



PvuI (7)
SgfI (6)
 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCGCCCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535) **AgeI (552)** **BspLU11I (560)** **Acc65I (595)**
 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAACATGTGGCTGGAAGAATCCAAATGAAATCAAAGGTAC
 601 CCGACATCCCAACTGATCCCTTGCCTCTCGCTGTTGTTCCATCTCGTTCCTTAGTGTCTTATTTCAACTGTTTGGTGACTCATCATTACTTT
 13▶ R H P Q L I P C V F A V V S I S F L S A C F I S T C L V T H H Y F
 701 TTACGCTGGACGAGAGGAAGTGGTGAAGTGTGAGACTACACACGAGAGTAACGTGCATCCGAGAGGACACAGCCTGGAGCTACAGGAGTACTT
 47▶ L R W T R G S V V K L S D Y H T R V T C I R E E P Q P G A T G G T
 801 GGACCTGTGTCCGTGTTAGCTGGAGAGCCTCCAGTCTAACTGTTACTTTCCTCTTAATGACAACAGACCTGGCATGAGAGCGAGAGAACTGCTCAGG
 80▶ W T C C P V S W R A F Q S N C Y F P L N D N Q T W H E S E R N C S G

BstEII (915) **XcmI (1079)**
 901 GATGAGCAGTCATCTGGTGACCATCAACACCGAAGCAGAACAGAAATTTGTGACCCAGCTTTGGATAAACGTTTTCTATTTCTGGGACTTGCTGAT
 113▶ M S S H L V T I N T E A E Q N F V T Q L L D K R F S Y F L G L A D
 1001 GAGAATGTGGAAGGCCAATGGCAGTGGGTGGACAAGACGCCATTTAACCCACACACGGTATTCTGGGAAAAGGGGAATCCAATGACTTTATGGAGAAG
 147▶ E N V E G Q W Q W V D K T P F N P H T V F W E K G E S N D F M E E
 1101 ACTGTGTTGCTCTGTTTCATGTCATGAAAAATGGGTCTGAAATGACTTTCCTGTCACTTTGAGGTGAGAAGGATTTGTAATTTACCTGGAATAACATT
 180▶ D C V V L V H V H E K W V W N D F P C H F E V R R I C K L P G I T F

MscI (1256) **NheI (1250)**
 1201 CAATTGGAAGCCCTCGAAGTGATCCTTGATGAGGATGAAGAAGATGAACCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCCAC
 213▶ N W K P S K •

HpaI (1388)
 1301 AACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAAC

EcoRI (1484)
 1401 AATTGCATTCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTCAAATACAG
 1501 CATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAG

SapI (1666)
 1601 CTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTGTATTTCCCAAGGTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGAC

SspI (1723) **Swal (1737)** **EcoO109I**
 1701 CTCCACATTCCTTTTTAGTAAATATTTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAG
 1801 GCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTC
 141▶ • N

BstXI (2027) **SacI (1998)**
 1901 CTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGA
 138▶ 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 L

StuI (2162)
 2001 GCTCTGTGCATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTG
 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
 2101 CCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCAGACAGAGTACCCTGCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCCAGTC
 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
 2201 TTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGTGAGAGA
 38▶ 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 I

XmnI (2304) **AseI (2370)**
 2301 TGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGTGATGATTACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTC
 5▶ N F T K M

SacI (2427)
 2401 TCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACG

SpeI (2525)
 2501 ACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCA

2601 CGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAAGTCATGTACT

SnaBI (2653)

2701 GGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCG

NdeI (2758)

2801 TAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCTTGGGCGGT

PacI (2944)
PstI (2937)
SdaI (2936) BspLU11I (2954)

2901 CAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGC

3001 CGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGA

3101 TACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGG

ApaLI (3268)

3201 CGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTG

3301 CGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT

3401 GTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG

3501 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATC

3601 TCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAA

PacI (3684) SmaI (3693)

EagI (3704)
NotI (3703)

3701 TCAGCGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAA

3801 ACAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA