



PvuI (7) SgfI (6) MfeI (82) EcoNI (96)
 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) Bsu36I (291)
 Psp1406I (203) PvuII (239) EcoNI (287)
 201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTCGCGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGTTGCTCAACTCTACGTCTTTGTTTCGTTT

BspLU11I (560) PvuI (590)
 AgeI (552)
 501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCAACATGTCGTCCATCTGCCTTTCACTCCCCGATCGTAA
 1 M S S I L P F T P P I V K
 601 CGCCTGCTGGGCTGGAAGAAGGGCGAGCAGAACGGGAGGAGAGAAATGGTGCAGAAAGGGTCAAGAGCCTGGTCAAGAAACTCAAGAAGACGGGG
 13 R L L G W K K G E Q N G Q E E K W C E K A V K S L V K K L K K T G

PvuII (700) DraIII (744)
 701 CAGCTGGACGAGCTGGAGAAGGCCATCACACGAGAAGCTCAACACCAAGTGCATCACCATCCCCAGTCCCTGGATGGCCGGTTGAGGTGTCCCATC
 47 Q L D E L E K A I T T Q N V N T K C I T I P R S L D G R L Q V S H

MscI (841) NcoI (875)
 801 GGAAGGGGCTCCCTCATGTCATCTACTGCCCTGTGGCGATGGCCAGACTGCACAGCCACCACGAGCTGCGGGCCATGGAGCTGTGTGAGTTCGCCTT
 80 R K G L P H V I Y C R L W R W P D L H S H H E L R A M E L C E F A F

Tth11II (913)
 901 CAATATGAAGAAGGACGAGGTCTGCGTGAATCCCTACCACTACCAGAGAGTAGAGACACCAGTCTACCTCCTGTGTTGGTGCACGCCACACAGAGATC
 113 N M K K D E V C V N P Y H Y Q R V E T P V L P P V L V P R H T E I

EagI (1001) SspI (1084)
 1001 CCGCCGAGTTCCCCCACTGGACGACTACAGCATTCCATCCCCGAAAACACTAATTCCTCCGAGGCATCGAGCCCCAGAGCAATATTCAGAGACCC
 147 P A E F P P L D D Y S H S I P E N T N F P A G I E P Q S N I P E T
 1101 CACCCCTGGCTACTGAGTGAAGATGGAGAAACAGTACCACAGATGAACCACAGCATGGACGCAGGTTCTCAAACCTATCCCCGAATCCGATGTC
 180 P P P G Y L S E D G E T S D H Q M N H S M D A G S P N L S P N P M S

PstI (1222) NgoMIV (1245)
 1201 CCCAGCACATAATAAATTGGACCTGCAGCCAGTTACCTACTGCGAGCCGCTTCTGGTGTCCATCTCTACTACGAGCTGAACCAGCGCGTCGGGGAG
 213 P A H N N L D L Q P V T Y C E P A F W C S I S Y Y E L N Q R V G E

AvrII (1371)
 1301 ACATTCCACGCTCGCAGCCATCCATGACTGTGGATGGCTTACCAGCCCTCCAATTCGGAGCGCTTCTGCCTAGGGCTGCTCCTCAATGTCAACAGGA
 247 T F H A S Q P S M T V D G F T D P S N S E R F C L G L L S N V N R
 1401 ATGCAGCAGTGGAGCTGACACGGAGACACATCGGAAGAGGGCTGCGGCTCTACTACATCGGAGGGGAGTCTTCGAGAGTGCCTCAGTGACAGCGCTAT
 280 N A A V E L T R R H I G R G V R L Y Y I G G E V F A E C L S D S A I

BglIII (1583) XmnI (1581)
 1501 TTTTGTCCAGTCTCCCAACTGTAACCAGCGCTATGGCTGGCACCCGGCCACCGTCTGCAAGATCCACCAGGATGCAACCTGAAGATCTTCAACAACCG
 313 F V Q S P N C N Q R Y G W H P A T V C K I P P G C N L K I F N N Q

ApaLI (1668)
 1601 GAGTTCGCTGCCCTCCTGGCCAGTCGGTCAACCAGGGCTTTGAGGCTGTCTACCAGTTGACCCGAATGTGCACCATCCGCATGAGCTTCGTCAAAGGCT
 347 E F A A L L A Q S V N Q G F E A V Y Q L T R M C T I R M S F V K G

BsrBI (1703) Tth11II (1783)
 1701 GGGGAGCGGAGTACAGGAGACAGACTGTGACCACTACCCCTGCTGGATTGAGCTGCACCTGAATGGGCTTTGAGTGGCTTGAACAAGGTCCTACCCA
 380 W G A E Y R R Q T V T S T P C W I E L H L N G P L Q W L D K V L T Q

MscI (1870) NheI (1864)
 1801 GATGGGCTCCCCAAGCATCCGCTGTTCCAGTGTGCTTATAGAGACATCAAGTATGGTAGGGGAGGGCTAGCTGGCCAGACATGATAAGATACATTGATGAG
 413 M G S P S I R C S S V S •

1901 TTTGGACAAACCACAAGTGAATGACAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAC

HpaI (2002) MfeI (2013) EcoRI (2098)
 2001 AAGTTAACAAACAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGA
 2101 ATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTG

SapI (2280)
 2201 CCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATAGTGTATTTTCCAAGTTTGAAGTACTCTTCAATTTCTTTATGTT

SspI (2337) SmaI (2351)
 2301 TTAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAA
 2401 TCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAATAGAAATTGGACAGCAAGAAAGCGAGCT
 2501 TCTAGCTTTAGTTCCTGGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTCGCAATTCATCTCAATGAGCACAAAGCAGTCAGGAGC
 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 (2612)
 2601 ATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTG
 110 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

StuI (2776)
 2701 TCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGA
 76 D 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

2801 TGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTGCTTGTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAG
 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

XmnI (2918) AseI (2984)
 2901 ATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGTGCTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACA
 10 D Q Q S I N F T K M

SacI (3041)
 3001 GCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGG

SpeI (3139)
 3101 GCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGT

SnaBI (3267)
 3201 CAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCA

NdeI (3372)
 3301 TAAGGTCATGTACTGGGCATAATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAG
 3401 TGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGG

PacI (3558) PstI (3551) SdaI (3550) BspLU11I (3568)
 3501 GGTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGG
 3601 AACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGA
 3701 CAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCC

ApaLI (3882)
 3801 TTCGGAAGCGTGGCGCTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGCTT
 3901 CAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTA
 4001 GCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAA
 4101 GCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTGCAAGCAGCAGATTACGGCG

PacI (4298)
 4201 AGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTT

EagI (4318) SwaI (4307) NotI (4317)
 4301 AATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACATAACGCTCTCCAT
 4401 CAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTCAAGTGCAGGTGCCAGAACATTTCTATCGAA