



PvuI (7)
SgfI (6)
 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCGCCCTACCTGAGGCC
 301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

SmaI (567)
EcoO109I (567)
 501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACTCTGAGATCACCGGTCAACATGTCGGGACCCGTGCCAAGCAGGGCCAGAGTTTACAC
 1 M S G P V P S R A R V Y T

ScaI (626) **BstBI (686)**
 601 AGATGTTAACACACAGACCCCGAGAGTACTGGGATTATGAATCACATGTGGTGAATGGGGGAATCAAGATGACTATCAGCTTGTTCGAAAATTAGGT
 13 D V N T H R P R E Y W D Y E S H V V E W G N Q D D Y Q L V R K L G
 701 AGGGGCAAATACAGTGAAGTGTTTGAAGCCATCAACATCACAATAATGAAAAAGTTGTTGTTAAAATTCTCAAGCCAGTAAAAAAGAAGAAAATTAAGC
 47 R G K Y S E V F E A I N I T N N E K V V V K I L K P V K K K K I K

Bsp120I (832)
 801 GTGAAATAAAGATTTTGGAGAATTTGAGAGGTGGGCCAACATCATCACACTTGCAGACATTGTAAGACCCCTGTGCACGAACCCCTGCCTTGGTTTT
 80 R E I K I L E N L R G G P N I I T L A D I V K D P V S R T P A L V F
 901 TGAACATGTAACAACACAGACTTCAAGCAATTGTACCAGACGTTAACAGACTATGACATTCGATTTTACATGTATGAAATCTGAAAGCCCTGGATTAT
 113 E H V N N T D F K Q L Y Q T L T D Y D I R F Y M Y E I L K A L D Y

BspHI [m] (1054) **HindIII (1069)**
 1001 TGTACAGCATGGGATTATGCACAGAGATGTGAAACCCATAATGTCATGATTGATCATGAGCACAGAAAGCTTCGGCTAATAGACTGGGGTTAGCTG
 147 C H S M G I M H R D V K P H N V M I D H E H R K L R L I D W G L A
 1101 AGTTTTACCATCCAGGCAAGAGTATAATGTCCGAGTTGCTTCTCGATATTTCAAAGTCCAGAGCTACTTGTAGATTATCAGATGTACGATTATAGTTT
 180 E F Y H P G Q E Y N V R V A S R Y F K G P E L L V D Y Q M Y D Y S L

MscI (1226) **BspEI (1241)**
 1201 GGATATGTGGAGCTTGGGTTGTATGCTGGCCAGTATGATCTTCCGGAAGGAGCCATTTTTCCATGGACATGACAATTATGATCAGTTGGTGAGGATAGCC
 213 D M W S L G C M L A S M I F R K E P F F H G H D N Y D Q L V R I A

EcoRV (1372)
 1301 AAGTTTCTGGGAACAGAAGATTTATATGACTATATTGACAAGTACAACATTGAATTAGATCCACGTTTCAACGATATCTTGGGAGACACTCCCGTAAGC
 247 K V L G T E D L Y D Y I D K Y N I E L D P R F N D I L G R H S R K

StuI (1448) **Bsu36I (1444)**
 1401 GATGGAAACGCTTTGTCCACAGTGAACACCAGCATCTTGTGAGCCCTGAGGCCTTGGATTTTCTGGACAAGCTGCTTCGATATGACCACAGTCACGGCT
 280 R W E R F V H S E N Q H L V S P E A L D F L D K L L R Y D H Q S R L

XmnI (1559)
 1501 CACTGCAAGAGAGCCATGGAGCACCTTACTTCTACTGTTGTGAAGGACAGGCTCGAATGAGTTCCACTAGCATGGCAGGGGGCAGCACACCTGTC
 313 T A R E A M E H P Y F Y T V V K D Q A R M S S T S M A G G S T P V
 1601 AGCAGCGCCAATATGATGTCAGGGATTTCTTCACTGCAACTCCTTCAACCCCTGGACCTCTGGCAGGCTCACCAGTATTGCCGCTGCCAACTCACTTG
 347 S S A N M M S G I S S V P T P S P L G P L A G S P V I A A A N S L

MscI (1769)
PvuII (1712) **NheI (1763)**
 1701 GGATACCTGTTCCAGCTGCTGCTGGCGCTCAGCAGTAATGACCCCATCTACCTTCTGATGCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAT
 380 G I P V P A A A G A Q Q •
 1801 TTGGACAAACCACAAC TAGAATGCAGTGAAGAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAC

EcoRI (1997)
 1901 AGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAA
 2001 TTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGC

SapI (2179)
 2101 CAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGAGTAAAGATATAGTGTATTTCCCAAGTGTGAACTAGCTCTTCACTTCTTATGTTT

SspI (2236) **SwaI (2250)**
 2201 TAAATGCACTGACCTCCACATTCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAAT

EcoO109I (2311)
2301 CCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTT

2401 CTAGCTTTAGTTCCTGGTACTTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCA
141 • N 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

SacI (2511)
2501 TAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGT
109 Y D S I 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

StuI (2675)
2601 CAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTACGACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGAT
76 F D K 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

2701 GATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGA
43 I E G T 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

BbsI (2821)
XmnI (2817) AseI (2883)
2801 TCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAAGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAG
9 D Q Q S I N F T K M

SacI (2940)
2901 CGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGG

SpeI (3038)
3001 CGGAGTTGTTACGACATTTTGGAAAGTCCCCTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTC

SnaBI (3166)
3101 AAACCGCTATCCAGCCCATTTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCAT

NdeI (3271)
3201 AAGTCATGTAAGTGGCATAATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCTCAAGT
3301 GGGCAGTTTACCCTAAACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATATTGACGTCAATGGGGCGGG

PacI (3457)
PstI (3450)
SdaI (3449)
3401 GTCGTTGGGCGGTGACCCAGGCGGGCCATTTACCGTAAGTTATGTAACCGCTGAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGA
3501 ACCGTA AAAAGGCCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCAAAACCCGAC
3601 AGGACTATAAAGATACCAGGCGTTTCCCTGGAAGTCCCTCGTGGCTCTCTGTTCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCT

ApaLI (3781)
3701 TCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCC
3801 AGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG
3901 CAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTGTGCTGAAG
4001 CCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACACCCGCTGGTAGCGGTGTTTTTTTGTGCAAGCAGCAGATTACGCGCA

PacI (4197)
4101 GAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTA

EagI (4217)
SwaI (4206) NotI (4216)
4201 ATTAACATTTAAATCAGCGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATC
4301 AAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCGAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA