



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

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
AgeI (552)
 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCACCATGGCAGAAGGCAACCACAGAAAAAGCCACTTAAGGT
 601 GTTGAATCCTGGGCAAAGATTTCTCACTGGTGTGGTAACTTAGTGAACAATAATGTACTGAACTGGAAGGAAGGAAAAAAGAAATATTAC
 13▶ L E S L G K D F L T G V L D N L V E Q N V L N W K E E E K K K Y Y

BbsI (712)
 701 GATGCTAAAACCTGAAGACAAAGTTCGGGTCATGGCAGACTCTATGCAAGAGAAGCAACGTATGGCAGGACAAATGCTTCTTCAAACCTTTTTAACATAG
 47▶ D A K T E D K V R V M A D S M Q E K Q R M A G Q M L L Q T F F N I

EcoRI (898)
 801 ACCAAATATCCCCAATAAAAAAGCTCATCCGAATATGGAGGCTGGACCACCTGAGTCAGGAGAATCTACAGATGCCCTCAAGCTTTGTCCTCATGAAGA
 80▶ D Q I S P N K K A H P N M E A G P P E S G E S T D A L K L C P H E E

BglII (932) **NdeI (981)**
 901 ATTCCTGAGACTATGTAAGAAAGAGCTGAAGAGATCTATCCAATAAAGGAGAGAAACAACCGCACACGCCTGGCTCTCATCATATGCAATACAGAGTTT
 113▶ F L R L C K E R A E E I Y P I K E R N N R T R L A L I I C N T E F
 1001 GACCATCTGCCTCCGAGGAATGGAGCTGACTTTGACATCACAGGGATGAAGGAGCTACTTGGGGTCTGGACTATAGTGTAGATGTAGAAGAGAATCTGA
 147▶ D H L P P R N G A D F D I T G M K E L L E G L D Y S V D V E E N L

BstXI (1103) **Eco47III (1119)**
 1101 CAGCCAGGGATATGGAGTCAGCGCTGAGGGCATTGCTACCAGACCAGAGCACAAGTCTCTGACAGCACATTCTTGGTACTCATGTCTCATGGCATCCT
 180▶ T A R D M E S A L R A F A T R P E H K S S D S T F L V L M S H G I L
 1201 GGAGGAACTCTGCGGAAGTGTGCATGATGAGAAAAACAGATGTGCTGCTTTATGACACCATCTCCAGATATTCAACAACCGCAACTGCCTCAGTCTG
 213▶ E G I C G T V H D E K K P D V L L Y D T I F Q I F N N R N C L S L

PstI (1332) **StuI (1328)**
 1301 AAGGACAAACCAAGGTCATCATTGTCCAGGCCTGCAGAGGTGCAAAACCGTGGGGAAGTGTGGGTCAGAGACTCTCCAGCATCCTTGGAAAGTGGCCTCTT
 247▶ K D K P K V I I V Q A C R G A N R G E L W V R D S P A S L E V A S

BbrPI (1444) **SapI (1472)** **DraIII (1486)**
 1401 CACAGTCATCTGAGAACCTGGAGGAAGATGCTGTTTACAAGACCCAGTGGAGAAGGACTTCATTGCTTTCTGCTCTTCAACGCCACACAACGTGCTCCTG
 280▶ S Q S S E N L E E D A V Y K T H V E K D F I A F C S S T P H N V S W
 1501 GAGAGACAGCACAACTGGGCTCTATCTTCATCACACAACCTACATGCTTCCAGAAATATTCTTGGTGTGCCACCTAGAGGAAGTATTTCCGGAAGGTA
 313▶ R D S T M G S I F I T Q L I T C T F Q K Y S W C C H L E E V F R K V
 1601 CAGCAATCATTTGAAACTCCAAGGGCCAAAGCTCAAATGCCACCATAGAACGACTGTCCATGACAAGATATTTCTACCTCTTTCTGCAATTGAAAT
 347▶ Q Q S F E T P R A K A Q M P T I E R L S M T R Y F Y L F P G N •

MscI (1758) **NheI (1752)**
 1701 GGAAGCCACAAGCAGCCAGCCCTCCTTAATCAACTTCAAGGAGCACCTTCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAAACC

HpaI (1890)
 1801 ACAACTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA

EcoRI (1986)
 1901 ACAATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATCTAAAATAC
 2001 AGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATT

SapI (2168)
 2101 AGCTGTTTGACGCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACCTG

SwaI (2239)
 2201 ACCTCCACATTCCTTTTTAGTAAATATTGAGAAATAATTAATACATCATTGCAATGAAATAAATGTTTTTATTAGGAGAATCCAGATGCTCA

EcoO109I (2300)
 2301 AGGCCCTTCATAATATCCCCAGTTTAGTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGT
 141▶ • N

2401 TCCTGGTGTACTTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGAT
 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

SacI (2500) BstXI (2529)
 2501 GAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTC
 106 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
 StuI (2664)
 2601 TGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAG
 72 Q 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
 2701 TCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGA
 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
 BbsI (2810) AseI (2872)
 2801 GATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCG
 6 I N F T K M
 SacI (2929)
 2901 TCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTA
 SpeI (3027)
 3001 CGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATC
 SnaBI (3155)
 3101 CACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGTAGCTAATAACGTAGTGTACTGCCAAGTAGGAAAGTCCATAAAGTCATGTA
 NdeI (3260)
 3201 CTGGGCATAATGCCAGGGCGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGAGTTTAC
 3301 CGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGGTCTGTTGGGGC
 PacI (3446)
 PstI (3439) SdaI (3438) BspLU11I (3456)
 3401 GTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGAAAAGGCCAGGAACCGTAAAAAG
 3501 GCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAA
 3601 GATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGT
 ApaLI (3770)
 3701 GCGCTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGC
 3801 TGCGCCTTATCCGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGT
 3901 ATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT
 4001 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGA
 PacI (4186) SmaI (4195)
 4101 TCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTTCATGGCTAGTTAATTAACATTTA
 EagI (4206)
 NotI (4205)
 4201 AATC AGCGGCCGCAATAAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACG
 4301 AAACAAAACAAACTAGCAAAATAGGCTGTCCCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA