAT

EagI (4103)
NotI (4102)
 4101 CAGCGGCCCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAACAAAACGAAA
 4201 CAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA