



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) 501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCCATGGAGCCACGCTTGCTGATGTTGGGTTTCTCTCATT
NcoI (560) 1 M E P R L L M L G F L S L
601 AACCATAGTACCCAGTTGTGGGAGAACTGTGTCTGTATGACCCACCGAGGTCCCAATGCCACATTCAAAGCCCTCTCTACAAGAACGGCACCATC
13 T I V P S C R A E L C L Y D P P E V P N A T F K A L S Y K N G T I

BbsI (728) 701 CTAAACTGTGAATGCAAGAGAGGTTTCCGAAGACTAAAGGAATGGTCTATATGCGTTGCTTAGGAACTCCTGGAGCAGCACTGCCAGTGCACCAGCA
BstAPI (776) 47 L N C E C K R G F R R L K E L V Y M R C L G N S W S S N C Q C T S
ApaLI (789) 801 ACTCCCATGACAAATCGAGAAAGCAAGTTACAGCTCAACTTGAACACCAGAAAAGAGCAACAAACCACACAGACATGCAGAAGCCAACACAGTCTATGCA
80 N S H D K S R K Q V T A Q L E H Q K E Q Q T T T D M Q K P T Q S M H

PstI (921) 901 CCAAGAGAACCTTACAGGTCAGTGCAGGGAGCCACCTCCTTGAAACATGAAGATTCCAAGAGAATCTATCATTTCGTGGAAGGACAGAGTGTCACTAC
BstXI (931) 113 Q E N L T G H C R E P P P W K H E D S K R I Y H F V E G Q S V H Y

BspLU11I (1096) 1001 GAGTGTATTCCGGGATACAAGGCTCTACAGAGAGGTCCTGCTATTAGCATCTGCAAGATGAAGTGTGGGAAAACGGGGTGGACTCAGCCCCAGCTCACAT
147 E C I P G Y K A L Q R G P A I S I C K M K C G K T G W T Q P Q L T

XmnI (1157) 1101 GTGTAGATGAAAGAGAACCACCGATTCTGGCTAGTGAGGAATCTCAAGGAAGCAGAAATCTTCTCCCGAGAGTGAAGTTCCTGCCCCATAACCAC
180 C V D E R E H H R F L A S E E S Q G S R N S S P E S E T S C P I T T

PvuII (1281) 1201 CACAGACTTCCACAACCACAGAAACAACTGCAATGACGGAGACATTTGTGCTTACAATGGAGTATAAGGTAGCAGTGGCCAGCTGCCTCTTCTGCTC
MscI (1277) 213 T D F P Q P T E T T A M T E T F V L T M E Y K V A V A S C L F L L

MscI (1397) 1301 ATCAGCATCTCCTCCTGAGCGGGCTCACCTGGCAACACAGATGGAGGAGAGCAGAAGAACCATCTAGCAAGCTAGAAAAGTCAGAGCCCCGTAGCTGG
BsrBI (1317) 247 I S I L L L S G L T W Q H R W R K S R R T I •
SapI (1347) 1401 CCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTAT

HpaI (1529) 1501 TTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAA
MfeI (1540)

EcoRI (1625) 1601 GTAAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTGAATCCTTTTCTGAGGGATGA
1701 ATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCTCACCTTCTTCATGGAGTTAAGATATAGTGATTTTCCCAAGTT

SapI (1807) 1801 TGAAGTACTCTTCATTTCTTTATGTTTTAAATGACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATG
SspI (1864) 1901 AAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAAT
Swal (1878) 2001 AGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTACAT

SacI (2139) 2101 CTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCACCTCATCAGAG
119 E I L V F C D P A Y D S I L E R C M G C P S V R I S R D V E D S
BstXI (2168) 2201 TAGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCCGTTGCTCAGCAGACCCAAATGGCAATGGCTTCAGCACAGACAGTGACCTGCCAA
85 Y P H R V A V I T 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

StuI (2303) 2301 TGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCAGCTTGGTCTGATGGCCGCCCGACATGGTGTCTGTTGCTCATAGAGCATGGTGTCTT
52 Y A E I H V A S I I E G T K T R I A A G V H H K N D E Y L M T I K

BbsI (2449)
XmnI (2445)

2401 CTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATA
19 E T A V E V L E L D Q Q S I N F T K M ←

AseI (2511) SacI (2568)

2501 CTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCCACCGTACA
←

SpeI (2666)

2601 CGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGICAAAACAAACTCCCATTGACGTCAATGG
←

SnaBI (2794)

2701 GGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTA
←

NdeI (2899)

2801 GATGTACTGCCAAGTAGGAAAGTCCCATAAAGTCACTGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGC
←

2901 ATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACAT
←

PacI (3085)
PstI (3078)
SdaI (3077) BspLU11I (3095)

3001 ACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATG
←

3101 TGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGAC
←

3201 GCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCTTTCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCCGCT
←

3301 TACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAG
←

ApaLI (3409)

3401 CTGGGCTGTGTGCACGAACCCCGTTCAGCCCAGCCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATGCCAC
←

3501 TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAC
←

3601 AGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTT
←

3701 TTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACTCAC
←

EagI (3845)
PacI (3825) SwaI (3834) NotI (3844)

3801 GTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGTG
←

3901 GAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAAGTGCCAGGAGCCAGAACATTTCC
←

4001 TCTATCGAA